### ST,C-Biotech/ChemLib

84786

From: Sent:	
To: Subject:	

Chan, Christina

Tuesday, January 21, 2003 12:07 PM Davis, Minh-Tam; STIC-Biotech/ChemLib RE: Rush search request for 09/767215

### Please rush. Thanks Chris

Chris Chan ,TC 1600 New Hire Training Coordinator and SPE 1644 308-3973 CM-1, 9B19

> ----Original Message-----From: Davis, Minh-Tam

Sent: Tuesday, January 21, 2003 11:58 AM

To: Chan, Christina

Subject: Rush search request for 09/767215

Please search in commercial database and in issued patent files:

1) Oligomer search for SEQ ID NO:2.

2) Amino acids 10-116, 126-420, 568-660, 676-745, 826-1004 of SEQ ID NO:2.

Thank you.

MINH TAM DAVIS

ART UNIT 1642, ROOM 8A01, MB 8E12

305-2008

Edward Hart Technicai Info. Specialist STIC/Biotech CMI 6B02 Tel: 305-9203 fol nothig Heat is even 25 aa as pui art

2/2000

Searcher:
Phone:
Location:
Date Picked Up:
Date Completed:
Searcher Prep/Rev/ew:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

/ENDOR/COST (w	here applic.)
STN:	
DIALOG:	
Questel/Orbit:	
DRLink:	
Lexis/Nexis:	
Sequence Sys.:	DY.
WWW/Internet:_	
Other (specify):_	

HIS PAGE BLANK (USPTO)

```
January 22, 2003, 08:53:00 ; Search time 43 Seconds (without alignments) 3111.247 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1004
1 MGELCRRDSALTALDEETLW.......VRQAIADEQKKVVWTEQSPR 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*/SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1983.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1984.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1986.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1986.DAT:*/SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1986.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990.DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS2/gcgdata/geneseq/genesegp-embl/AA2000.DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SIDS2/gcgdata/geneseg/genesegp-embl/AA1991.
/SIDS2/gcgdata/geneseg/genesegp-embl/AA1992.
/SIDS2/gcgdata/geneseg/genesegp-embl/AA1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS2/gcgdata/geneseq/genesegp-emb1/AA1998
/SIDS2/gcgdata/geneseq/genesegp-emb1/AA1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS2/gcgdata/geneseq/genesegp-embl/AA1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS2/gcgdata/geneseq/genesegp-embl/AA1980.
/SIDS2/gcgdata/geneseq/genesegp-embl/AA1981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     908470
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             908470 segs, 133250620 residues
                                                                                                                                                                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A_Geneseq_101002:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-767-215-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Human caspase recr	Human predicted ca	Human EST encoded	Human prostate tum	Formaldehyde senso	Novel human secret	Membrane antiqen p	Peptide #4509 enco	Protein #4316 enco	Human brain expres
SUMMARIES			ar	AAE07164		AAM24402	AAY73852	AAB82496	AAU30127	AAR51227	ABB37003	ABB22317	AAM57730
			DB ::	22	22	22	20	22	22	15	22	22	22
			Score Match Length DB I	1004	1139	148	229	390	1139	334	348	348	348
	æ	Query	Match	100.0	34.2	1.0	1.0	1.0	1.0	6.0	6.0	6.0	6.0
			Score	1004	343	10	10	10	10	6	9	6	6
		Result	No.	1	7	æ	4	5	9	7	80	σ	10

/note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"

10..116 /label= CARD\_domain

Modified-site Modified-site Modified-site

Domain

Location/Qualifiers 6..9

Key Modified-site

Homo sapiens.

18..21 /note= "Casein kinase II phosphorylation site" 25..27 /note= "Protein kinase C phosphorylation site"

12.15 /note= "Casein kinase II phosphorylation site"

	11	o (		<u> </u>	348	22		one mar
	12	י ע			24.0	77		#4400v
	13	ית			348	77		Peptide #4518 enco
	14	א עב		~ .	348	7.5		le #4292
	15	ית			348	53		peptide
	16	ۍ د د		<b>.</b>	599	22		secreted
	17	o 0			n,	22		Human protein segu
	18	ת			1147	7.7		uman caspase recr
	19	σ,			_	22		Drosophila melanog
	20	<b>x</b> (		~ .	т б	21		RCA1-associated R
	21	<b>20</b> 0		~ ~	20 0	77		RCA1-associated R
	77	<b>10</b> C		~ ~	4. C	77		KCAI-associated K
	57	<b>20</b> C		<b>n</b> c	10	77		uman Okra Okrabb
	4 7	<b>20</b> c		n 1	α α τ	7 .		uman okra protein
	0.0	oα		<b>n</b> 1	907	20		. pneumoniae prot
	070	<b>20</b> C		n 1	100	1,5	<i>.</i>	S. pneumoniae LSSA
	7 0	<b>0</b> 0		2	130	7.7	€ •	rabidopsis thalla
	9 0	ם מ		n 1	140	7 7		Arabidopsis thalla
	200	pα		<b>n</b> (	144	7 7		ropionipacterium
	30	<b>20</b> 0		n c	44.7	77		rabidopsis thalla
	31	<b>.</b>		n ,	100	T.7		rabidopsis thalla
	32	ω,		m .	170	23		taphylococcus aur
	33	æ		m	197	21		rabidopsis thalia
	34	æ		<u>~</u>	250	21		rabidopsis thalia
	35	<b>&amp;</b>		<u>~</u>	274	21		rabidopsis thalia
	36	80		<u>~</u>	274	22		ovel human diagno
	37	8		m	291	21		rabidopsis thalia
	38	. 00			315	21		Arabidopsis thalia
	39	· œ			321	21		Arabidopsis thalia
	40	ο α		. ~	321	21		ď
	41	α		. ~	322	2.5		٠,
	42	οα		. ~	3 6	15		U
	4.3	000			342	1.5		) U
	4.0	οα		. ~	2 7 8	4 5		ic thali
	45	ω ω	~	- ∞	416	21	AAG13047 A.	dopsis
							ALIGNMENTS	
í								
RESULT	RESULT I							
3 4	0/104 AAF07164		4		standard. Drotein.		1004	
×			5	;				
AC	AAE07164							
×								
TO	06-NOV-2001	100	(F	irst	(first entry)	2		
×	1							
ς Ε	Human caspase	spase		scru	recruıtment		domain-14 (CAKD-14).	
4 2 2		0		5		÷		, 77
X N	Human; C	caspase.	ם י	Gecr	utciller P	יין ביי מייי	♥	
¥ 3	nuclear ractor-kappa B; NF-KB; Cell	racte	Ä .	cor-kappa	D .	Y F - K	B; cell growth; cell death; cancer;	nerapy;
K Z	Alabaimer's	יות מיוי	0 0	Tana		T I I I	Systemic lupus elytmematosus; meulologicai o Darkinson's dispass: inflammatoru disordor:	togical disorder;
KK	hapmatological	בייהסי	- 1	של ה מיי	, rai.	0.00	On a disease, initianumacoly d	anaellia
X	atroke:	enimmi.	1 0	310	rder	ָלְינ <u>ָ</u>	rodyspiesere symme, myocardie hn's dispass, slibraic rhinitis.	
KW	cell signalling	rnalli	b d	disc	order	5 5	ling disorder; cytostatic; immunosuppressive;	noot
ΚW	neuroprotective;	tecti	V.	an,	antiviral	31;	antibacterial.	
×	CaCh	2						

```
Note= "Leucine zipper pattern"
//note= "Leucine zipper pattern"
449..452
//note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .466
e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                            .262
e- "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .283
e- "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300
.e- "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309
e= "Protein Kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .310
e- "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .368
.e= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .369
.e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .381
te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .386
.e= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..465
te- "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .472
e= "Protein Kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .504
e- "Casein kinase II phosphorylation site"
                                                                                                                                                                                             ..137
:e- "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                          note= "Tyrosine Aimac".
21..224
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                        .252
e- "Protein kinase C phosphorylation site"
                                                                                                          .123
.e= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                 .
e- "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                              .243
.e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .365
e- "Tyrosine kinase phosphorylation site"
60..62
/note= "Protein kinase C phosphorylation site"
91..93
                                     note- "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                             . 227
ce- "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                  .256
.e- "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              587..592
/note= "N-myristoylation site"
589..592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .516
e= "N-myristoylation site"
                                                                                                                                                                               "N-myristoylation site"
                                                                                                                                                                                                                                       "N-myristoylation site"
                                                                                             note= "N-myristoylation site"
                                                  label= Coiled_Coil_domain
                                                                                                                                                                                                                                                                                                                                                  label- k-Box_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note-
                                                                                                                                                                               'note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
 Modified-site
                           Modified-site
                                                     Modified-site
                                                                                 Modified-site
                                                                                                           Modified-site
                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                     Domain
```

/note= "Protein kinase C phosphorylation side 760..763
/note= "cAMP- and cGMP-dependent protein kinase phosphorylation site" rnote= "Protein Kinass . . 725..728 7note= "Casein Kinase II phosphorylation site" note= "N-glycusyturic... 59..761 /note= "Protein kinase C phosphorylation site" .844 e= "Protein kinase C phosphorylation site" .863 e= "Casein kinase II phosphorylation site" site" /note= "N-myristoylation site" 1002..1004 /note= "Protein kinase C phosphorylation site" Note= "Protein kinase c pucchases 74.677 74.677 /note= "Casein kinase II phosphorylation site" "Casein kinase II phosphorylation site" site" "Casein kinase II phosphorylation site" ..727 te= "Protein kinase C phosphorylation site" .637 | e= "Casein kinase II phosphorylation site" 653..655 /note= "Protein kinase C phosphorylation site" An isolated caspase recruitment domain polypeptide useful for "Casein kinase II phosphorylation site" note= "Caseln Almer.]
168.870
Anote= "Protein kinase C phosphorylation" fiote= "Casein Ainer. 326..929 /note= "Casein kinase II phosphorylation 896 e= "Casein kinase II phosphorylation ..979 te= "Casein kinase II phosphorylation /note= "Peroxisomal targetting signal" 196..799 ..949 Le= "Peroxisomal targetting signal" 872 .e= "RGD cell attachment sequence" label = Guanylate\_kinase\_domain note= "Casein kinase II phospr 33. 738 'note= "N-myristoylation site" 'note= "Caseıu .... 300..805 ^^^te= "N-myristoylation site" "N-myristoylation site" /note= "N-glycosylation site" 602..605 'label- SH3\_domain (MILL-) MILLENNIUM PHARM INC. 22-JAN-2001; 2001WO-US02087. 09-FEB-2000; 2000US-0181159 JO. /note= .1004 344..947 ..740 745 note= 'note= WPI; 2001-497073/54 N-PSDB; AAD13447. WO200159065-A2 Modified-site Andified-site Modified-site Modified-site Modified-site Addified-site 16-AUG-2001 Bertin J; Peptide Peptide Domain Region Domain

```
ö
                                                                                                 The present sequence is human caspase recruitment domain-14 (CARD-14). The CARD-14 gene is located on chromosome 17. The CARD-14 is used for the detection of modulators that modulates the ability of CARD-14 to bind to Bci-10 and stimulates phosphorylation of Bci-10 or activation of nuclear factor-kappa B (NF-kB). The CARD-14 is useful for regulating growth and cell death and useful for the treatment of cancer. It is also useful for the treatment of autoimmune disorders (e.g., systemic lupus erythematosus), neurological disorders e.g., Alzheimer's and Parkinson's disease, inflammatory disorders, haematological disorders etc., a naemia, myelodysplastic syndromes), myocardial infarctions, strokes, immune disorders (e.g., Crohn's disease, allergic rhinitis), cell signalling disorders and certain viral and bacterial infections.
regulating growth and cell death and useful for the treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PRLTNSAMRAGHLLDLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFSNFSGLME 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSKLTECLAGAIGSLQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MGELCRRDSALTALDEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGELCRRDSALTALDEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KREVSAHFHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1004; 100.0%; Pred. No. 0;
                                                             Claim 1; Fig 1A-1E; 109pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 100.
Matches 1004; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  1004 AA;
                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  οŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

09-FEB-2000; Homo sapiens 16-AUG-2001 Bertin J; 480 420 540 009 099 VNSYTMKDTAAHGTIPNYSRAQQQLIALIQDMTQQCTVTRKPSSGGPQKLVRIVSMDKAK 780 YKRLLQDLEAKVATSGDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHAHR 720 SCELELQEQSLRTASDQESGDEELNRLKEENEKLRSLTFSLAEKDILEQSLDEARGSRQE **LVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKE** YKRLLQDLEAKVATSGDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHAHR QQSLYKRVAEDFGEEPWSFSSCLEIPEGDPGALPGAKAGDPHLDYELLDTADLPQLESSL QPVSPGRLDVSESGVLMRRRPARRILSQVTMLAFQGDALLEQISVIGGNLTGIFIHRVTP REPCPREKQRLVRMHAICPRDDSDCSLVSSTESQLLSDLSATSSRELVDSFRSSSPAPPS GSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTDG RDQAYSARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLRQLQAEPPGVLKQEART 241 199 721 301 301 361 361 421 421 481 481 541 541 601 601 199

ò

g

δ

00 Oy 00 OO

δ

```
Human; caspase recruitment domain-14; CARD-14; chromosome 17; nuclear factor-Kappa B: NE-kB; cell growth; cell death; cancer; therapy; autoimmune disorder; systemic lupus erythematosus; neurological disorder; Alzheimer's disease; Parkinson's disease; inflammatory disorder; anaemia haematological disorder; myelodysplastic syndrome; myocardial infarction; stroke; immune disorder; Crohn's disease; allergic rhinitis; infection; cell signalling disorder; cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is predicted human caspase recruitment domain-14 (CARD-14). The CARD-14 gene is located on chromosome 17. The CARD-14 is used for the detection of modulators that modulates the ability of CARD-14 to bind to Bel-10 and stimulates phosphorylation of Bel-10 or activation of nuclear factor-kappa B (Nr-kB). The CARD-14 is useful for regulating growth and cell death and useful for the treatment of cancer. It is also useful for the treatment of autoimmune disorders (e.g.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              An isolated caspase recruitment domain polypeptide useful for regulating growth and cell death and useful for the treatment of cancer
LSEKLCLLQGFKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTH
                                                                                                                             LSEKLCLLQGFKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTH
                                                                                                                                                                                         ALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRLGTSEEQLLEAARQEEGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                 predicted caspase recruitment domain-14 (CARD-14).
                                                                                                                                                                                                                                                        DRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTEQSPR 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Encoded by TGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 2A-2C; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                    AAE07165 standard; Protein; 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JAN-2001; 2001WO-US02087
                                                                                                                                                                                                                                                                                                                                                                                                                  06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-497073/54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAD13448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200159065-A2
                                                                                                                                                                                                                                                                                                                                                                                    AAE07165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human
                                                                                                           841
                                                                                                                                                                                                                                                                     961
                721
                                                                            781
                                                                                                                                          841
                                                                                                                                                                        901
                                                                                                                                                                                                      901
                                                                                                                                                                                                                                       961
                                              781
                                                                                                                                                                                                                                                                                                                     RESULT 2
                                                                                                                                                                                                                                                                                                                                     AAE07165
                                                                            a
                                                                                                                                       Q
                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                   Op
                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                         δ
                                                                                                                                                                        ò
```

```
(HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                              treatment.
                                                                                                                                                                                         Sednence
                                                                                                                                                                                                                                                                                                                    AAY73852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteins
                                                                                                                                                                                                                                                                                           AAY73852
ID AAY7
                                                                                                                                                                                                                                                                                   RESULT 4
                                                                                                                                                                                                                                                                                                             QQ
                                                                                                                                                                                                                                          δλ
 ó:
systemic lupus erythematosus), neurological disorders e.g., Alzheimer's and Parkinson's disease, inflammatory disorders, haematological disorders (e.g., ameamia, myelodysplastic syndromes), myocardial infarctions, strokes, immune disorders (e.g., Crohn's disease, allergic rhinitis), cell signalling disorders and certain viral and bacterial infections.
                                                                                                                                                                                                                                                                                                                      KCLAEYLSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCT 912
                                                                                                                                                                                                                                                                                    792
                                                                                                                                                                                                                 LDPSRMEGSSTCFWAESCLTLVPYTLVWPHRPARPRPVLLVPRAVGKILSEKLCLLQGFK 852
                                                                                                                 ATSGDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAH 732
                                                                                                                                                                                 TQIVMVDYEASEPLFKAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTDGYKRLLQDLEAKV 672
                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
                                                                                                                                                                                                                                                                                                             LHRMDIFPIVIHVSVNEKMAKKLKKGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSSLAP
                                                                                                     SGVLMRRRPARRILSQVTMLAFQGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPG
                                                                                                                                                GTIPNYSRAQQQLIALIQDMTQQCTVTRKPSSGGPQKLVRIVSMDKAKASPLRLSFDRGQ
                                                                                     ;
0
                                                                      Length 1139;
                                                                                      1; Indels
                                                                     DB 22;
                                                                      Score 343; DB Pred. No. 0; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human EST encoded protein SEQ ID NO: 1927.
                                                                                                                                                                                                                                                                                                                                                                                                          Ā
                                                                                                                                                                                                                                                                                                                                                         1023 DGWSDLDGLLSCVRQAIADEQKKV 1046
                                                                                                                                                                                                                                                                                                                                               DGWSDLDGLLSCVRQAIADEQKKV 996
                                                                                                                                                                                                                                                                                                                                                                                                         AAM24402 standard; Protein; 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0491404.
2000US-0617746.
2000US-0631451.
2000US-0663870.
                                                                      Match 34.2%;
Local Similarity 99.8%;
les 443; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JAN-2001; 2001WO-US02687
                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                      1139 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200154477-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-2000;
17-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-AUG-2000;
15-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                          12-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                          AAM24402
                                                      Sequence
                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                973
                                                                                                        553
                                                                                                                                                                                          723
                                                                                                                                                                                                           733
                                                                                                                                                                                                                           783
                                                                                                                                                                                                                                                            843
                                                                                                                                                                                                                                                                              853
                                                                                                                                         613
                                                                                                                                                                         673
                                                                                                                                                                                                                                            793
                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                          qq
                                                                                                                                                                                                           ò
                                                                                                                                                                                                                          Q
                                                                                                                                                                                                                                            ò
    8
                                                                                                         δ
                                                                                                                        g
                                                                                                                                         ò
                                                                                                                                                      a
                                                                                                                                                                         Ôχ
```

```
The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, blochesics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes novel polypeptides and their encoding nucleic acids derived from human pancreatic tumor tissue which have cytostatic activity. The sequences are also useful in producing pharmaceutical compositions for treatment of pancreatic tumors. AAY73814-Y74252 represent protein fragments encoded by the human pancreatic tumor CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human nucleic acid sequences from pancreatic tumors, and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                             Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dahl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pancreas; tumor; EST; expressed sequence tag; human; cytostatic;
  ;
`
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΰ
Asundi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pilarsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22; Length 148; 0.44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human prostate tumor EST fragment derived protein #39.
  Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schmitt A,
     2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Preu ...
       Wang
  Tang YT, Liu C, Zhou P, Qian XB, Wang
Cao Y, Drmanac RA, Zhang J, Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.0%; Score 10;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (META-) METAGEN GES GENOMFORSCHUNG MBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B,
                                                                                                                                                                                                                           Claim 20; Page $236; 1275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY73852 standard; Protein; 229 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 23; Page 325; 502pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hinzmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98DE-1020190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98DE-1020190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Specht T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-621386/54.
N-PSDB; AAZ52870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           823 RPARPRPVLL 832
                                                                              WPI; 2001-476164/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 AA;
                                                                                                        N-PSDB; AAH99061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DE19820190-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosenthal A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAR-2000
```

ö

us-09-767-215-2.rag

SSXS

g

ò

```
AAU30127
0000×0
                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                             ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oxidation of formaldehyde in a sample by adding a particular bacterial cell and detecting the decrease in formaldehyde
library derived expressed sequence tag (EST) sequences represented in AAZ52858-253014.
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oxidizing formaldehyde in a sample involves: (1) providing R. sphaeroides cells that comprise a glutathione-dependent formaldehyde dehydrogenase (GSH-FDH) gene, especially the R. formaldehyde adhl gene (SGH-FDH) gene, especially the R. linked to the GSH-FDH gene, a cis-acting operator, at least 1 protecten that senses formaldehyde (especially GGRs and GfGH), and a protectin that senses formaldehyde (especially GGRs and GfGH), and a protectin that senses formaldehyde (especially GGRs) that modulates trans-acting requiatory protein (especially GGRs) that modulates formaldehyde sensor protein(s), such that the promoter and operator together specifically direct transcription of the GSH-FDH gene in response to a signal from the formaldehyde sensor protein(s), such that the promoter and operator together specifically direct transcription of the GSH-FDH gene when the cell is exposed to formaldehyde; (2) adding the bacterial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gfdr encoded by an open reading from of the formaldehyde-inducible regulatory system (see AAF90616) of Rhodobacter sphaeroides. Hydropathy analysis of the sequence suggests Gfdr to be a transmembrane protein. A second open reading frame encodes Gfds (see AAB82497), a putative soluble protein. By analogy to other systems, it is thought that a His residue near the C-terminal end of Gfds may be dephosphorylated when formaldehyde binds to Gfdr. In the absence of formaldehyde, the phosphate on Gfds may be transferred to an Asp residue of the repressor GfdR (see AAB82495). These proteins are utilised in methods of the invention for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of the formaldehyde sensor protein
                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detecting and remediating formaldehyde. A claimed method for
                                                                                               Length 229;
                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repressor; sensor; GfdT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection; biosensor; bioremediation; pollutant.
                                                                                          Score 10; DB 20;
Pred. No. 0.65;
                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Column 31-34; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (WISC ) WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                                                                                                                                                                                  AAB82496 standard; Protein; 390 AA.
                                                                                               1.00,0%; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                       Formaldehyde sensor protein GfdT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0192983.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Formaldehyde dehydrogenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0608241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0919953
                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                 Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhodobacter sphaeroides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Donohue T, Barber R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-380473/40.
N-PSDB; AAF90616.
                                                                                                                                                                         823 RPARPRPVLL 832
                                                                                                                                                                                                111111111
77 RPARPRPVLL 86
                                                       229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6242244-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                05-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUN-2001
                                                                                                                                                                                                                                                                                                                                                         AAB82496;
                                                         Sequence
                                                                                               Query Match
                                                                                                                                                                                                                                                                            RESULT 5
                                                                                                                                                                                                                                                                                             AAB82496
```

```
.;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding a range of human polypeptides, useful in genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically the nucleic are useful for useful for producing the proteins.
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration;
to the sample; and (3) detecting a decrease in formaldehyde in the sample. A biosensor and bioremediation system for environmental
                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1139;
                                                                                                                                                                                                  22; Length 390;
                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.0%; Score 10; DB 22; 100.0%; Pred. No. 2.8;
                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                              Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU30127 standard; Protein; 1139 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; Page 247; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccination, testing and therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human secreted protein #618.
                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                             100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-APR-2001; 2001WO-US08656.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-APR-2000; 2000US-0552929.
26-JAN-2001; 2001US-0770160.
                                                                    formaldehyde are obtained.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-DEC-2001 (first entry)
                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-611725/70.
                                                                                                                                                                                                                                                                                                                                308 LRERAVABER 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1139 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                    390 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200179449-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU30127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
```

RESULT 7 AAR51227

à g

```
Protein #4316 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \operatorname{Human} genome-derived single exon nucleic acid probes useful for analyzing gene expression in \operatorname{human} fetal liver .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        claim 27; SEQ ID NO 29638; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 9;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                       Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB22317 standard; Protein; 348 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.9%; Scc.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
                                                                                                                                                                                        2000US-0207456
2000US-0608408
2000US-0632366
2000US-0234687
2000US-0234687
2000US-024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-2001; 2001WO-US00666
                                                                                                                     30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-483447/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
tes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   348 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLKEENEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200157274-A2
                    WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2000; 26-MAY-2000; 20-JUN-2000; 03-AUG-2000;
                                                                                                                                                                                             26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                  21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001
                                                                     09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB22317;
                                                                                                                                                                                                                                                                                                                                                                                                                       Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB22317
QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TO NOT THE PER NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR51227 showes the antigen peptide for a monoclonal antibody having immobility action of human sperm and inhibitory action of fertilisation. It is useful for a contraception vaccine and for the
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1..335
/label- membrane antigen peptide of human sperm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide #4509 encoded by human foetal liver single exon probe
                                                                                                                                                                                                                                                                                                                                                                                                                       Membrane antigen peptide; human sperm; contraceptive vaccine; diagnosis of infertility; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.9%; Score 9; DB 15; Length 334; 100.0%; Pred. No. 8.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Membrane antigen peptide of human sperm and its coding -
a contraceptive vaccine and for diagnosis of infertility
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                         Membrane antigen peptide of human sperm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB37003 standard; Peptide; 348 AA.
                                                                                                                                                                                                                       AAR51227 standard; Protein; 334 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 8-9; 10pp; Japanese.
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92JP-0228449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92JP-0228449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis of fertilisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 9; Conservative
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1994-128676/16.
N-PSDB; AAQ45175.
                                                                            PDVDFSNFSG 117
                                                PDVDFSNFSG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266 RLKEENEKL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ISOJ/) ISOJIMA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                334 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP06070775-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-AUG-1992;
                                                                                                                                                                                                                                                                                                                        23-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAR-1994
  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB37003;
                                                                                                                                                                                                                                                                          AAR51227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
     Matches
                                                108
                                                                                                 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB37003
```

g

ò

; 0

Gaps

.; 0

STATE OF STA

```
WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                      microarray;
                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001
                                                                                                                                                                                                                                                                                                 AAM70143;
                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Penn SG,
                                                                                                                                                                     Query Match
                     Single
                                                                                                                                                                                                                                                                                                                                                            Human;
                             brains
                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                            RESULT 11
                                                                                                                                                                                                                                                                     AAM70143
  δy
                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                       ;
                                                                                                                                             The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human brain expressed single exon probe encoded protein SEQ ID NO: 29835
                                                                                               Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                Length 348;
                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                Score 9; DB 22;
Pred. No. 9.1;
                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                            Claim 15; SEQ ID No 24087; 530pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rank DR;
                                                          Rank DR;
                                                                                                                                                                                                                                                                                                  Score 9;
                                                                                                                                                                                                                                                                                                                                                                                                          AAM57730 standard; Protein; 348 AA
                                                                                                                                                                                                                                                                                                0.9%;
100.0%; Piv
                                       (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC
                                                          Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK, Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
21-SEP-2000; 2000US-0234687. 27-SEP-2000; 2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0180312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001; 2001WO-US00667
                   2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                     Conservative
                                                         Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
9, Conserve
                                                                           WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                       266 RLKEENEKL 274
                                                                                                                                                                                                                                                                                                                                                          224 RIKEENEKL 232
                                                                                                                                                                                                                                                                               348 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200157275-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                   04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo saptens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn SG,
                                                                                                                                                                                                                                                                                Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                             AAM57730;
                                                                                                           hearts
                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                         q
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bonce marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimmer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                             The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bone marrow expressed exon; gene expression analysis; probe; rray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human bone marrow expressed probe encoded protein SEQ ID NO: 30449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for
                                                                                   Example 4; SEQ ID NO: 29835; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; SEQ ID NO: 30449; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Prea. ...
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 9; I
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen W, Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM70143 standard; Protein; 348 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111111111
224 RLKEENEKL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266 RLKEENEKL 274
                                                                                                                                                                                                                                                                                                                                                                                                348 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200157276-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-AUG-2000; 2
21-SEP-2000; 2
27-SEP-2000; 2
```

Š

g

ò

```
Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                     Peptide #4518 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide #4292 encoded by probe for measuring breast gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                    Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            analyzing gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.9%; Score 9; 1
100.0%; Pred. No.
ive 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM05610 standard; Protein; 348 AA.
                                                AAM30481 standard; Protein; 348 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 27; SEQ ID No 30750; 654pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                            26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen W,
                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US00663.
                                                                                                                                                                                                                                                                                                                                                                                2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11111111
224 RLKEENEKL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266 RLKEENEKL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    348 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanzel
                                                                                                                                                                                                                                                                           40200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-OCT-2001
                                                                                                                   17-OCT-2001
                                                                                                                                                                                                                                                                                                           09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                  AAM30481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM05610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
AAM05610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                  AAM30481
                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ő
                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to human single exon nucleic acid probes (SEMP: see AAIIO08-AAIIS459). The present sequence is a peptide encoded by one such probe. The SEMPs are derived from human HeLa calls. The SEMPs can be used to produce a single exon microarray, which can be used for massuring human gene expression in a sample derived from human cervical epithelial calls. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                             Peptide #4409 encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                               human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·;
                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.9%; Score 9; DB 22; Length 348; 100.0%; Pred. No. 9.1; ive 0; Mismatches 0; Indels
                                DB 22; Length 348; 0. 9.1;
                                                                  0; Indels
                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 27; SEQ ID No 22801; 487pp; English
                                                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rank DR;
                              0.9%; Score 9;
100.0%; Pred. No
:ive .0; Mismato
                                                                                                                                                                                                                          AAM17975 standard; Protein; 348 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanzel DK, Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0180312.
2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US00670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0632366
2000US-0234687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-488901/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RLKEENEKL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1||||||||
224 RLKEENEKL 232
                                                                                                      266 RLKEENEKL 274
                                                                                                                          224 RLKEENEKL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 348 AA;
348 AA;
                                                                                                                                                                                                                                                                                                                                                                                   cervical cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200157278-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000; 2
26-MAY-2000; 3
30-JUN-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                             12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                            AAM17975;
   Sednence
                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                 Probe;
```

NAME OF COLOR OF STREET OF

ö

Gaps

ò

266

ŏ g

Length 348; 0; Indels σ

```
WO200186003-A2
     \mathbb{R} 	imes \mathbb{R} 	ime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to novel single exon nucleic acid probes (see AA10010-AA110067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human peptide encoded by genome-derived single exon probe SEQ ID 29447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel single exon nucleic acid probe used to measuring gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histlocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary histlocytosis; Iymphangioleiomyomtosis; Karagener syndrome; pulmonary histlocyteiosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 348; . 9.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; SEQ ID No 14350; 322pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          breast disease and non-carcinoma tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG39782 standard; Peptide; 348 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.9%; Scc.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                     21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                               29-JAN-2001; 2001WO-US00661.
                                                                                                                                                                                                                                                                 2000US-0632366.
                                                                                                                                                                                    2000US-0180312
                                                                                                                                                                                                             2000US-0207456
2000US-0608408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-476286/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                266 RLKEENEKL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11111111
224 RLKEENEKL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       348 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in a human breast
                      WO200157270-A2
                                                                                                                                                                                                                                                                    03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                      30-JUN-2000;
                                                                                                                                                                                 04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-AUG-2002
                                                                          09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG39782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG39782
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression nallysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases (COPD), interstitial lung disease (LID), familial idiopathic pulmonary (fibrosis, neurofibromatosis, therens solerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoldosis, pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probes. Also included are a microarray comprising the novel set of probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a mucletc acid expressed in the human lung; measuring gene expression in a sample derived from human lung; measuring gene expression in a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spatially-addressable \ set \ of \ single \ exon \ nucleic \ acid \ probes, \ used \ to \ measure \ gene \ expression \ in \ human \ lung \ samples \ -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 23;
. 9.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 9.1
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 27; SEQ ID No 29447; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; P.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                           2000US-207456P.
2000US-0608408.
2000US-0632366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.98;
                                                                                                                                                                                                                                                                                                             2000US-234687P.
2000US-236359P.
                                                                             30-JAN-2001; 2001WO-US00665
                                                                                                                                                           2000US-180312P
                                                                                                                                                                                                                                                                                                                                                                                               04-OCT-2000; 2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-114183/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348 AA;
                                                                                                                                                                                                                                                                                                             21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                               26-MAY-2000;
                                                                                                                                                                                                                                                                             03-AUG-2000;
                                                                                                                                                                                                                                    30-JUN-2000;
                                                                                                                                                           04-FEB-2000;
15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Penn SG,
```

;;

266 RLKEENEKL 274

δŏ

11111111 224 RLKEENEKL 232 qq Search completed: January 22, 2003, 08:58:20 Job time : 47 secs

us-09-767-215-2.rag

S. Commission of the Commissio

```
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308 LRERAVAAER 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 LRERAVABER 13
 00000000000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
US-08-858-207A-326
δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 326, App
Sequence 6, Appli
Sequence 2, Appli
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188, App
307, App
188, App
188, App
11, Appl
126, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36, Appl
13, Appl
79, Appl
13, Appl
3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127, App
13, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3, Appli
36, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Appl
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Appl
                                                                                                                                               (without alignments)
1554.769 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127,
                                                                                                                                                                                                                   1004
1 MGELCRRDSALTALDEETLW.....VRQAIADEQKKVVWTEQSPR 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sedineuroe 
                                                                                                                           ; Search time 19 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-858-207A-326
US-08-874-118-6
US-08-747-116-2
US-08-871-818-8
US-08-874-59A-307
US-08-874-59A-307
US-08-974-50-188
US-09-430-323-188
US-09-395-689-3
US-09-395-689-3
US-08-985-689-3
US-09-154-750A-79
US-08-985-689-3
US-08-985-689-3
US-08-985-689-3
US-08-985-689-3
US-08-985-689-3
US-08-985-689-3
US-08-652-877-127
                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -09-100-664A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-100-664A-3
US-09-100-664A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-192-983-5
                                                                                                                                                                                                                                                                                                                                   262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Listing first 45 summaries
                                                                                         - protein search, using sw model
                                                                                                                         January 22, 2003, 08:58:25
                                                                                                                                                                                                                                                                             OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                               length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                   US-09-767-215-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . . . . .
                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                 sed
                                                                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                      Word size :
                                                                                         OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                                            Sednence:
                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ь.
В
```

```
ö
                                                                                                        Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                            Appl
Appl
Appl
Appl
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Appli
Appli
Appli
Appli
Appli
Sequence 2, A Sequence 3, A Sequence 2, A Sequence 2, A Sequence 2, A Sequence 22, B Sequence 23, B Sequence 24, B Sequence 2, A Sequence 2, A Sequence 2, A Sequence 3, A Sequence 3, A Sequence 6, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1
US-09-192-983-5
Sequence 5, Application US/09192983A
Sequence 5, Application US/09192983A
Patent No. 6242244
GENERAL INFORMATION:
APPLICANT: Donohue, Timothy
APPLICANT: Witthuhn, Vernon
TITLE OF INVENTION: Microbial System for Formaldehyde Sensing and
TITLE OF INVENTION: Remediation
FILE REFERENCE: 960296.95505
CURRENT FAPLICATION NUMBER: US/09/192,983A
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/6919,953
EARLIER FILING DATE: 1996-02-29
EARLIER FILING DATE: 1996-02-28
SOFWWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 390
TYPE: PRT
CORGANISM: Rhodobacter sphaeroides
US-09-192-983-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 326, Application US/08858207A
Patent No. 6348328
GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
0.32;
                               US-09-335-983-3
US-09-335-983-4
US-09-155-983-4
US-09-155-98-2
US-09-329-535-2
US-09-329-535-9
US-09-155-036-22
US-09-155-036-23
US-09-155-036-24
US-09-155-036-26
US-09-137-077-2
US-09-135-036-5
US-09-135-036-5
US-09-155-036-5
US-09-155-036-5
US-09-155-036-5
US-09-155-036-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 10; DB 4
Pred. No. 0.32
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.0%; SCUL
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.0
Best Local Similarity 100.
Matches 10; Conservative
```

ö

```
;
                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                Length 446;
                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/879,941
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.8%; Score 8; DB 4;
100.0%; Pred. No. 31;
                                                                                                                                                                                                              Query Match 0.8%; Score 8; DB 2; Best Local Similarity 100.0%; Pred. No. 31; Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Wallis, Nicola
TITLE OF INVENTION: NOVEL HISTIDINE KINASE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Prea. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GM10021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 2, Application US/08879941; Patent No. 6268172
                                                           INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 446 amino acids amino acid
   TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                           ; TOPOLOGY: linear
US-08-874-138-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 LQEELNOE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220 LQEELNQE 227
                                                                                                                                                                                                                                                                                             135 LQEELNQE 142
                                                                                                                                                                                                                                                                                                                               220 LQEELNQE 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-879-941-2
                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
US-08-879-941-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA
ZIP: 08543
                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/858,207A
FILING DATE: 09-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY, AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/POCKET NUMBER: P50475
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.8%; Score 8; DB 4; Best Local Similarity 100.0%; Pred. No. 8.4; Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SURFUARRE: FastERD for Windows Version 2.0
SUGRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/874,138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
GAPPLICANT: Wallis, Nicola
TITLE OF INVENTION: No. 5882889el Compounds
WUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOOKET NUMBER: GM10015
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08874138 Patent No. 5882889
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
TOWNITER: IBM COMPATIBLE
TOWNITER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 326:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
; MOLECULE TYPE: No. 6348328e
US-08-858-207A-326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 LOEELNOE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-08-874-138-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

```
Sequence 307, Application US/08974549A
Fatent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Chapmen, March B.
APPLICANT: Chapmen, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Morin, Gregg B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 24;
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CARRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.7%; Score 7; DB 3;
100.0%; Pred. No. 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNDBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNDBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/974,549P
                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.,č,
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/CDOCKET NUMBER: 015:
TELECOMMUNICATION IRFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                 Randolph T.
JMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity luv...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94111-3834
                                                                                                                        FILING DATE: 0 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         759 TRKPSSG 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
US-08-974-549A-307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-851-843A-188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                           APPLICANT: Walls, Nicola
TITLE OF INVENTION: NOVEL HISTIDINE KINASE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
STATE: NJ
STATE: NJ
STATE: USA
ZIP: 08543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: No. 6093809el Telomerase NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSE: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/747,116
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Andrews, William H.
VENTION: No. 6093809el Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.8%; Score 8; D
100.0%; Pred. No.
live 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 188, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Makamura, Toru
APPLICANT: Morin, Gragg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GM10021
                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APLICATION NUMBER: 08/879,941
FILING DATE:
                  Sequence 2, Application US/09747116
Patent No. 6348340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: GM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 609-520-3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM CONTONERS OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 8; Conserv
                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 LQEELNQE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1111111
220 LQEELNQE 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-851-843A-188
  US-09-747-116-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q
```

ò

.; 0

.; 0

```
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 05-MAY-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
?: Two Embarcadero Center, 8th Floor
San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DGCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.7%; Score 7; DB 4
100.0%; Pred. No. 20;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION: 330
PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION DATA.
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION DATA.
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION DATA.
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/74,643
FILING DATE: 01-OCT-1996
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: US 08/724,643
                                                                                                United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 188, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.7
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGIH: 24 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: peptide US-08-854-050-188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  759 TRKPSSG 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 TRKPSSG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
US-09-430-323-188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.7%; Score 7; DB 4;
100.0%; Pred. No. 20;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                PELLING DATA:

PELLING DATA:

APPLICATION NUMBER:

BFILING DATE:

PRIOR APPLICATION NUMBER:

APPLICATION NUMBER:

APPLICATION NUMBER:

BFILING DATE:

APPLICATION NUMBER:

BRIOR APPLICATION DATA:

APPLICATION NUMBER:

APPLICATION NUMBER:

BRIOR APPLICATION DATA:

APPLICATION NUMBER:

APPLICATION NUMBER:

APPLICATION NUMBER:

BRIOR APPLICATION DATA:

APPLICATION NUMBER:

APPLICATION NUMBER:

BRIOR APPLICATION NUMBER:

APPLICATI
                                                      CLASSIFICATION: 330
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 188, Application US/08854050 Patent No. 6261836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Greeg B.
APPLICANT: Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 307:
            FILING DATE: 19-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity الاسن.
الا کانت
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: peptide US-08-974-549A-307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   759 TRKPSSG 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-854-050-188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
```

Gaps ö

> g õ

ô

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ## Sequence 3, Application US/09395689

## Sequence 3, Application

## APPLICANT: Hwang, Jaulang

## APPLICANT: Chen, Tacing Yueh

## TITLE OF INVENTION: TOPOISOMERASE 1-MEDIATED DNA DELIVERY

## FILE REFERENCE: 089191/024001

## CURRENT APPLICATION NUMBER: 05/09/395,689

## CURRENT FILING DATE: 1999-09-13

## NUMBER OF SEQ ID NOS: 6

## SOFTWARE: FastSEQ for Windows Version 4.0

## SEQ ID NO 3

## LENGTH: 105
                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 97; . 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                               Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/09/562,737
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 7;
                                                                                                                                                                                                                                                                                                                                                               Score 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 126, Application US/09562737 Patent No. 6428967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0./v,
100.0%; Pr
                                                                                  REFERENCE/DOCKET NUMBER: P501
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEPHONE: (215) 270-5090
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
                                                                                                                                                                                                                                                                                                                                                           Query Match 0.7%; Sc
Best Local Similarity 100.0%; P
Matches 7; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Pseudomonas aeruginosa
US-09-395-689-3
                  ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                             ; TOPOLOGY: circular
; MOLECULE TYPE: peptide
PCT-US94-06655-11
                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      900 HALLDVQ 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               365 YSARDSA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 HALLDVQ 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 YSARDSA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: human US-09-562-737-126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-562-737-126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Pa
SEQ ID NO 126
LENGTH: 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Datentin Release #1.0, Version #1.30
CURRIN APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: -UNKNOWN>
PRIOR APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas
APPLICANT: Graddis, Thomas
APPLICANT: Myszka, David
TILE OF INVENTION: Coiled-Coil Stem Loop Templates
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: SMITHKINE Beecham Corporation
STREET: CORPORATE PATENTS / P.O. Box 1539
CITY: King of Prussia
STATE: PA
COMPUTER: PA
COMPUTER: PA
COMPUTER: FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: PATENTING DATA:
APPLICATION NUMBER: PCT/US94/06655
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:

NAME: APple, Randolph T.
RECISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 188:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.7%; Score 7; DB 4;
100.0%; Pred. No. 20;
:ive 0; Mismatches
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 188:
US-09-430-323-188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US94-06655-11; Sequence 11, Application PC/TUS9406655; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 24 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 0.7°
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    759 TRKPSSG 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
```

ŝ qq

ò

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
AUPLICATION NUMBER: US/08/946,914 FILLING DATE: Herewith
                                                                                                                                                                                                                                                                                                                           1488.0560001/EKS/SGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.7%; Score 7; DB 4;
100.0%; Pred. No. 97;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 79, Application US/09154750A

Sequence 79, Application US/09154750A

Patent No. 6432640

GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Polyak, Kornelia
TITLE OF INVENTION: P53-Induced Apoptosis
FILE REFERENCE: 1107.75357

CURRENT APPLICATION NUMBER: US/09/154,750A

CURRENT FILING DATE: 1998-09-17

PRIOR FILING DATE: 1998-09-17

PRIOR FILING DATE: 1998-09-17

PRIOR FILING DATE: 1998-03-30

NUMBER OF SEQ ID NOS: 93

SOFTWARE: FASSEQ for Windows Version 3.0

SEQ ID NO 79

LEMENT 10 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 7; D
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: January 22, 2003, 09:00:57 Job time: 22 secs
                                                                                                                                                                           CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,093
FILING DATE: 09-0CT-1996
ATTORNEY AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.05600/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                  PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.7%; Sox
Best Local Similarity 100.0%; P:
Matches 7; Conservative 0;
                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-946-914-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
CORGANISM: Homo sapiens
US-09-154-750A-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     904 DVQLDSV 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 DVQLDSV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           904 DVQLDSV 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 DVQLDSV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-154-750A-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ÓΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                APPLICANT: Wong, K.K.; Saffer, J.D.
TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Paul W. Zinnerman
ADDRESSEE: Battelle Memorial Institute
ADDRESSEE: Battelle Memorial Institute
ADDRESSEE: PINL P.O. Box 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ... LUDY
STREE: Sterne, Kessler, Goldstein, & Fox P.L.L.C.
STREE Hashington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 121;
  Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13, Application US/08946914
Patent No. 6027916
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Galectin 8, 9, 10 and 10SV
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein, & Fox P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage COMPUTER: IBM PC/XT/AT
0.7%; Score 7; DB 4;
100.0%; Pred. No. 76;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.7%; Score 7; DB 2;
100.0%; Pred. No. 87;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Processor (WordPerfect 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/853,659A
FILING DATE: Unknown
CLASSIFICATION: 435
FRICH APPLICATION DATA:
APPLICATION NUMBER: none
FILING DATE: n/a
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                         Sequence 36, Application US/08853659A Patent No. 5925522
                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Intellectual ADDRESSEE: Battelle Memoraboressee: Partelle Memoraboressee: Partelle Memoraboressee: Partelle Memoraboressee: Partelle Memoraboressee: Partelle May CITY: Richland STATE: Washington COUNTRY: U.S.A.
ZIP: 99352
COMPUTER READABLE FORM: MEDIUM TYPE: Diskette 3:3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 7; Conservative
                   Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  456 LSDLSAT 462
                                                                                268 KEENEKL 274
                                                                                                         |||||||||
58 KEENEKL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 LSDLSAT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-853-659A-36
                                                                                                                                                                                   RESULT 13
US-08-853-659A-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-08-946-914-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                          q
```

ő

ö

THIS PAGE BLANK (USPTO)

```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Appli
Sequence 16, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 37615, A
Sequence 2, Appli
Sequence 188, App
Sequence 188, App
Sequence 35935, A
Sequence 35935, A
Sequence 35935, A
Sequence 5287, Ap
Sequence 5287, Ap
Sequence 5287, Ap
Sequence 10, Appl
Sequence 13, Appli
Sequence 13, Appli
Sequence 26, Appli
                                                             (without alignments)
1447.090 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                            1 MGELCRRDSALTALDEETLW.......VRQAIADEQKKVVWTEQSPR 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                    2003, 08:57:45 ; Search time 14 Seconds
                                                                                                                                                                                                                                                                  5.1.3
Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-032-159A-16

US-10-032-159A-18

US-09-864-761-37615

US-09-864-761-37615

US-09-843-676-188

US-09-483-486-188

US-09-864-761-35935

US-09-864-761-35935

US-09-864-761-33346

US-09-864-761-33346

US-09-984-761-33346

US-09-9815-22-5046

US-09-913-626-5287

US-09-913-626-5287

US-09-913-626-5287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-728-479-9
US-09-263-689-13
US-09-866-582-26
                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-767-215-2
US-09-767-215-5
                                                                                                                                                         122226 segs, 20178551 residues
GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                             Published_Applications_AA:*
                                                                                                                                                                                                                                          Post-processing: Listing first 45 summaries
                                    - protein search, using sw model
                                                                                                                             OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq length: 0 seq length: 2000000000
                                                                                       US-09-767-215-2
1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match Length
                                                     January 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                              Scoring table:
                                                                                                                                                                          Word size :
                                                                                                                                                                                                               Minimum DB
Maximum DB
                                    OM protein
                                                                                                                                                                                                                                                             Database :
                                                                                                            Sequence:
                                                                                                                                                         Searched:
                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Result
No.
```

Sequence 110, Appl Sequence 13, Appl Sequence 1468, Ap Sequence 226, Appl Sequence 1, Appli Sequence 1, Appli Sequence 20, Appl Sequence 20, Appli Sequence 18, Appli Sequence 199, Appl Sequence 199, Appl Sequence 219, Appl Sequence 210, Appl Sequence 100, Appl Sequence 100, Appl Sequence 100, Appl Sequence 100, Appl Sequence 100, Appl Sequence 101, Appl	Sequence 103, App Sequence 104, App Sequence 105, App Sequence 106, App
US-10-001-876-210 US-09-767-041-13 US-09-925-300-1468 US-09-925-300-1468 US-09-925-300-1468 US-09-935-299-963 US-09-935-299-963 US-09-931-381A-2 US-09-931-381A-2 US-09-931-381A-2 US-09-931-381A-2 US-09-931-381A-2 US-09-931-381A-3 US-09-931-381A-3 US-09-931-381A-3 US-09-931-381A-3 US-09-931-381A-3 US-09-931-381A-3 US-09-931-381A-3 US-09-798-990-99 US-09-796-990-99 US-09-796-990-99 US-09-796-990-99 US-09-796-990-102	US-09-796-990-103 US-09-796-990-104 US-09-796-990-105 US-09-796-990-106
	, , ,
22266666666666666666666666666666666666	473 473 473
00000000000000000000000000000000000000	0.7
01000000000000000000000000000000000000	4 4 4 4 4 5 4 4 4 5 4 4 5 7

## ALIGNMENTS

```
61 PRLTNSAMRAGHLLDLLKTRCKNCALAFLESLKFHNPDVYTLVTGLQPDVDFSNFSGLME 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSKLTECLAGAIGSLQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 SCELELQEQSIRTASDQESGDEELNRIKEENEKIRSITFSLAEKDILEQSIDEARGSRQE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 KREVSAHFHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGELCRRDSALTALDEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1004;
               Sequence 2, Application US/09767215
| Patent No. US2002001636A1
| GENERAL INFORMATION:
| APPLICANT: Bettin, John
| TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
| TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
| TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
| CURRENT APPLICATION NUMBER: US/09/767,215
| CURRENT APPLICATION NUMBER: 05.01-02
| PRIOR APPLICATION NUMBER: 60/181,159
| PRIOR APPLICATION NUMBER: 60/181,159
| WUMBER OF SEQ ID NOS: 10
| SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1004;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Sco
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 100.
Matches 1004; Conservative
                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
US-09-767-215-2
                                                                                                                                                                                                                                                                                                                           LENGTH: 1004
US-09-767-215-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
```

; 0 2

```
Query Match
                                                                                                                                                                                                                    Db
                                                                                                                                                                                                                                                            Dρ
                                                                                                                                                                                                                                                                                                  Op
                                                                                                                                                                                                                                                                                                                                         Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    öγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                        δλ
                                                          g
                                                                                                 pp
                                                                                                                     ^{\circ}
                                                                                                                                        g
                                                                                                                                                           Ω
                                                                                                                                                                              g
                                                                                                                                                                                                   Qγ
                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                       QΥ
                                                                               Qγ
                                                                                                                                                                                                                                                                                                             780
                                                                    420
                                                                                        420
                                                                                                                                                   540
                                                                                                                                                            900
                                                                                                                                                                                                                               999
                                                                                                                                                                                                                                                   099
                                                                                                                                                                                                                                                                     960
                                                                                                                     REPCPREKQRLVRMHAICPRDDSDCSLVSSTESQLLSDLSATSSRELVDSFRSSSPAPPS 480
                                                                                                                                                                                                   ASPLRLSFDRGQLDPSRMEGSSTCFWAESCLTLVPYTLVWPHRPARPRPVLLVPRAVGKI
                                                                                                                                                                                                                                                                                                                                                              LSEKLCLLQGFKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTH
                                                                                                                                                                                                                                                                                                                                                                                                                                  ALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRLGTSEEQLLEAARQEEGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                            GSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTDG
                                                                                                                                                                                                                                        VNSYTMKDTAAHGTIPNYSRAQQQLIALIQDMTQQCTVTRKPSSGGPQKLVRIVSMDKAK
LVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKE
                                                                               QPVSPGRLDVSESGVLMRRRPARRILSQVTMLAFQGDALLEQISVIGGNLTGIFIHRVTP
                                                                     RDQAYSARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLRQLQAEPPGVLKQEART
                                                                                                                                                    QQSLYKRVAEDFGEEPWSFSSCLEIPEGDPGALPGAKAGDPHLDYELLDTADLPQLESSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-142001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTEQSPR 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/767,215 CURRENT FILING DATE: 2001-01-22 PRIOR APPLICATION NUMBER: 60/181,159 PRIOR FILING DATE: 2000-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09767215
Patent No. US20020081636A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRGANISM: Homo sapiens US-09-767-215-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-767-215-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                            541
                                                                                                                                                                                                                                                                                                                                                                       781
                                                                                       361
                                                                                                                                                                                                                               601
                                                                                                                                                                                                                                                                                         661
                                                                                                                                                                                                                                                                                                                                                                                           841
                                                                                                                                                                                                                                                                                                                                                                                                              841
                                                                                                                                                                                                                                                                                                                                                                                                                                 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                    901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          961
                                                                                                                                                                                         541
                                                                                                                                                                                                                                                                       661
                                                                                                                                                                                                                                                                                                             721
          241
                              301
                                                 301
                                                                                                                              421
                                                                                                                                                                                                                                                  601
                                                                    361
                                                                                                            421
                                                                                                                                                  481
                                                                                                                                                                                                                                                                                                                                                                     Db
                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                             δ
                                                g
                                                                    Qγ
                                                                                    Q
                                                                                                          ò
                                                                                                                              g
                                                                                                                                                  ò
                                                                                                                                                                 Q
                                                                                                                                                                                        Ω
                                                                                                                                                                                                        g
                                                                                                                                                                                                                          οy
                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                      οy
                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                              οq
                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

```
.;
0
                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGVLMRRRPARRILSQVTMLAFQGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPG 612
                                                                                                                                                   TQIVMVDYEASEPLFKAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTDGYKRLLQDLEAKV 672
                                                                                                                                                                      GTIPNYSRAQQQLIALIQDMTQQCTVTRKPSSGGPQKLVRIVSMDKAKASPLRLSFDRGQ 792
                                                                                                                                                                                                                                                                                                                                                                        LDPSRMEGSSTCFWAESCLTLVPYTLVWPHRPARPRPVLLVPRAVGKILSEKLCLLQGFK 852
                                                                                                                                                                                                                                                                                                                                                                                           LHRMDIFPIVIHVSVNEKMAKKLKKGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSSLAP 972
                                                                                           902 KCLAEYLSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCT 961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PRLTNSAMRAGHLLDLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFSNFSG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MGELCRRDSALTALDEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHS
                                                                                                                                                                                                                          ATSGDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAH
                                                                                                                                                                                                                                                                                                                      KCLAEYLSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USE
Length 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Reda, John C.
TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,
TITLE OF INVENTION: CARD-DOMAIN COLEIC ACIDS, AND METHODS OF (FILE REFERENCE: P-LJ 5100
CURRENT APPLICATION NUMBER: US/10/032,159A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 60/257,457
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF.
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.7%; Score 117; DB 9; Le
100.0%; Pred. No. 1.6e-104;
iive 0; Mismatches 0;
                                      ï
 10;
   DB
                                      0; Mismatches
                   ö
   Score 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Xaa - Any Amino Acid US-10-032-159A-16
                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16, Application US/10032159A Patent No. US20020164703A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            973 DGWSDLDGLLSCVRQAIADEQKKV 996
 34.2%;
99.8%;
                     Best Local Similarity 99.8
Matches 443; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity
Matches 117; Conserv
                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-032-159A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                               602
                                                                                                                                                                                                                                                                                                                                                                                                                                              853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1022
                                                                          553
                                                                                                                                                   613
                                                                                                                                                                                                                          673
                                                                                                                                                                                                                                                            722
                                                                                                                                                                                                                                                                                                   733
                                                                                                                                                                                                                                                                                                                                     782
                                                                                                                                                                                                                                                                                                                                                                        793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
```

g

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PAWLOWSKI, KZZYSZŁOF
APPLICANT: Reed, John C.
APPLICANT: GOGZIK, Adam
TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,
TITLE OF INVENTION: ENCODING NUCLEIC ACIDS, AND METHODS OF USE
FILE REFERENCE: P-LJ 5100
CURRENT APPLICATION NUMBER: US/10/032,159A
CURRENT APPLICATION NUMBER: US 60/257,457
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 1247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N: MAP TO AC004702.1

N: EXPRESSED IN HBL100, SIGNAL = 1.2

N: EXPRESSED IN PLACENTA, SIGNAL = 0.97

N: EXPRESSED IN FETAL LIVER, SIGNAL = 2.4

N: EXPRESSED IN BRAIN, SIGNAL = 3.2

N: EXPRESSED IN HUNG, SIGNAL = 1.5

N: EXPRESSED IN BONE MARROW, SIGNAL = 1.5

N: EXPRESSED IN HEART, SIGNAL = 1.3

N: EXPRESSED IN HEART, SIGNAL = 1.3

N: EXPRESSED IN HEART, SIGNAL = 3.7

N: EXPRESSED IN HEAR, SIGNAL = 3.7

N: EXPRESSED IN HTT: P30622, EVALUE 1.00e-89

N: SWISSPROT HIT: P30622, EVALUE 1.00e-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.9%; Score 9; DB 10; Length 348; 100.0%; Pred. No. 1.5; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                        PRIOR APPLICATION UNMBER: PCT/USO1/00668
PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/USO1/00663
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-50
PRIOR FILING DATE: 2001-01-50
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-50
PRIOR FILING DATE: 2001-01-50
PRIOR PRIOR PRIOR DATE: 2001-01-50
PRIOR FILING DATE: 2001-01-50
PRIOR PRIOR APPLICATION NUMBER: US 09/774, 203
PRIOR FILING DATE: 2001-01-29
PRIOR PILING DATE: 2001-01-29
PRIOR PRIOR PRIOR DATE: 2001-01-29
PRIOR PILING DATE: 2001-01-29
PRIOR PRIOR PRIOR DATE: 2001-01-29
PRIOR PILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.9%; Score 9; DB 9;
100.0%; Pred. No. 4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 4..
Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 8, Application US/10032159A; Patent No. US20020164703A1
      FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: BA
OTHER INFORMATION: EX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266 RLKEENEKL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             224 RLKEENEKL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-032-159A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: HUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-37
PRIOR FILING DATE: 2000-09-37
PRIOR PRIOR FILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-01-03
PRIOR FILING DATE: 2001-01-03
PRIOR FILING DATE: 2001-01-03
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR PRIOR NUMBER: PCT/USO1/00664
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR PRIOR NUMBER: PCT/USO1/00664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 EETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGHLLD 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 PRLTNSAMRAGHLLDLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFSNFSG 117
                                                                                                                                        Account of Sequence 18, Application US/10032159A
; Sequence 18, Application US/10032159A
; Sequence 18, Application US/10032159A
; Patent No. US202020164703A1
; GENERAL INFORMATION:
; APPLICANT: PawLowski, Krzysztof
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,
; TITLE OF INVENTION: CARD-DOMAIN CONTECT ACIDS, AND METHODS OF USE
; FILE REFERENCE: P-LJ 5100
; CURRENT APPLICATION NUMBER: US/10/032,159A
; PRIOR FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.2%; Score 92; DB 9; Length 92; 100.0%; Pred. No. 1e-80; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 LLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQ 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LLKTRGKNGAIAFLESLKFHNPDVYTLVTGLO 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00669 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 37615, Application US/09864761 Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 9.2%
Best Local Similarity 100.(
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
US-09-864-761-37615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-032-159A-18
```

q ò QQ

ò

ö

0

```
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 24;
                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Adapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Nakamura, No. US20030009019Alel Telomerase
NUMBER OF SEQUENCES: 223
STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor FITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.7%; Score 7; DB 9;
100.0%; Pred. No. 10;
ative 0; Mismatches
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
                                                         United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 188:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States of America ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 188, Application US/09438486
; Publication No. US20030009019A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 188:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                   ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.7
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 759 TRKPSSG 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-438-486-188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-843-676-188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dβ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.8%; Score 8; DB 10; Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                       US-09-747-116-2
Sequence 2, Application US/09747116
Fatent No. US2001006799A1
GENERAL INFORMATION:
APPLICANT: Wallis, Nicola
TITLE OF INVENTION: NOVEL HISTIDINE KINASE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/747,116
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.08; Prea. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GM10021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/879,941
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFRENCE/DOCKET NUMBER: GM10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 446 amino acids TYPE: amino acid rives: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          Diskette
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
 674 TSGDSFYIR 682
|||||||||||||||
896 TSGDSFYIR 904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 LQEELNQE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1111111
220 LQEELNQE 227
                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                               STATE: NJ
COUNTRY: US
ZIP: 08543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
US-09-843-676-188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                              RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
     ογ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
```

ö

0; Gaps

```
RESULT 11
US-09-864-761-37819
Sequence 37819, Application US/09864761
Sequence 37819, Application US/09864761
Sequence 37819, Application US/09864761
Sequence 37819, Application US/09864761
Sequence 37819, Application Sequence 37819
Sequence 37819
Sequence 37819
Sequence 37819
Sequence 37819
Sequence 37819
Sequence 37810
Sequence 3781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.92
OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 2
OTHER INFORMATION: SATSSPROT HIT: O14607, EVALUE 4.00e-07
OTHER INFORMATION: EST_HUMAN HIT: AA330221.1, EVALUE 7.00e-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.7%; Score 7; DB 10; Length 39;
100.0%; Pred. No. 16;
7ative 0; Mismatches 0; Indels
                                                              PRIOR APPLICATION UNBER: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-01-30
PRIOR PILING DATE: 2000-01-30
PRIOR PILING DATE: 2000-01-30
PRIOR PILING DATE: 2000-01-30
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 35335
LENGTH: 39
               APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP T
OTHER INFORMATION: EXPRE
OTHER INFORMATION: EXPRE
OTHER INFORMATION: EXPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267 LKEENEK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INCORMATION:
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US 60/180, 312
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207, 456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207, 456
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR PRILITATION NUMBER: US 60/236, 359
PRIOR PRILITAGION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        015389-002931US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                           CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997
CLASSIFICATION NABER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 13-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 10-0CT-1996
CLASSIFICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION: 536
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
TELENGENCE/DOCKET NUMBER: 015389-002(
TELEFRAX: (415) 576-0300
TELEFRAX: (415) 576-0300
TELEFRAX: (415) 576-0300
TELEFRAX: CHARATICRESTICS:
LENGTH: 24 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.7%; Score 7; Best Local Similarity 100.0%; Pred. No Matches 7; Conservative 0; Mismat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 35935, Application US/09864761
Patent No. US20020048763A1
                                                                                                                    UMBER: US/09/438,486
12-NOV-1999
                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide US-09-438-486-188
                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   759 TRKPSSG 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 TRKPSSG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NN: EXPRESSED IN PLACENTA, SIGNAL = 4

NN: EXPRESSED IN BT474, SIGNAL = 3.7

NN: EXPRESSED IN BT474, SIGNAL = 3.7

NN: EXPRESSED IN ADDIT LIVER, SIGNAL = 4.4

NN: EXPRESSED IN HEART, SIGNAL = 3.9

NN: EXPRESSED IN BEAIN, SIGNAL = 4.7

NN: EXPRESSED IN HELA, SIGNAL = 4.7

NN: EXPRESSED IN HELA, SIGNAL = 4.7

NN: EXPRESSED IN HELA, SIGNAL = 4.6

NN: EXPRESSED IN HELA, SIGNAL = 3.9

NN: EXT-HUMAN HIT: AW385142.1, EVALUE 5.20e-02

NN: SWISSPROT HIT: P41246, EVALUE 5.00e+00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                              PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR PAPLICATION NUMBER: US 62263.6

PRIOR PILING DATE: 2000-09-03

PRIOR PILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2001-01-03

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PRIOR DATE: 2001-01-30

PRIOR PRIOR DATE: 2001-01-30

PRIOR PRIOR DATE: 2001-01-30

PRIOR PILING DATE: 2000-09-21

PRIOR PILING DATE: 2000-09-21

PRIOR PILING DATE: 2000-09-30

PRIOR PILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.7%; Score 7; DB 1
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches
US 60/207,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 5287, Application US/09738626; Publication No. US20020197605A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAP TO AC002470.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO OTHER INFORMATION: EXPREOTHER INFORMATION: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 472 RSSSPAP 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 RSSSPAP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-864-761-33346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-09-738-626-5287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 33346, Application US/09864761

Pageuence 33346, Application US/09864761

Pageuence 33346, Application US/09864761

GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENEE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23

PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N: EXPRESSED IN BT474, SIGNAL = 2.1
N: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8
N: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
N: EXPRESSED IN LUNG, SIGNAL = 2
N: EXPRESSED IN LUNG, SIGNAL = 1.5
N: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
N: EXPRESSED IN PLACINY, SIGNAL = 1.9
N: EXPRESSED IN PLACIONY, SIGNAL = 1.9
N: EXPRESSED IN HELA, SIGNAL = 1.8
N: EXPRESSED IN HELA, SIGNAL = 1.8
N: EXPRESSED IN HELA, SIGNAL = 1.8
N: EXPRESSED IN HERAFY, SIGNAL = 1.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.7%; Score 7; DB 10; Length 45;
100.0%; Pred. No. 18;
ive 0; Mismatches 0; Indels
                         PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-30
     APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      540 LQPVSPG 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1111111
20 LQPVSPG 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-09-864-761-33346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-864-761-37819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

ö

;; 0

Gaps

; 0

Length 78; Indels

```
US-10-032-159A-10

Sequence 10, Application US/10032159A

Patent No. US20020164703A1

GENERAL INFORMATION:
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Reed, John C.
APPLICANT: Reed, John C.
APPLICANT: BROODING NUCLEIC ACIDS, AND METHODS OF USE
TITLE OF INVENTION: ENCODING NUCLEIC ACIDS, AND METHODS OF USE
FILE REPRENCE: P-LJ 5100
CURRENT APPLICATION NUMBER: US/10/032,159A

CURRENT FILING DATE: 2000-12-19

PRIOR APPLICATION NUMBER: US 60/257,457

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10
                                                   Query Match 0.7%; Score 7; DB 10; Best Local Similarity 100.0%; Pred. No. 31; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.7%; Score 7; DB 9; Best Local Similarity 100.0%; Pred. No. 36; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: January 22, 2003, 09:00:30 Job time : 16 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-10-032-159A-10
                                                                                                                                                                625 PLFKAVL 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 LTPYLRQ 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111111
24 LTPYLRO 30
                                                                                                                                                                                             US-09-815-242-5046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                   ολ
                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INVORMATION:
GENERAL INVORMATION:
APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Yaskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Garr, Grant J.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamanoto, Robert T.
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-2
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.7%; Score 7; DB 9; Best Local Similarity 100.0%; Pred. No. 28; Matches 7; Conservative 0; Mismatches
        ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-09-815-242-5046
Sequence 5046, Application US/09815242
; Petent No. US/0020061569A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 QEKELAA 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1111111
17 QEKELAA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pp
```

ö

Gaps

; 0

0; Indels Length 92;

THIS PAGE BLANK (USPTG)

```
5.1.3
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2003
```

- protein search, using sw model OM protein Run on:

January 22, 2003, 08:56:55 ; Search time 26 Seconds (without alignments) 3712.268 Million cell updates/sec

US-09-767-215-2 1004 Perfect score:

1 MGELCRRDSALTALDEETLW.......VRQAIADEQKKVVWTEQSPR 1004 Sequence:

Scoring table:

283224 seqs, 96134422 residues OLIGO Gapop 60.0 , Gapext 60.0 Searched:

Total number of hits satisfying chosen parameters:

0

Word size :

seq length: 0 seq length: 2000000000 Minimum DB s Maximum DB s Post-processing: Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
Result No.	Score	% Query Match	Length	DB	ID	Description
-	10	0.	738		вбовба	saes taeacamos-owt
١٥	o c		162		٠.	٩
'n	ο α	0.8	167	2		
4	σ.		245	ι ,	XXXXXX	
S	60		245	~	A91294	mosome repli
9	80		245	~	D86135	
7	80		270	7	G71061	ധ
8	80		324	7	AB3548	
6	80	-	332	~	T26436	$\overline{}$
10	ω		346	7	A12229	syn
11	æ	•	348	7	T28806	olfactory receptor
12	œ		366	7	B75481	
13	α		381	7	S73665	hypothetical prote
14	80	•	388	7	E95177	-
15	80		388	7	G98043	aminotransferase (
16	80		418	7	T45807	translation initia
17	80		446	7	н97929	histidine kinase (
18	8		662	7	н95934	probable MPA1 fami
19	80		750	7	T21534	hypothetical prote
20	ω		752	7	S40780	Ψ
21	ω		772	7	T27907.	
22	œ		851	7	T06722	_
23	ω		996	7	S43878	-
24	7		62	7	T30666	hypothetical prote
25	7		68	-	VZA	
26	7	•	73	7		hypothetical prote
27	7		74	~	3622	_
28	7	0.7	94	7	g	ical
29	7	0.7	79	7	53	ם

<u> </u>	nypotherical prote hypothetical prote conserved hypothet	hypothetical prote alpha, 1-6-glucosi	hypothetical prote hypothetical prote	ribosomal protein T-cell receptor al	D5L protein - vari hypothetical prote	B6L protein - vari hypothetical prote	
B95283 T40431	H8428/ T48522 AC3244	T49389 T50029	T30769 T14871	S78145 A31557	E36837 T28442	F72150 AH2322	155469
000	7 77 77	0.0	0 0	7 7	7 7	7 0	7
883	93 109	111 116	120	122	126 126	126	136
0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7
7 7 1		7	~ ~	r r	7	~ ~	7
30 31	333 34	35 36	37 38	39 40	41 42	43	. 4.

## ALIGNMENTS

_	
_	,,
٦	V
⊃	α
	О
Ŧ	V

two-component sensor histidine kinase homolog ykrQ - Bacillus subtilis

C.Species: Bacillus subtilis
C.Species: Bacillus subtilis
C.Species: Bacillus subtilis
C.Species: Bacillus subtilis
C.Species: Bacillus subtilis
C.Specession: B68863
C.Saccession: B68863
C.Saccessio

A;Cross-references: GB:299111; GB:AL009126; NID:g2633699; PIDN:CAB13226.1; PID:e11849 A;Experimental source: strain 168 C;Genetics:

A; Gene: ykrQ

Gaps ö 1.0%; Score 10; DB 2; Length 738; 100.0%; Pred. No. 0.35; tive 0; Mismatches 0; Indels Best Local Similarity 100. Matches 10; Conservative Query Match

ö

# 262 EELNRLKEEN 271 ò

|||||||||||||||| EELNRLKEEN 23 14 q

hypothetical protein SA1058 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-oct-2001
C;Accession: B89894
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ona, M.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

A,Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A,Reference number: A89758; MUID:21311952; PMID:11418146

```
A; Description: this protein is one of the components of the prepriming protein comple le-stranded DNA for DNA polymerase reaction
A; Pathway: DNA biosynthesis
C; Superfamily: DNA replication protein dnaC
C; Keywords: DNA biosynthesis; P-loop
F;106-113/Region: nucleotide-F;inding motif A (P-loop) #status atypical
F;165-169/Region; nucleotide-binding motif B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-5,'D',7-245 <BLAT>
A;Cross-references: GB:AE000507; GB:U00096; NID:g2367380; PIDN:AAC77317.1; PID:g17908
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: dnaC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-5, Tb', 7-245 < SUR>
A; Residues: 1-5, Tb', 7-245 < SUR>
A; Cross-references: EMBL: U14003; NID: 91263172; PIDN: AAA97260.1; PID: 9537204
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
B; Masai, H.; Bond, M.W.; Arai, K.I.
Proc. Natl. Acad. Sci. U.S.A. 83, 1256-1260, 1986
A; Title: Cloning of the Escherichia coli gene for primosomal protein i: the relations
A; Reference number: A94085; MUID: 86149284; PMID: 3006041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:J04030; GB:J02785; GB:M13005; NID:g145788
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Tile: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: C65251
C,Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 01-Mar-2002
C;Accession: A28484; S55588; B25124; C65251
R;Nakayama, N.; Bond, M.W.; Miyajima, A.; Kobori, J.; Arai, K.
Diol. Chem. 262, 10475-10480, 1987
A;Title: Structure of Escherichia coli dnac. Identification of a cysteine residue pos A;Reference number: A92600; MUID:87280100; PMID:3301836
                                                                                                                                                                                                                                                                                                                                                                                      A, Molecule type: DNA
A, Residues: 1-245 <NAK>
R; Butland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A; Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from A, Reference number: S56314; MUID:95334362; PMID:7610040
A; Accession: S56588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002
C;Accession: A91294
G;Accession: Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome replication protein DnaC [imported] - Escherichia coli (strain O157:H7, C; Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.8%; Score 8; DB 1;
100.0%; Pred. No. 15;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
'... 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-14 <MAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 99 min C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      943 GISEEQLL 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||||||||
|150 GTSEEQLL 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nypothetical protein ylxL - Bacillus subtilis

NyAlternate names: s1903 '-region hypothetical protein C
C.Species: Bacillus subtilis
C.Species: Bacillus S.Species: Bacillus S.Species: Bacillus S.Species: Bacillus
A.Authors: Foulger
D.Species: Park, S. Summano, V. C.Species: Bacillus
A.Authors: Foulger
D.Species: Bacillus
A.Authors: Foulger
D.Species: Bacillus
A.Authors: Collida A.Species: Bacillus
A.Authors: Collida A.Species: B.Species
D.Species: B.Species: B.Species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         · · ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
           A; Accession: B89894
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-references: GB:BA000018; PID:g13701015; PIDN:BAB42310.1; GSPDB:GN00149
A; Cross-references: strain N315
C; Genetics: A; Genetics: Genetics: A; Genetics: Genetics: A; Genetics: Genetics: Genetics: A; Genetics: Genetics: Genetics: Genetics: A; Genetics: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA replication protein dnaC - Escherichia coli (strain K-12)
C;Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.8%; Scc.
100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.8%; ;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.،
المالية عند المالية ا
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1.67 < MAR>
A; Cross-references: GB:M20144
C; Genetics:
A; Gene: y1xL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKEENEKL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        662 KRLLQDLE 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 KRLLODLE 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               XMECNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

C

 $s_{u}$ 

ö

Gaps

ô

g

us-09-767-215-2.rpr

ò g

```
vegetatible incompatibility protein het-e-1 [imported] - Brucella melitensis (strain C; Species: Brucella melitensis
C; Species: Brucella melitensis
C; Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C; Accession: AB3548
R; DelVecchio, V. G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov
; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melit
A;Reference number: AB3552; PMID:11776688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 9, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule Lype: DNA
A; Residues: 1-33 - VNIL>
A; Residues: 1-33 - VNIL>
A; Cross-references: EMBL: ALI10477; NID: e1542121; PIDN: CAB54324.1; CESP: Y113G7B.1
A; Cross-references: Clone Y113G7B
C; Genetics:
A; Gene: CESP: Y113G7B.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A12229
cobalamin synthesis protein [imported] - Nostoc sp. (strain PCC 7120)
c)Species: Nostoc sp.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: A12229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE008918; PIDN:AAL53549.1; PID:g17984458; GSPDB:GN00191
A;Experimental source: strain 16M
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein Y113G7B.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T26436
R;Lennard, N.
submitted to the EMBL Data Library, September 1999
A;Reference number: Z20215
A;Reference number: Z20215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.08; Preu. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.8%; Score 8; DB 2
100.0%; Pred. No. 20;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 8; D. Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Introns: 23/2; 49/2; 259/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-324 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1111111
283 QKEVLLRR 290
          115 LKEENEKL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 OKEVLLRR 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           928 NEKMAKKL 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: BMEII0307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
T26436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΟY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cispecias: Escherichia coli (strain O157:H7, subst chromosome replication protein DnaC [imported] - Escherichia coli (strain O157:H7, subst chromosome replication protein DnaC [imported] - Escherichia coli (strain O157:H7, subst cispecias: Escherichia coli disequence_revision 16-Feb-2001 #text_change 17-May-2002 C;Accession: D86135 C;Accession: D86136 C;Accession: D86126 C;Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: G71061
hypothetical protein PH1189 - Pyrococcus horikoshii
C;Species: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Nov-1999
C;Accession: G71061
R;Kawarabayasi, Y:; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamacoto, S.; Sekir
M; Ohluku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: G71061
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-270 <ARA>
A;Residues: 1-270 <ARA>
A;Coss-references: GB:AP000005; NID:93236132; PIDN:BAA30289:1; PID:d1031232; PID:g32576
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                             ö
A;Residues: 1-245 <hAY>
A;Cross-references: GB:BA000007; PIDN:BAB38744.1; PID:g13364799; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECS5321
C;Superfamily: DNA replication protein dnaC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 270;
                                                                                                                                                                                                                                             Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.8%; Score 8; DB 2;
100.0%; Pred. No. 16;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.8%; Score 8; DB 2;
100.0%; Pred. No. 15;
ative 0; Mismatches
                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                         / Match 0.8%; Score 8; DB 2 Local Similarity 100.0%; Pred. No. 15; Nes 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.8
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           943 GTSEEQLL 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    943 GTSEEQLL 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                150 GTSEEQLL 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267 LKEENEKL 274
                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
```

δ q

ö

ö

ò

RESULT 11

ò pp

```
C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
A;Variety: ATCC 29342
C;Dates: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999
C;Accession: S73665
B;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumon A;Reference number: S73327; MUID:97105885; PMID:8948633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 17-81 A:Residues: 17-81 A:Residues: 18-81 A:Residues: EMBL:AE000032; GB:U00089; NID:g1674011; PIDN:AAB95987.1; PID:g167 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Elsen, J.A.; Read, T.D.; Peterson, S.; H on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzappl nson, T.; Hickey, E.K.; Holt, I.E. science 293, 499-506, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris A; Ailtie. Complete Genome Sequence of a virulent isolate of Streptococcus pneumonlae. A; Accession: E95177
A; Accession: E95177
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-388 <a href="https://www.new.accessions.com/">www.new.accessions.com//www.new.accessions.com/</a>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE005672; PIDN:AAK75614.1; PID:914973014; GSPDB:GN00164; TIGR: A;Experimental source: strain TIGRA C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
G98043
aminotransferase (EC 2.6.1.-) [imported] - Streptococcus pneumoniae (strain R6)
c;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aminotransferase, class II [imported] - Streptococcus pneumoniae (strain TIGR4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C:Accession: E95177
                                                                                                                                                                                                                                                                                                                                        - Mycoplasma pneumoniae (strain ATCC 29342)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                        Indels
                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 8; DB 2;
Pred. No. 23;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 22;
; Mismatches
          21;
                                        Mismatches
          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.8%; Score 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.8%; Scc.
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                     .,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.08;
          100.08;
                                                                                                                                                                                                                                                                                                                                        hypothetical protein P02_orf381
   Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 SLVEKDSL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         447 LVSSTESQ 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLVEKDSL 385
                                                                                                            RVTPGSAA 604
                                                                                                                                                                     274 RVTPGSAA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVSSTESQ 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: SP1524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics:
                                                                                                            597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
                                                                                                                                                                                                                                                                           RESULT 13
                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
B75481

periplasmic serine proteinase, HtrA/DegQ/DegS family - Deinococcus radiodurans (strain F C; Species: Deinococcus radiodurans
C; Species: Deinococcus radiodurans
C; Species: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2002
C; Accession: B75481

R;White, O: Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma S.; Smith, H.O; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: B75481
A;Residues: 1-366 <WHI>
A;Residues: DRA A;Residues: BRAE001930; GB:AE000513; NID:96458450; PIDN:AAF10323.1; PID:9645845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Map position: 1 :scherichia coli trypsin-like proteinase; GLGF domain homology; trypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Olfactory receptor ODR-10 - Caenorhabditis elegans
Olfactory receptor ODR-10 - Caenorhabditis elegans
CiSpecies: Caenorhabditis elegans
CiSpecies: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C;Accession: T28806
R;Bu, Z.
Submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid C53B7.
A;Reference number: 220526
A;Accession: T28806
A;Reference number: 220526
A;Gession: T28806
A;
                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
A;Accession: A12229
A;Status: preliminary
A;Nolecule type: DNA
A;Rolecule type: DNA
A;Rosidues: 1-346 < KUR>
A;Cross-references: GB:BA000019; PIDN:BAB75091.1; PID:g17132487; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene cobw
C;Superfamily: cobw protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.8%; Score 8; DB 2; Length 366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 348;
                                                                                                                                                                                                                                                                                                                                        Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                    DB 2;
. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. No. 20; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                    Score 8; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.8%; Score 8;
                                                                                                                                                                                                                                                                                                                0.8%; Scc.
100.0%; Pred
0; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.8
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                              789 DRGQLDPS 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11111111
216 DRGQLDPS 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||||||||||||
|LLKTRGKN 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 LLKTRGKN 83
```

31

ò op ·

Query Match

```
C; Accession: G98043
R; Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; F e, R.; Leblanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M y. P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A; Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; Aritle: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A; Reference number: A97872; MUID:21429245; PMID:11544234
A; Residues: praliminary
A; Molecule type: DNA
A; Residues: 1-388 < KUR>
A; Rossidues: 1-388 < KUR>
A; Cross references: GB:AE007317; PIDN:AAL00180.1; PID:g15459025; GSPDB:GN00174
C; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match

O.8%; Score 8; DB 2; Length 388; Best Local Similarity 100.0%; Pred. No. 23; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        378 SLVEKDSL 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          οy
```

Search completed: January 22, 2003, 09:00:11 Job time : 30 secs

qq

THIS PAGE BLANK (USPTO)

· Chart

```
GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
```

- protein search, using sw model OM protein January 22, 2003, 08:53:45 ; Search time 16 Seconds (without alignments) 2602.640 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-767-215-2 1004 1 MGELCRRDSALTALDEETLW......VRQAIADEQKKVVWTEQSPR 1004

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

112892 seqs, 41476328 residues

Searched:

Total number of hits satisfying chosen parameters: 0 Word size :

112892

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hom	mus m	Q9bx17 homo sapien	bacil	P07905 escherichia	Q9scw4 arabidopsis		598	P75283 mycoplasma	~	۲.	217		P37852 polytrichum		P47929 homo sapien	4	m		Q9bw83 homo sapien	Q9d0p8 mus musculu	P74901 thermus the	Q9xt48 macropus eu			_		Q9x7r6 streptomyce		P73451 synechocyst	0	109 stre	20
SUMMARIES	ID	- 2≥	CARE_MOUSE	CARB_HUMAN	YLXL_BACSU	DNAC_ECOL1	HSF6_ARATH	PEP1_GADMO	PLSX_CLOTS	YF03_MYCPN	EFGM_RAT	YH07_VACCV	GVPB_BACME	CHLB_PLESC	CHLB_POLCU	RM14_RECAM	LEG7_HUMAN	YN77_RHIME	RPC_BPPH1	DRTS_PLAVN	RAYL_HUMAN	RAYL_MOUSE	VATE_THETH	TNFB_MACEU	RPOC_PROHO	V281_ARATH	V282_ARATH	HIS1_BACHD	RNH_STRCO	JOIN_LYCES	NRTB_SYNY3	YKJ5_YEAST	- 1	OIF_BOVIN
	DB	П	П	-	7	7	٦	П	Н	-	<del>-</del>	-	7	7	П	П	7	7	-	П	1	_	_	7	_	П	7	7	Т	٦.	Н	Н.	н.	4
	Length	1004	666	1147	167	245	588	324	333	381	752	68	88	100	100	122	135	142	144	182	186	186	188	201	203	508	209	212	231	265	275	278	299	677
dŧ	Query		•		•	•			0.8		٠	٠	•				•		•		0.7			•	٠	0.7		•		0.7		0.7	0.7	:
	Score	1004	28	6	80	80	80	80	<b>ω</b>	00	ω	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	۲ ر	•
	Result No.	1	7	æ	4	Ŋ	9	7	80	on ·	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	ז

_	P18394 streptomyce	050098 pyrococcus	P23148 photorhabdu	P45349 haemophilus	Q9qzv1 homo sapien	084638 chlamydia t	P52204 canis famil	P35906 felis silve	Q11167 mycobacteri	~	P46092 homo sapien
PANE_PYRAB	AFSA_STRGR	PANE_PYRHO	LXD2_PHOLU	METR_HAEIN	ANR2_HUMAN	HEM2_CHLTR	RDS_CANFA	RDS_FELCA	Y502_MYCTU	WNT2_CAEEL	CKRA_HUMAN
⊣	Н	-	٦	7	٦	1	Н	П	٦	-	-
300	301	301	307	309	333	338	346	346	358	360	362
0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7
7	7	7	7	7	7	7	7	7	7	7	7
34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

RE_HUMAN CARE_HUMAN STANDAR Q9BXL6; Q9BVB5;	15-JUN-2 15-JUN-2 15-JUN-2 Caspase	CARD14 OR CARD14 OR Homo sapié Eukaryota; Mammalia; NCBI_TaxII			- 21 0 12 -		LOCATION: Cytoplasmic. FICITY: Expressed in placenta. t not in the other cancer cell CONTAINS I CARD DOMAIN. CONTAINS I BDZ/DHR DOMAIN. CONTAINS I GUANYLATE KINASE-LI posed to contain a SH3 domain m or SMART.	Thir
---	---	---	--	--	-------------	--	--	------

a

```
GSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTDG 660
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 82-743 FROM N.A.
                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                         2) (Bimp2).
CARD14 OR BIMP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Breast;
                                                                                                                                                                                                                                         CARE_MOUSE
                                                                                                                                                                                                                                 CARE_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This
                                661
                                                                721
                                                                                781
                                                                                                 781
                                                                                                                 841
                                                                                                                                841
                                                                                                                                                901
                                                                                                                                                                901
                                                                                                                                                                                961
                                                                                                                                                                                                961
                 661
                                                 721
                                                                                                                                                                                                                         RESULT 2
                                                                                                                                                                                                                                          g
                                                                                                g
                                                                                                                               g
                                                                                                                                                                QQ
                                                                                                                                                                                δy
                               g
                                                                                ò
                                                                                                               δy
                                                                                                                                                ŏ
               Q
                                                QΣ
                                                                                                                                                                                                                                         0;
 and for commercial
        (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                GYKRLLQDLEAK -> SRARPLLSPGLLMGTVAAGGVTQAD
FTSPRRCRSTLGWASALSWADVKRSAHL (IN REF. 2;
                                                                                                                                                                         DYEASEPLFKAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTD
                                                                                                                                                                                                                                                                                                                                                                         240
                                                                                                                                                                                                                                                                                                                         240
                                                                                                                                                                                                                                                                                                                                                                                          300
                                                                                                                                                                                                                                                                                                                                                                                                        300
                                                                                                                                                                                                                                                                                                                                                                                                                          360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           099
                                                                                                                                                                                                                                                                                                  360
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RDQAYSARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLRQLRQAEPPGVLKQEART 420
                                                                                                                                                                                                                                                                                          PRLTNSAMRAGHLLDLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFSNFSGLME 120
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                  MGELCRRDSALTALDEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHS 60
                                                                                                                                                                                                                                                                                                                                                          KREVSAHFHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANNVS
                                                                                                                                                                                                                                                                                                                                                                  SCELELQEQSLRTASDQESGDEELNRLKEENEKLRSLTFSLAEKDILEQSLDEARGSRQE
                                                                                                                                                                                                                                                                                                                                                                                                  REPCPREKQRLVRMHAICPRDDSDCSLVSSTESQLLSDLSATSSRELVDSFRSSSPAPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QPVSPGRLDVSESGVLMRRRPARRILSQVTMLAFQGDALLEQISVIGGNLTGIFIHRVTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSAADQMALRPGTQIVWUYEASEPLFKAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTDG
                                                                                                                                                                                                                                                                                                                                                                                                                         LVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQSLYKRVAEDFGEEPWSFSSCLEIPEGDPGALPGAKAGDPHLDYELLDTADLPQLESSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                        Length 1004;
                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                       7469B8B56BE06073 CRC64;
 ρλ
                                                                                                                                        CARD. COIL (POTENTIAL)
Usage
                                                                                                                                                                                                                         DB 1;
                                                                                               PROSITE; PS50209; CARD; 1.
PROSITE; PS50209; CARD; 1.
PROSITE; PS500856; GUANYLATE KINASE_1; FALSE_NEG
PROSITE; PS50106; PDZ; 1.
Coiled coil.
                                                                                                                                                                GUANYLATE KINASE
modified and this statement is not removed.
                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                        100.0%; Score 1004; 100.0%; Pred. No. 0;
         entities requires a license agreement (;
or send an email to license@isb-sib.ch)
                              EMBL; AF322642; AAG53403.1; -.
EMBL; AY032927; AAK54453.1; -.
EMBL; BC018142; AAH18142.1; -.
EMBL; BC001326; AAH01326.1; AIT_INIT.
INTERPRO; IPRO00619; Guanylate_kin.
INTERPRO; IPRO1478; PDZ.
SMART; SM00072; GuKc; 1.
SMART; SM001228; PDZ.; 1.
                                                                                                                                                                                                AAH01326)
                                                                                                                                                                                                        1004 AA; 113299
                                                                                                                                                                                                                                        Matches 1004; Conservative
                                                                                                                                        107
409
658
990
671
                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                        15
128
568
858
619
                                                                                                                                                        DOMAIN
DOMAIN
CONFLICT
                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                         Query Match
                                                                                                                                                 DOMAIN
                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                         -
                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         541
                                                                                                                                                                                                                                                                                                                                                                                                                                                         361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          601
                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                        241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421
                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                                                                                         301
                                                                                                                                                                                                                                                                                                                                                                                                                                         301
g
                                                                                                                                                                                                                                                                                          á
                                                                                                                                                                                                                                                                                                        Dp
                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                        Db
                                                                                                                                                                                                                                                                                                                                                        οy
                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                       QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                         οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 14 (Bcl10-interacting MAGUK protein
                                                                                                                                   840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Bimpl, a MAGUK family member linking protein kinase C activation to Bcl10-mediated NF-kappa B induction."; J. Biol. Chem. 276:30589-30597(2001).
YKRLLQDLEAKVATSGDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHAHR
                      VNSYTMKDTAAHGTIPNYSRAQQQLIALIQDMTQQCTVTRKPSSGGPQKLVRIVSMDKAK
                                                                                                                                                                                                                   ASPLRLSFDRGQLDPSRMEGSSTCFWAESCLTLVPYTLVWPHRPARPRVLLVPRAVGKI
                                                                                                                                                                                                                                               LSEKLCLLQGFKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTH
                                                                                                                                                                                                                                                                                                                                                            LSEKLCLLQGFKKCLAEYLSQEEYBAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTH
                                                                                                                                                                                                                                                                                                                                                                                                                                      ALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRLGTSEEQLLEAARQEEGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-21391892; PubMed-11387339;
MEDLINE-21391892; PubMed-11387339;
MEDLINE-21391892; PubMed-11387339;
Li Q., Chen S., Chen F.F., Yamaoka S., Verma I.M., Mak T.W.
Nunez G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTEGSPR 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
```

```
PROSITE,
                                                                                                                                                                                                                                                                Coiled coil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YLXL_BACSU
P40405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=168;
                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YLXL_BACSU
                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY: Detected in adult peripheral blood leukocytes, thymus, spleen and liver. Also found in promyelocytic leukemia HL-60 cells, chronic myelogenous leukemia K562 cells, Burkitt's lymphoma Raji cells and colorectal adenocarcinoma SW480 cells. Not detected in Hela S3, Molt-4, A549 and G431 cells. Not SIMILARITY: CONTAINS I CARD DOMAIN.
SIMILARITY: CONTAINS I GARD DOMAIN.
SIMILARITY: CONTAINS I GUANYLATE KINASE-LIKE DOMAIN.
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 11 (CARD-containing MAGUK protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-21255663; PubMed-11356195; Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.; Carmal, a CARD-containing binding partner of Bc110, induces Bc110 phosphorylation and NF-kappa activation."; FEBS Lett. 496:121-127(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.; FEBS Lett. 505:198-198(2001).
-!- FUNCTION: Activates NF-kappaB via Bcll0 and IKK. Stimulates the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bertin J., Wang L., Guo Y., Jacobson M.D., Poyet J.-L., Srinivasula S.M., Merriam S., DiStefano P.S., Alnemri E.S.; "CARD11 and CARD14 are novel caspase recruitment domain ("CARD)/membrane-associated quanylate kinase (MAGUK) family members that interact with Bcll0 and activate NF-kappaB."; J. Biol. Chem. 276:11877-11882(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphorylation of Bc110. SUBUNIT: CARD11 and Bc110 bind to each other by CARD-CARD interaction.
                                                                                                                                                                                 5
                                                                                                                                                                                 QAQQQLLA -> HLLEDHRS (IN REF. ; D18350DA12430255 CRC64;
                                                                                                                                                                                                                     Length 999;
                                                                                                                                                                                                                                               0; Indels
                                                                                                                              CARD. COIL (POTENTIAL).
                                                                                                                                                                                                                       Score 28; DB 1; Le
Pred. No. 5.9e-20;
                                                                            FALSE_NEG.
                                                                                                                                                        PDZ.
GUANYLATE KINASE.
                                                                                                                                                                                                               2.8%; >cc.
100.0%; Pred. No. c.
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     PRT; 1147 AA
                                            Pfam; PF0095; PD2; 1.
PROSITE: PS50209; CARD. 1.
PROSITE: PS0856; GUANTLATE_KINASE_1;
PROSITE: PS50052; GUANTLATE_KINASE_2;
PROSITE: PS50106; PD2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                        80 RGKNGAIAFLESLKFHNPDVYTLVTGLQ 107
            EMBL; BC004692; AAH04692.1; -.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-21192234; PubMed-11278692;
                                                                                                                                                                                             113496 MW;
EMBL; AF363457; AAK60137.1;
                                                                                                                                                                                                                                               28; Conservative
                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                           411
655
986
743
                                                                                                                                                                                            999 AA;
                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 3) (Carma 1).
CARD11 OR CARMA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                 Coiled coil.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                   CARB_HUMAN
                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERRATUM.
                                                                                                                                            DOMAIN
                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                 09BXL7
                                                                                                                                                                                                                                                                                                                                                       CARB_HUMAN
                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                    Best
à
                                                                                                                                                                                                                                                                                                  g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
A Bouriss R., Boursier L., Brans A., Braun M., Brighnell S.C., Bron S.,
Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
A. Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N.,
Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C. R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Parro V., Pohl T.M., Portetelle B., Rapoport G., Rey M., Reynolds S.,
Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
Supposed to contain a SH3 domain which is not detected by Pfam or {\rm SMART}_{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GUANYLATE KINASE.
P -> L (IN REF. 2).
W; 913A4B015D2B36CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COILED COIL (POTENTIAL). PDZ.
                                                                                                                                                                                                                                                                                                                                                                                   FALSE_NEG.
FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 9; DB 1;
Pred. No. 2.3;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 AA
                                                                                                                                                                                                                                                                                                                                     SMART; SM00228; PDZ; 1.
PROSITE; PS50209; CARD; 1.
PROSITE; PS00856; GUANYLATE_KINASE_1;
PROSITE; PS50052; GUANYLATE_KINASE_2;
PROSITE; PS50106; PDZ; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein ylxL precursor
                                                                                                                                                                                                                                                                   Genew; HGNC:16393; CARD11.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-98044033; PubMed-9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132641 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                              EMBL; AF322641; AAG53402.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103
442
748
1133
808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             674 TSGDSFYIR 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     764 TSGDSFYIR 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11
123
673
966
808
1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1423;
```

```
Biol. Chem. 263:15083-15093(1988).
                                                                             Blattner F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; B2512'
ECO2DBASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-K12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SITE
      This SWISS-PROT entry is copyright. It is produced through a collaboration between the SAISS institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorokin A., Tacconi T., Takagai T., Takahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zunstein E., Yoshikawa H., Danchin A., The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                            Helmann J.D., Marquez L.M., Chamberlin M.J.; "Cloning, sequencing, and disruption of the Bacillus subtilis sigma 28 gene."; J. Bacteriol. 170:1568-1574(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Masai H., Arai K.-I.; "Operon structure of dnaT and dnaC genes essential for normal and stable DNA replication of Escherichia coli chromosome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakayama N., Bond M.W., Miyajima A., Kobori J., Arai K.-I.; "Structure of Escherichia coli dac. Identification of a cysteine residue possibly involved in association with dnaB protein."; J. Biol. Chem. 262:10475-10480(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli, and
Escherichia coli 0157:H7.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.8%; Score 8; DB 1; Length 167;
100.0%; Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL PROTEIN YLXL. 356021A73B679B69 CRC64;
                                                                                                                                                                                                                                                                                                                                                            EMBL; M20144; ...-
Subtilist; BG10752; ylxL.
Hypothetical protein; Signal; Complete proteome.
19 POTENTIAL.
19 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1988 (Rel. 08, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNAC replication protein dnaC.
DNAC OR DNAD OR B4361 OR Z5961 OR ECS5321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                       SEQUENCE OF 1-67 FROM N.A. MEDLINE-88169477; Pubmed-2832368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-87280100; PubMed-3301836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-89008392; PubMed-2844800;
                                                                                                                                                                                                                                                                                                                                                                                                                          167 AA; 19119 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.08;
                                                                                                                                                                                                                                                                                                                                                EMBL; 299112; CAB13521.1;
                                                                                                                              Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia.
NCBL_TaxID=562, 83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267 LKEENEKL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 LKEENEKL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNAC_ECOLI
P07905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-K12
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNAC_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Masai H., Bond M.W., Arai K.-I.;
"Cloning of the Escherichia coli gene for primosomal protein i: the relationship to dnar, essential for chromosomal DNA replication.";
Proc. Natl. Acad. Sci. U.S.A. 83:1256-1266(1986).

-!- FUNCTION: THIS PROTEIN IS REQUIRED FOR CHROMOSOMAL REPLICATION. IT FORMS, IN CONCERT WITH DNAB PROTEIN AND OTHER PREPRIMING PROTEINS DNAT, N. N. N. N. A PREPRIMING PROTEIN COMPLEX ON THE SPECIFIC SITE OF THE TEMPLARE DNA RECOGNIZED BY PROTEIN N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Complete genome sequence of enterchemorrhadic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=0157:H7 / EDL933 / ATCC 700927;

MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROBABLY INVOLVED IN THE INTERACTION WITH THE DNAB PROPEIN.

D -> A (IN REF. I AND 6).

CSCC7232221FIIFI CRC64;
                                                                                                                                                                                                              "Analysis of the Escherichia coli genome VI: DNA sequence of the
                                                                                                                                 Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA replication; Primosome; Complete proteome.
                                                                                                                                                                                                                                                  region from 92.8 through 100 minutes."; Nucleic Acids Res. 23:2105-2119(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-0157:H7 / RIMD 0509952;
MEDLINE-21156231; PubMed=11258796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=86149284; PubMed=3006041;
                                                                                            MEDLINE=95334362; PubMed=7610040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003593; AAA_ATPase.
SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1030.3, 6TH EDITION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE000507; AAC77317.1; -. EMBL; AE005667; AAG59544.1; -. EMBL; AP002569; BAB38744.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27935 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; J04030; AAA23700.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U14003; AAA97260.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-14 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EcoGene; EG10237; dnaC.
InterPro; IPR003593; AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A28484; XMECNC
PIR; B25124; B25124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245 AA;
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69
```

Length 245;

DB 1;

Score 8;

0.88;

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                   SECONDENCE FROM N.A.
STRAIN=cv. Columbia; TISSUE=Green siliques;
Schoefil F., Praendl R., Praendl R.,
"De-repression of heat shock protein synthesis in transgenic plants.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                 Autoloopsis thaliana (Mouse-ear cress).
Bukaryota, Viidiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; Rosidae,
eurosids II; Brassicales; Brassicaceae, Arabidopsis.
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Structural analysis of Arabidopsis thaliana chromosome 5. VII. Sequence features of the regions of 1,013,767 bp covered by sixteen physically assigned Pl and TAC clones.";
DNA Res. 5:297-308(1998).
-!- FUNCTION: DNA-BINDING PROTEIN THAT SPECIFICALLY BINDS HEAT SHOCK PROMOTER ELEMENTS (HSE) AND ACTIVATES TRANSCRIPTION (BY SIMILARITY).
                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Heat shock factor protein 6 (HSF 6) (Heat shock transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-cv. Columbia;
MEDLINE-99087489; Pubmed-9872454;
Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA-binding; Activator;
                               ö
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: HÖMOTRIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Nuclear (By similarity).
PTM: EXHIBITS TEMPERATURE-DEPENDENT PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04D86398693B1997 CRC64;
                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PSO0434; HSF_DOMAIN; 1. Transcription regulation; Nuclear protein; DNA Phosphorylation; Heat shock; Multigene family.
               Pred. No. 5.9;
                                                                                                                                                                                   299 AA
                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY POLY-ASN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE HSF FAMILY.
                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00056; HSFDOMAIN.
ProDom; PD001788; HSF_DNA_bind; 1.
SMART; SM00415; HSF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P22813; 1HKT.
InterPro; IPR000232; HSF_DNA_bind.
InterPro; IPR002341; HSF_ETS.
Pfam: PF00447; HSF_DNA-bind; 1.
100.08; Pt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AJ251867; CAB63802.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AB016880; BAB10163.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34051 MW;
                                                                                                                                                                                                                                                                                     6) (HSTF 6).
HSF6 OR AT5G62020 OR MTG10.4.
                               8; Conservative
                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             299 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY)
               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                               943 GTSEEQLL 950
                                                                                  150 GTSEEQLL 157
                                                                                                                                                                                   HSF6_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
SEQUENCE
                                                                                                                                                 RESULT 6
HSF6_ARATH
                             Matches
                                                                ó
                                                                                              qq
```

```
ö
                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Stomach;
Karlisen S., Hough E., Olsen R.L.;
Structure and proposed amino-acid sequence of a pepsin from Atlantic cod (Gadus morhus).";
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        Gadus morhua (Atlantic cod).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Deleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interruc, and interruce, and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=DSM 571;
van Rinsum A.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
submitted (MAR-1998) to PROBABLY INVOLVED IN FATTY ACID OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thermosaccharolyticum).
Bacteria, Firmicutes; Clostridia; Thermoanaerobacteriales;
Length 299
                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium thermosaccharolyticum (Thermoanaerobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-077-2001 (Rel. 40, Last annotation update)
Fatty acid/phospholipid synthesis protein plsx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermoanaerobacteriaceae; Thermoanaerobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COURT CIVETAILOGY. D 54:32-46(1998).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY Al.
PDB; 1AM5; 24-DEC-97.
InterPro; IPR001461; Aspprotease_site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
DB 1;
                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 41, Last annotation update)
Pepsin IIB (EC 3.4.23.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   333 AA.
                                                                                                                                                                                                                                                                          324 AA
                       red. No. 7;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 7.(
Mismatches
                         Pred. No.
0.8%; Score 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE, AND X-RAY CRYSTALLOGRAPHY.
                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.5°,
100.0%; Pre-
0,
0.00,
100.08; Pie
                                                 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 8; Conserv
                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                               269 EENEKLRS 276
                                                                                                                            177 EENEKLRS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         376 SQSLVEKD 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 SQSLVEKD 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLSX_CLOTS
O65984;
                                                                                                                                                                                                                                                                          PEP1_GADMO
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLSX_CLOTS
                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLSX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
                                                                                                  ò
                                                                                                                                              da
                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

752 AA.

9

```
-!- SUBCELLULAR LOCATION: Mitochondrial.
-!- TISSUB SPECIFICITY: DETECTED IN ALL TISSUES WITH THE HIGHEST LEVEL IN LIVER, THYMOS AND BRAIN.
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-G/EF-2 SUBFAMILY.
                                                                                                                                                                                                                                                                                                     factor G in mammals.";
Nucleic Acids Res. 21:2641-2647(1993)
-!- FUNCTION: THE PROPEIN PROMOTES THE GTP-DEPENDENT TRANSLOCATION
OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE
                                                                                                                                                                        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-93324327; PubMed-8332461; Barker C.S., Makris A., Patriotis C., Bear S.E., Tsichlis P.N.; "Identification of the gene encoding the mitochondrial elongation
                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi;
                                                     01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Elongation factor G, mitochondrial precursor (MEF-G).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP, P1351; TFNM.
InterPro: IPR004540; EF-G.
InterPro: IPR00040; EF-G.
InterPro: IPR0004161; EFTU_D2.
InterPro: IPR000795; EF_GTPbind.
InterPro: IPR0005255; Small_GTP.
Pfam; PF00009; GTP_EFTU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.55,
100.08; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83770 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L14684; AAA41107.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S40780; S40780.
                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            752 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           429 QRLVRMHA 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                396 QRLVRMHA 403
                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YH07_VACCV
P17357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NP_BIND
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
                     δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycoplasma pneumoniae.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.8%; Score 8; DB 1; Length 381;
100.0%; Pred. No. 8.8;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                               Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Very hypothetical mgpC-like protein MPN503 (P02_orf381).
MPN503 OR MP339.
                                                                                                                                                                                                                                                                                                       Phospholipid biosynthesis.
0 MW; 8A932B1A96D88EC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     al protein; Complete proteome.
381 AA; 40896 MW; 5CFD05505E344852 CRC64;
                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                   0.8%; Scor
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           381 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pneumoniae.";
Nucleic Acids Res. 24:4420-4449(1996).
-!- SIMILARITY: BELONGS TO THE MGPC FAMILY.
PHOSPHOLIPID SYNTHESIS (BY SIMILARITY). SIMILARITY: BELONGS TO THE PLSX FAMILY.
                                                                                                                                                                                                          EMBL; AJ004870; CAA06178.1; ALT_INIT.
InterPro; IPR003664; FA_Synthesis.
Pfam; PF02504; FA_Synthesis, 1.
ProDom; PD006974; FA_Synthesis; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129; '
MEDLINE-97105885; Pubmed-8948633;
                                                                                                                                                                                                                                                                                                                         333 AA; 35930 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE000032; AAB95987.1; -
                                                                                                                                                                                                                                                                  ProDom; PD006974; FA_synthesi:
TIGRFAMS; TIGR00182; plsx; 1.
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                   Fatty acid biosynthesis; SEQUENCE 333 AA; 35930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1111111
241 LLKQELOR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                          228 LLKQELQR 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      447 LVSSTESQ 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 LVSSTESQ 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Herrmann R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YF03_MYCPN
P75283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
```

Db

ò

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 8; DB 1; Length 752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELONGATION FACTOR G.
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
W. DFBA6108D38A72E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                           Pram; PF00679; EFG_C; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
TIGRFAMS; TIGR00231; Small_GTP: 1.
PROSTIE; PS00301; EFGCTOR_GTP: 1.
PROSTIE; PS00301; EFACTOR_GTP: 1.
Transit peptide; GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 15, Created)
(Rel. 15, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 16;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P1/35/;
01-AUG-1990 (
01-AUG-1990 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YH07_VACCV

ID YH07_VP

AC P17357;

DT 01-AUG-

DT 01-AUG-
```

RESULT 10

q

ó

```
NON_TER
SEQUENCE
                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
                                                                                                                                                                                                                                RESULT 13
CHLB_PLESC
                                                                                                                                                                                                                                                                                                                                                          CHLB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
  DR DR DR DR SQ SQ
                                                                                                                                                                δλ
                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                       ō
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Li N., Cannon M.C.;

"Gas vesicle genes identified in Bacillus megaterium and functional expression in Escherichia coli."

"Bacteriol. 180:2450-2458 (1998).

"In FUNCTION: Gas vesicles are small, hollow, gas filled protein structures that are found in several microbial planktonic microorganisms. They allow the positioning of the organism at the favorable depth for growth. Gypa type proteins form the essential core of the structure.

"SUBCELLULAR LOCATION: GAS VESICLE MEMBRANE."

"SUBCELLULAR LOCATION: GAS VESICLE PROTEIN TYPE A FAMILY.
                          Vaccinia virus (strain WR).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                        MEDLINE-89073756; PubMed-2849238; Kotwal G.J., Moss B.; Analysis of a large cluster of nonessential genes deleted from vaccinia virus terminal transposition mutant."; virology 167:524-537(1988).
                                                                                                                                                                                                                                                                                                                                                                                                 .;
                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                    Length 68;
                                                                                                                                                                                                                                                                                                             PIR; B31829; WZVZA2.
Hypothetical protein; Early protein.
SEQUENCE 68 AA; 7814 MW; 47DF7558D134D949 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Gas vesicle structural protein B (GVP B).
01-FEB-1991 (Rel. 17, Last annotation update)
Hypothetical 7.8 kDa HINDIII-C protein.
                                                                                                                                                                                                                                                                                                                                                                   Score 7; DB 1;
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                            0.7%; Scor.
100.0%; Pred. No. 1...
7. 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=VT1660;
MEDLINE=98233742; PubMed=9573198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF053765; AAC38416.1; -.
                                                                                                                                                                                                                                                                                                  EMBL; M22812; AAA69593.1; -.
                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 100.vv
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus megaterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                           SEQUENCE FROM N.A.
                                                                  NCBI_TaxID=10254;
                                                                                                                                                                                                                                                                                                                                                                                                                         702 VLHVTDT 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1404;
                                                                                                                                                                                                                                                                                                                                                                                                                                        111111
36 VLHVTDT 42
                                                       Orthopoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUN-2002 (
15-JUN-2002 (
15-JUN-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVPB_BACME
068677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
GVPB_BACME
 ô
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96426856; PubMed=8812302;
A Boivin R., Richard M., Beauseigle D., Bousquet J., Bellemare G.:
Boivin R., Richard M., Beauseigle D., Bousquet J., Bellemare G.:
Thylogenetic inferences from chloroplast chilb gene sequences of
The sequences of an experimental sequences of and diverse land plants.
The sequences and plants.
The sequences of an experimental sequences of and diverse land plants.
The sequence of the sequence of the sequences of composition of protochlorophyllide (Pohlide) to form chlorophyllide a (Chlide)
C protochlorophyllide (Pohlide) to form chlorophyllide a (Chlide)
C PATHWAY: Light-independent chlorophyll biosynthesis.
C II SUBUNIT: Protochlorophyllide reductase is thought to be composed of three subunits; chil., chln and chlb. Could form a heteroteetramer of two chila and two chila subunits (By similarity).
C II SIMILARITY: BELONGS TO THE CHLB / BCHB / BCHZ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000510; Oxred_nitrognsel.
Pfam; PF00148; oxidored_nitro; 1.
Oxidoreductase; Photosynthesis; Chlorophyll biosynthesis; Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Bryidae; Hypnales; Hylocomiaceae; Pleurozium.
NCBL_TaxID=34163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Light-independent protochlorophyllide reductase subunit B
(EC 1.18...) (LI-POR subunit B) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.7%; Score 7; DB 1; Length 100;
100.0%; Pred. No. 27;
live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                   Length 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 AA; 11659 MW; 40B101BE6D66B5E0 CRC64;
                                                                                                                                                                                                               5F089DE77358D84A CRC64;
                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                            0.7%; Score 7; DB 1
100.0%; Pred. No. 24;
iive 0; Mismatches
InterPro; IPR000638; Gas_vesicle.
Pfam: PF00741; Gas_vesicle: 1.
Pr000m: PD003358; Gas_vesicle: 1.
PROSITE: PS00234; GAS_VESICLE.A_1: 1.
PROSITE; PS00669; GAS_VESICLE_A_2: 1.
                                                                                                                                                                                                               9618 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pleurozium schreberi (Moss).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L25774; AAC37495.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Conservative
                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                               88 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           662 KRLLQDL 668
                                                                                                                                                                                                                                                                                                                                                                                                                   638 EAVGLLR 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 EAVGLLR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||||||||
1 KRLLQDL 7
                                                                                                                                                                                  Gas vesicle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHLB_PLESC
```

œ

```
STRAIN-ATCC 50394;
    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                              Definition of the composition of the composition of three subunits; childen to the childen to the composition of three subunits; childen the childen to the composition of three subunits; childen the childen to the composition of three subunits; childen the childen to the composition of three subunits; childen the childen the childen to the composition of three subunits; childen the chi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000510; Oxred_nitrognsel.
Pfam; PF00148; oxidored_nitro; 1.
Oxidoreductase; Photosynthesis; Chlorophyll biosynthesis; Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                           Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Polytrichopsida; Polytrichaceae; Polytrichum.
NCBI_TaxID=3213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·,
                                                                                                                01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Light-independent protochlorophyllide reductase subunit B
(EC 1.18.-.-) (LI-POR subunit B) (Pragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.7%; Score 7; DB 1; Length 100;
100.0%; Pred. No. 27;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11573 MW; 984F131F432400A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Mitochondrial 60s ribosomal protein L14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 AA
                                                                     100 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; core jakobids; Reclinomonas
NCBI_TaxID=48483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-96426856; PubMed-8812302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L25772; AAC37494.1; -.
                                                                                                                                                                                                                                                        Polytrichum commune (Moss).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reclinomonas americana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 AA;
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          662 KRLLQDL 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KRLLQDL 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitochondrion.
                                                                CHLB_POLCU
P37852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RM14_RECAM
021251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
RM14_RECAM
                          RESULT 14
CHLB_POLCU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPL14
                                                                                                                                                                                                                                  CHLB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
MEDLINE-97311393; PubMed-9168110;
Lang B.F., Burger G., O'Kelly C.J., Cedergren R., Golding G.B.,
Lemieux C., Sankoff D., Turmel M., Gray M.W.;
"An ancestral mitochondrial DNA resembling a eubacterial genome in
                                                                                                                                                 Nature 387:493-497(1997).
-!- SUBCELLULAR LOCATION: Mitochondrial.
-!- SIMILARITY: BELONGS TO THE L14P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13415 MW; F942C64410D4EE53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.7%; Score 7; DB 1;
100.0%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: January 22, 2003, 08:58:42
Job time : 20 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P04450; IWHI.
InterPro; IPR000218; Ribosomal_L14.
Pfam: PF00238; Ribosomal_L14; 1.
ProDom: PD001093; Ribosomal_L14; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGREAMS; TIGRO1067; rplN bact, 1.
PROSITE; PS00049; RIBOSOMAL_L14; 1.
Ribosomal protein; Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF007261; AAD11878.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             769 KLVRIVS 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 KEVRIVS 116
                                                                                                                              miniature.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
```

Q8yd70 brucella me Q9u2yl caenorhabdi Q18807 caenorhabdi

OByrg2 anabaena sp O9rwc4 deinococcus O97ps5 streptococc

Q9h6g7 homo sapien Q9m218 arabidopsis Q60552 mesocricetu

Q8xQ66 meurospora Q9m4t7 arabidopsis Q9c53 arabidopsis Q9f2f5 streptococc Q8rsb5 halomonas c Q9bkq7 caenorhabdi Q43061 porphyridiu Q43061 porphyridiu Q9fhk7 arabidopsis Q9zvq1 rhizobium m Q9zvq1 ralstonia s Q8xvq1 ralstonia s Q8xvq1 caenorhabdi

Word size :

Searched:

Sequence:

Minimum DB Maximum DB

Database :

Q924i0 mus musculu Q92id6 mus musculu Q23529 caenorhabdi O15083 homo sapien Q9acu8 streptomyce

OM protein

Run on:

```
SEQUENCE FROM N.A.
Witthuhn V.C. Jr., Donohue T.J.;
Witthuhn V.C. Jr., Jr.,
Witthuhn V.C. Jr.,
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AF435819; AAL30776.1;
SEQUENCE 390 AA: 41929 MW; BDA7AC33D3F5AE84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
Rhodobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 10; DB 2; Length 390;
Pred. No. 0.33;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                08YRQ2
09RRQ4
09PR55
09H67
09M218
060552
08X0E6
09M477
09E2F5
09E2F5
09E7F7
043060
043060
043060
092YRQ7
092YRQ7
092YRQ7
092YRQ1
092YR
Q9FIG5
Q9ZSE0
Q8YD70
Q9U2Y1
Q18807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 1.0%; Sc
Local Similarity 100.0%; P
hes 10; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 20, (TrEMBLrel. 20, I
                                                                                                                                                               10
                                                                                                                                                                                          2
2
2
10
10
16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  031661;
01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         308 LRERAVAAER 317
 NCBI_TaxID=1063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002
01-MAR-2002
 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     031661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8VV27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GfdT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       031661

1D 03

AC 03

DT 03

DT 03
 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          031661 bacillus su
Obnft4 trichomonas
Ogfry1 ceratopteri
Obhcg3 homo sapien
095u22 drosophila
P91635 drosophila
08vu84 homo sapien
08vu84 homo sapien
08vu84 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8th14 methanosarc
Q99ug3 staphylococ
Q9an71 bradyrhizob
Q9fsr5 oryza sativ
O58907 pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08vvz7 rhodobacter
                                                                                                       (without alignments)
4309.819 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                          I MGELCRRDSALTALDEETLW.......VRQAIADEQKKVVWTEQSPR 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                             ; Search time 48 Seconds
            5.1.3
Compugen Ltd.
                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                             671580 segs, 206047115 residues
            GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                     summaries
                                                                protein search, using sw model
                                                                                          2003, 08:54:50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9FRY1
Q9HCQ3
Q95U22
P91635
Q8WU84
Q9W1M7
Q8TES3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .Q8VVZ7
6 031661
Q9NFT4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q99UQ3
Q9AN71
                                                                                                                                                                                                     OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8THL4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_human:*
sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Listing first 45
                                                                                                                                                                                                                                                                                                                                                                                                            sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                                                            seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
11
12
12
17
                                                                                                                                                 US-09-767-215-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                          January 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               00000000000000
                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perfect score:
                                                                                                                                                                                                       Scoring table:
```

ö

;

Result No.

11110084311008431110084311110084311

YKRQ protein.

435 AA

```
MEDLINE=20382201; PubNed=10928457;
Bricheux G., Coffe G., Bayle D., Brugerolle G.;
Bricheux G., Coffe G., Bayle D., Brugerolle G.;
"Characterization, cloning and immunolocalization of a coronin homologue in Trichomonas vaginalis.";
Bur. J. Cell Biol. 79:413-422(2000).
-!- SIMILARITY: CONTAINS 2 WD REPEATS (TRP-ASP DOMAINS).
BMBL; AJ271374; CAB76208.1;
-- InterPro; IPR001680; WD40.
Prodom: PP00400; W040.
Prodom: PP00400; W040.
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Parabasalidea; Trichomonadida; Trichomonadidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50082; WD_REPEATS_2; 2.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
Repeat; WD repeat.
SEQUENCE 435 AA, 48204 MW; F63ADC16D5DCE6C5 CRC64;
                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=HNN, TISSUE=SHOOT APEX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ceratopteris richardii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM00320; WD40;
                                                                                                                                                                                                                                                                                                                 Prichomonas vaginalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            267 LKEENEKLR 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=5722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                 Coronin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRKNOX1
                                                                                                    O9NFT4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRKNOX1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9FRY1
                                                                    Q9NFT4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4atches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
RESULT 3
                                   Q9NFT4
                                                                                                    ōλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC CON REPARED DRAWN REPARED BRANK REPARED B
                                                                                                                                                                                                                                                                                            Runst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouillet S., Boursler L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Britz C., Fulita M., Fulita Y., Emril S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Pabret C., Ferrari E., Foulger D.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kurita K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Kurita K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Mone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Brescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Sato T., Scanlan E., Schleich S., Schroeber, Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeber, Rose M., Sator T.,
RA Takeuchi M., Tamakoshi A., Takagi T., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Takagi T., Takemaru R.,
RA Takeuchi M., Tamakoshi A., Takagi T., Takemaru R.,
RA Takeuchi M., Wannelte R., Wedler H., Weitzeneyger T.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA The complete genome sequence of the gram-positive bacterium Bacillus
RH The complete genome sequence of the gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                     Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales; Bacillacea; Bacillus.
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.0%; Score 10; DB 16; Length 738;
100.0%; Pred. No. 0.58;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00091; PAS; 4.
TIGREAMs; TIGR00229; sensory_box; 4.
Kinase; Phosphorylation; Sensory transduction; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        738 AA; 85513 MW; FE27DAB7F08AC64B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, 29911; CAB13266.1;
InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR003661; His_KinA.
InterPro; IPR003661; His_KinA.
InterPro; IPR0001459; HIS_KIN_Sig.
InterPro; IPR000149; PAS_domain.
Pfam; PF00512; HATPase_c; 1.
PRIWTS; PR00344; BCTRLSENSOR.
SMART; SM00387; HATPase_c; 1.
SMART; SM00388; HisKA; 1.
SMART; SM00091; PAS; 4.
                                                                                                                                                                                                                                                                          MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 EELNRLKEEN 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                   Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome
SEQUENCE 738 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-168;
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sano R., Juarez C., Ito M., Basebe M.;
"KNOX class of homeobox genes potentially have similar function in both sporophytic unicellular and multicellular meristems, but not in gametophytic meristems.";
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Filicophyta; Filicophyta; Filicales; Pteridaceae; Ceratopteris.
NCBL_TaxID=49495;
                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 512;
Length 435;
                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AB043954; BAB18582.1; -.
HSSP; P41778; 1DU6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3EBFCE074AAE080B CRC64;
                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.9%; Score 9; DB 10; 100.0%; Pred. No. 4.7;
  Score 9; DB 5;
Pred. No. 4.1;
            100.0%; Pred. nc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00027; HOMEDBOX_1; UNKNOWN_1.
PROSITE; PS50071; HOMEDBOX_2; 1.
SROUENCE 512 AA; 57195 MW; 3EBFCE074!
                                                                                                                                                                                                                                                                                                                      01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
```

qq

ò

.; 0

qq

ò

```
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
1-phosphatidylinositol 3-kinase (EC 2.7.1.137) (PI3-kinase) (PtdIns-3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last amnotation update)
Hypothetical 113.9 kDa protein (Fragment).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 949;
  Length 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   949 AA; 107878 MW; 4867E3ECD1E22EEC CRC64;
                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5;
8.2;
DB 5;
                                                                                                                                                                                                                                                                                                     949 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1020 AA
                      100.0%; Pred. No. 8.2
live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.9%; Score 9; DB 5100.0%; Pred. No. 8.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00613; P13Ka; 1.
Pfam; PF00452; P13K_C2; 1.
Pfam; PF0045; P13K_C2; 1.
SMART: SW00145; P13Ra; 1.
SMART; SW00145; P13Ra; 1.
SMART; SW00142; P13Kc; 1.
PROSITE; PS00916; P13_4_KINASE_1; 1.
PROSITE; PS00916; P13_4_KINASE_2; 1.
PROSITE; PS00909; P13_4_KINASE_2; 1.
  0.9%; Score 9;
                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PI3K59F OR PI3K-59F OR CG5373.
                                                      9; Conservative
                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                      Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
tes 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=OREGON R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       456 LSDLSATSS 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       456 LSDLSATSS 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7227;
                                                                                                                                            443 LSDLSATSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transferase
SEQUENCE
  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                           RESULT 7
P91635
ID P91635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8WU84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8WU84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8WU84
                                                                                                             δý
                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Champe M., Charlin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
X. C., Lewis S.E., Rubin G.M., Celniker S.;
Champered (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AV058362; AAL13591.1;
ENBL, AV058362; AAL13591.1;
ENBL, AV058362; AAL13591.1;
ENBLS, AV058362; AAL13591.1;
ENBLS, AV058362; AAL13591.1,
ENBLS, AV058362; AAL13591.1,
ENGLS, AV058362; AAL13596CC09A3F3A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 759,
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "HCMOGT-1.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB041533; BAB16440.1; -.
SEQUENCE 759 AA; 84920 MW; A88E5B53B3E4269A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 100.0%; Score 9; DB 4; Similarity 100.0%; Pred. No. 6.7; 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                              759 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        949 AA
Mismatches
                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
9; Conservative
                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                   470 SFRSSSPAP 478
                                                                                   111111111
255 SFRSSSPAP 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           266 RLKEENEKL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          480 RLKEENEKL 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GH13170p.
PI3K59F OR CG5373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                  Sperm antigen.
HCMOGT-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Komori S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                           09нс03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        095022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
095022
10 095022
095022
001-D
DT 01--D

Matches
                                                                                                                                                                                     RESULT 5
09HCQ3
1D 09HCQ4
AC 09HCQ5
DT 01-M2
DT 01-M3
DT 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
```

ŏ Q ; 0

```
Q9H6O4
ID Q9H6O4
AC Q9H6O4;
DT 01-MAR-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8TES3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8TES3
QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAY AMBDLINE-2UJ9000B; Pubmed-10731132;

RA Admanatides P.G. Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G. Scherer S.E., Ilp P.W., Hoskins R.A., Galle R.F.,

RA CGOTGE R.A., Least S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Abliew R.M., Basu A., Baxendale J.P., Bhandari L., Beasley E.M.,

Ra Borkova D., Botchan M.R., Bouck J., Byraktaroglu L., Beasley E.M.,

Ra Borkova D., Botchan M.R., Bulker H., Cadleu E., Center A., Chandra I.,

Rosson K.Y., Bennos P.V., Bernan B.P., Bhandari D., Bolshakov S.,

Ra Borkova D., Botchan M.R., Bulker H., Cadleu E., Center A., Chandra I.,

Ra Borkova D., Botchan M.R., Bulker H., Cadleu E., Center A., Chandra I.,

Ra Borkova D., Botchan M.R., Bulker H., Cadleu E., Center A., Chandra I.,

Ra Borkova D., Botchan M.R., Bulker H., Cadleu E., Center A., Chandra I.,

Ra Borkova D., Botchan M.R., Bulker H., Cadleu E., Center A., Chandra I.,

Ra Borkova D., Botchan M.R., Bouck J., Harris P.,

Ra Durbin K.J., Evangelista C.C., Ferraz C., Ferraz
                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
P13K59F protein.
P13K59F or CG5373.
Drosophila melanogaster (Fruit fly).
Brkaryota: Merazoa Arthropoda: Tracheata; Hexapoda; Insecta;
Pterygota; Merazoa Arthropoda: Diptera; Brachycera; Muscomorpha;
Ephydroidea: Drosophilidae; Drosophila.
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                         Length 1020;
                            Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: BC021123; AAH21123.1;
INTERPO: IRR007115; Calponin-like.
Pfam: PF00307; CH: 1.
SMART: SM00033; CH: 1.
Hypothetical protein.
                                                                                                                                                           NON_TER 1 1 SEQUENCE 1020 AA; 113890 MW; 1F1D124CDF6AC8A3 CRC64;
                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                          DB 4;
8.8;
                                                                                                                                                                                               0.9%; Scc.
100.0%; Pred. No. c
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1157 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BERKELEY;
MEDLINE=20196006; Pubmed=10731132;
                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                          266 RLKEENEKL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                        463 RLKEENEKL 471
SEQUENCE FROM N.A.
                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                         09W1M7
                                                                                                                                                                                                                                                                                                                                                      RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                          õ
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
             Zheng L.,
Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohara O., Nagase T., Kikuno R., Okumura K.; "The nucleotide sequence of a long cDNA clone isolated from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
A Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhen Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smit Gibbs R.A., Wagers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";

Excience 287:2185-2195(2000).

"R EmBuf, AE003461; AAF47030.1; -.

"Interpro; IPR0010577; P3859F.

Interpro; IPR001217; PhospholipaseA2.

"Interpro; IPR001219; PhospholipaseA2.

"Interpro; IPR0012429; P13K_C2.

"Interpro; IPR000403; P13K_C2.

"Interpro; IPR000403; P13K_C2.

"Interpro; IPR001403; P13K_C2. 1.

"R Pfam; PF001513; P13K 2.1.

"R Pfam; PF00145; P13K 2.1.

"R SMART; SM00145; P13K 2.1.

"R PROSITE; PS00145; P13K_C2. 1.

"R PROSITE; PS00118; PAZ_HIS; UNRNOWN_1.

"R PROSITE; PS00118; PAZ_HIS; UNRNOWN_1.

"R PROSITE; PS00118; P13_4 KINASE_2: 1.

"R PROSITE; PS00116; P13_4 KINASE_2: 1.

"R PROSITE; PS00116; P13_4 KINASE_2: 1.

"R PROSITE; PS00116; P13_4 KINASE_3: 1.

"R PROSITE; PS00116; P13_4 KINASE_3: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1171 AA; 134966 MW; FA567ABBC8A703FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases EMBL; AK074049; BAB84875.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.9%; Score 9; DB 4;
100.0%; Pred. No. 9.9;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1171 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 9; L
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLJ00120 protein (Fragment). FLJ00120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    674 TSGDSFYIR 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11111111
788 TSGDSFYIR 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          456 LSDLSATSS 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          443 LSDLSATSS 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               spleen."
```

S

```
"Potential symbiosis-specific genes uncovered by sequencing a 410-kb DNA region of the Bradyrhizobium japonicum chromosome."; J. Bacteriol. 183:1405-1412(2001). Sectoriol; AR322013; AAG60905.1; SEQUENCE 223 AA; 25398 MM; 6F86C3C1D5D70315 CRC64;
                                                                                                                                                                                                                                                                                         SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
MEDLINE=21311952; PubMed=11418146;
MEDLINE=21311952; PubMed=11418146;
MEDLINE=21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchlyama I., Baba T., Yuzawa H., Kobayashi I.,
Kuroda M., Ohta T., Uchlyama I., Baba T., Yuzawa H., Kobayashi I.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R. I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizobium group; Bradyrhizobium.
                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gottfert M., Rothlisberger S., Kundig C., Beck C., Marty R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP003361; BAB57377.1; -
EMBL; AP003133; BAB42310.1; -
InterPro; IPPO0181; PPP_deformylase.
Pfam; PF0137; PPP_deformylase; 1.
PRINTS; PR01576; PDEFORMYLASE
ProDom; PD003844; PPP_deformylase; 1.
Hypothetical protein; Complete protecome.
SEQUENCE 162 AA; 18102 MW; 8E22824A4B2945AF CRC64;
                                                                                             Hypothetical protein SAV1215.
SAV1215 OR SA1058.
Staphylococcus aureus (strain Mu50 / ATCC 700699), and staphylococcus aureus (strain N315).
                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.8%; Score 8; DB 2; Best Local Similarity 100.0%; Pred. No. 25; Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. No. 19; ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=110SPC4;
MEDLINE=21101824; PubMed=11157954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lancet 357:1225-1240(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity luv...
8; Conservative
                                                                                                                                                                                                                                              NCBI_TaxID=158878, 158879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bradyrhizobium japonicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          662 KRLLQDLE 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 LDLLKTRG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=375;
                                                                                                                                                                                                                            Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (
01-JUN-2001 (
01-JUN-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hennecke H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09AN71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9AN71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ID481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ID481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9AN71
     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-C2A / ATCC 35395 / DSM 2834;
STRAIN-C2A / ATCC 35395 / DSM 2834;
MEDLINE-21929760; PubMed=11932238;
Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P., FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A., Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R., Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W., Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M., Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A., Hedderich R., Jim Y., Liu J., Mukhoppadhyay B., Reeve J.N., Smith K., Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C., Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
                                                                                                                                                                                                                          Okamoto S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The genome of Methanosarcina acetivorans reveals extensive metabolic and physiological diversity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE-SMALL INTESTINE;
Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto
Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
Tanaka T., Nakamura Y., Isogai T., Sugano S.;
Tanaka T., Nakamura Y., Isogai T., Sugano S.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AK026370; BAB15463.1; --
SEQUENCE 143 AA; 15296 MW; C1CRCF31219EBDF9 CRC64;
                                 Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 17; Length 157;
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea, Buryarchaeota, Methanococci, Methanosarcinales, Methanosarcinaceae, Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 AA; 18084 MW; A4ADC6D2CBA197AF CRC64;
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA: FLJ22717 fis, clone HSI13737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                 0.8%; Score 8; DB 4;
100.0%; Pred. No. 17;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 8; I
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Res. 12:532-542(2002).
EMBL; AEO11170; AAM07840.1; -.
Complete proteome.
SEQUENCE 157 AA; 18084 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.8%; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methanosarcina acetivorans.
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.8
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Predicted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    474 SSPAPPSQ 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         637 EEAVGLLR 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1111111
106 EEAVGLLR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 SSPAPPSQ 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=2214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Metcalf W.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8THL4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 099003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8THL4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          099003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8THL4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HDD COCCOS OCC COCCOS OCCOS OC
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

·:

Gaps

0;

0; Indels

223 AA.

Length 162;

DB 16;

ó

Gaps

; 0

Indels

Length 223;

```
the Han B., Zhou B., Feng Q., Huang Y.C., Chen Z.H., Li Y., Zhu J.J.,
Han B., Zhou B., Feng Q., Huang Y.C., Chen Z.H., Li Y., Zhu J.J.,
A Tang Y.S., Zhao Q., Liu Y.L., Wu J., Yu Z., Fan D.L., Chen L.,
Weng Q.J., Zhang D., Lu Y.Q., Yu S.L., Zhu J., Liu X.H. W.X.,
Lei H.Y., Zhang Y.J., Wang R., Li C., Lu Y., Chen X.C., Zhang Y.,
Hu H.Y., Jia P.X., Li T., Qian Y.M., Ying K., Hong G.F.;
A Hu H.Y., Ja P.X., Li T., Qian Y.M., Ying K., Hong G.F.;
Coryza sativa indica (Guangluai4) genomic DNA, chromosome4, BAC
R. Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
L. Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
REL: AL42007; CAC09359.1; -.
REL: AL42007; CAC09359.1; -.
REL: AL42007; Homeobox.
RICEPRO; IPR001036; Homeobox.
ROSITE: PS50071; HOMEOBOX. 1.
ROSITE: PS50071; HOMEOBOX. Nuclear protein.
SEQUENCE 262 AA: 29004 MW; CS4C573691F8CBF8 CRC64;
                                                                                                                                                                                                                                               OPESR5

OPERAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2001 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.8%; Score 8; DB 10; Length 262; 100.0%; Pred. No. 29; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.0
Matches 8; Conservative
11111111
29 LDLLKTRG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                   RESULT 15
                                                                                                                                                                                                                                 Q9FSR5
                                                  q
```

Search completed: January 22, 2003, 08:59:39 Job time : 54 secs

473 SSSPAPPS 480 

qq οy

ö

Gaps

ô

```
January 22, 2003, 08:49:35; Search time 20.8535 Seconds (without alignments) 683.714 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ALTALDEETLWEMMESHRHR......PDVYTLVTGLQPDVDFSNFS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . DAT: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980. DAT: */SIDS2/gcgdata/geneseqy-emb1,AA1981. DAT: */SIDS2/gcgdata/geneseqyeneseqp-emb1,AA1981. DAT: */SIDS2/gcgdata/geneseqyeneseqp-emb1,AA1981. DAT: */SIDS2/gcgdata/geneseqyeneseqp-emb1,AA1981. DAT: */SIDS2/gcgdata/geneseqyeneseqp-emb1,AA1981. DAT: */SIDS2/gcgdata/geneseqyeneseqp-emb1,AA1981. DAT: */SIDS2/gcgdata/geneseqyeneseqp-emb1,AA1986. DAT: */SIDS2/gcgdata/geneseqyeneseqp-emb1,AA1986. DAT: */SIDS2/gcgdata/geneseqyeneseqp-emb1,AA1988. DAT: */SIDS2/gcgdata/geneseqyeneseqyeneseqp-emb1,AA1988. DAT: */SIDS2/gcgdata/geneseqyeneseqyeneseqyeneseqp-emb1,AA1988. DAT: */SIDS2/gcgdata/geneseqyeneseqyeneseqp-emb1,AA1988. DAT: */SIDS2/gcgdata/geneseqyeneseqyeneseqyeneseqp-emb1,AA1988. DAT: */SIDS2/gcgdata/geneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyeneseqyene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1989.DAT:*/SIDS2/gcgdata/geneseg/genesegp-emb1/AA1990.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT.
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT.
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                908470
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTIMANDIDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-767-215-2_COPY_10_116
560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                       - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A_Geneseq_101002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                       OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
                                                                                                                                                                                                                                                                                                                                     Run on:
```

					SUMMAKIES	
		æ				
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
-	560	100.0	:	22	AAE07164	Human Caspase recr
7	260	100.0		22	AAE07165	Human predicted ca
m	270	48.2		22	AAU01207	Human caspase recr
4	246	43.9		22	AAU01206	Human caspase recr
Ŋ	246	43.9	1032	23	AAU73247	Human plakoglobin
9	217	38.8		22	AAU01204	Rat caspase recrui
7	209	37.3		21	AAB41067	Human ORFX ORF831
80	209	37.3		23	ABP10782	Human ORFX protein
6	209	37.3		22	AAB95617	Human protein sequ
10	209	37.3		22	AAU01205	Human caspase recr

Human plakoglobin Human CIPER protei Drosophila melanog CTAA-OVA-DD fusion Human Noltage-gate Novel human secret Human polypeptide, Human polypeptide, Human voltage-gate C glutamicum prote Drosophila melanog Hemolysin Serpul Human OSEX ORE2683 MOUSE LICAM F00 ** Ankyrin protein se Ankyrin protein se D. immitis ankyrin Ankyrin protein se D. immitis ankyrin Ankyrin protein se MOUSE LICAM F00 ** MYCOBACTERIUM tube MOUSE LICAM F00 to MUSE LICAM PROTEI F011 length ankyrin	4 (CARD-14).  4 (CARD-14; chromosome 17;  19 rowth; cell death; cancer; therapy;  11 growth; cell death; cancer; therapy;  12 serythematosus; neurological disorder;  13 sease; inflammatory disorder; anaemia;  14 chromosuppressive; myocardial infarction;  15 inmunosuppressive; nootropic;  16 cfMP-dependent protein kinase  17 cferial.  18 cGMP-dependent protein kinase  19 inase II phosphorylation site"  10 inase II phosphorylation site"  10 inase C phosphorylation site"
AAU73245 AAX59412 ABAY59413 ABB62651 AAX59413 AAX44570 AAV33386 AAM93214 AAX44572 AAX44572 AAX44572 AAX44572 AAX44572 AAX44571 AAX44572 AAX44572 AAX10658 AAM10657 AAM10657 AAM10657 AAM106660 ABB11515 AAM106660 AAM106660 AAM106670 AAM10669 AAM10670 AAM10669 AAM10670 AAM10669 AAM10670 AAM10670 AAM10670 AAM10670 AAM10670 AAM10670	in-14 (C? ain-14; C cell grc cell grc cell grc cell grc cell grc cell grc static; static; static; static; static; static; static; and cGMP-n site" nmase l
AAU AAAU AAAU AAAU AAAU AAAU AAAU AAAU	ein; 1004 AA.  ry)  nt domain-14 (C ent domain-14; NF-kB; cell gr stemic lupus er rkinson's disea rkinson's disea ; crohn's disea r; cytostatic; ral; antibacter n/Qualifiers "CAMP- and cGMP rylation site" "CARD_domain "casein kinase "Casein kinase
199333333331119333317	y)  y)  int do  int do
2337 22337 22337 1126653 2102 2103 2103 2103 2103 2103 2103 210	; Prot. st ent ruitme ruitme ruitme ppa B; se; Pa se; Pa se; Pa se; Sy se; Pa sorder isorde antivi note== note== note== note== note===
748222222222222222222222222222222222222	tandard tandard  (fir ase rec pase re ctor-ka disord s disea s disea ling d ling d ctive; ns. L t ite 6 ite 1 ite 2
<u> на пененененененененененене</u>	stan 01 01 01 02 04 04 04 04 04 04 04 04 04 04 04 04 04
1	T 1 164 AAE07164 sta AAE07164; 06-NOV-2001 Human caspas Human; caspa nuclear fact autoimmune d Alzheimer's haemerlogic stroke; immu cell signal1 neuroprotect Homo sapiens Key Modified-sit Modified-sit Modified-sit
11111111111111111111111111111111111111	SULT 1 E07164 AAE077 AAE077 06-NO Human Human Human nucles autoin Alzhei haemal stroke cell s neurop Homo s Key Modiff Modiff
	RESULA AABOUL AABOUL AABOUL AABOUL AABOUL AXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

```
/note= "N-glycosylation site"
                                                                                                   note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note=
                                                                                                                                                                                                                            note=
                                                                                                                           label.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-497073/54.
N-PSDB; AAD13447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200159065-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
           Modified-site
                                    Modified-site
                                                             Modified-site
                                                                                     Modified-site
                                                                                                                                       Modified-site
                                                                                                                                                               Modified-site
                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fodified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bertin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "N-myristoy<sub>1atto...</sub>
121.123
/note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                         hote= "Casein Aimace C phosphorylation site"
/hote= "Protein Kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                       .262
e- "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                               .283
.e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300
e- "Casein Kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309
- "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .310
e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        369
e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .452
e- "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             465
e- "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      472
e- "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .386
e= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  site"
60..62
/note= "Protein kinase C phosphorylation site"
91..93
                                   "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                          ...168
te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                              ..243
te- "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Casein kinase II phosphorylation site"
                                                                                                                                                                                       "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                         "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .365
:e= "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                   .227
e- "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                             .256
e= "Casein Kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .381
e= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .466
e= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .406
e= "Leucine zipper pattern"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       587..592
/note= "N-myristoylation site"
589..592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
516
e= "N-myristoylation site"
                                                                                                                                                ..135
te= "N-myristoylation site"
                                                                                                                                                                                                               "N-myristoylation site"
                                                                        .122
.e= "N-myristoylation site"
                                                14..117
'note= "N-glycosylation site"
                                                                                                                                       label Coiled_Coil_domain
                                                                                                                                                                                                                                                                                                                  label= k-Box_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label= PDZ_domain
                                                                                                                                                                                                                                                              /note= "T
221 . . 224
                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "C
390..293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 504
                                                                                                                                                                                                   .166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note-
                                                                                                                                                                                                                                         note=
                                                                                                                                                                                                                                                                                           note=
                                                                                                                                                                                                                                                                                                                                                                                                                       note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note=
                                        'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
Modified-site
                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                        Modified-site
                                                 Modified-site
                                                                          Modified-site
                                                                                                   Modified-site
                                                                                                                                                   Modified-site
                                                                                                                                                                          Modified-site
                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                           Domain
```

```
60. 763
Ynote= "CAMP- and CGMP-dependent protein kinase
phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   site"
                                                                                                                                                                                       /note= "Protein Aimwaca...
725..728
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                 note= "N-glycosytation."
59..761
'note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .844
.e= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .947
e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                               "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1002..1004
/note= "Protein kinase C phosphorylation site"
                               "Casein kinase II phosphorylation site"
                                            .655
e= "Protein kinase C phosphorylation site"
                                                                                              "Casein kinase II phosphorylation site"
"Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   An isolated caspase recruitment domain polypeptide useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "Proteru Armer.
360..863
Anote= "Casein kinase II phosphorylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "RGD cell clr...
193. 896
/note= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .029
e= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..979
te= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .949
.e= "Peroxisomal targetting signal"
                                                                                                                                                                                                                                                                                                                                                                                   85..793
note= "Peroxisomal targetting signal"
96..799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .872
e= "RGD cell attachment sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            label= Guanylate_kinase_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "N-myristoylation site"
1002..1004
                                                                                                                                        .719
e= "N-myristoylation site"
                                                                                                                                                                                                                                                    "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              "N-myristoylation site"
                                                                                                                                                                                                                                                                 .740
e= "N-glycosylation site"
                                                                                                                           SH3_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JAN-2001; 2001WO-US02087.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-FEB-2000; 2000US-0181159.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ju.
/note=
1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.
/note=
. 985
                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Ca
                                                                                                         .745
                                                                 /note= "P
574..677
                                                                                                                                                            'note= "N
725..727
```

```
ò
                                                                                                                                                                                                                                                                                                                                   QQ
                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                    Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nuclear factor-kappa B; NF-kB; cell growth; cell death; cancer; therapy; autolmnune disorder; systemic lupus erythematosus; neurological disorder; Alzheimer's disease; Parkinson's disease; inflammatory disorder; anaemia; haematological disorder; myelodysplastic syndrome; myocardial infarction; stroke; immune disorder; Crohn's disease; allergic rhinitis; infection; cell signalling disorder; cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antibacterial.
                                                         The present sequence is human caspase recruitment domain-14 (CARD-14). The CARD-14 gene is located on chromosome 17. The CARD-14 is used for the detection of modulators that modulates the ability of CARD-14 to bind to Bcl-10 and stimulates phosphorylation of Bcl-10 or activation of nuclear factor-kappa B (NF-kB). The CARD-14 is useful for regulating growth and cell death and useful for the treatment of cancer. It is also useful for the treatment of autoimmune disorders (e.g., systemic lupus erythematosus), neurological disorders e.g., Alzheimer's and ParkInson's disease, inflammatory disorders, haematological disorders (e.g., anaemia myelodysplastic syndromes), myocardial infarctions, strokes, immune disorders (e.g., Crohn's disease, allergic rhinitis), cell signalling disorders and certain viral and bacterial infections.
regulating growth and cell death and useful for the treatment of cancer
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                               1 ALTALDEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMR 60
                                                                                                                                                                                                                                                                                                             10 ALTALDEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMR 69
                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                Length 1004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     caspase recruitment domain-14; CARD-14; chromosome 17;
                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                           AGHLLDLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFSNFS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human predicted caspase recruitment domain-14 (CARD-14).
                                                                                                                                                                                                                                              100.0%; Score 560; DB 22;
100.0%; Pred. No. 1.6e-64;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Encoded by TGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE07165 standard; Protein; 1139 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
700
                                    Claim 1; Fig 1A-1E; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-FEB-2000; 2000US-0181159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JAN-2001; 2001WO-US02087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-497073/54.
                                                                                                                                                                                                                      1004 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAD13448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200159065-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bertin J;
                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE07165;
                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                      AAE07165
                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                     g
```

```
ö
                                                                                                                                                           The present sequence is predicted human caspase recruitment domain-14 (CARD-14). The CARD-14 gene is located on chromosome 17. The CARD-14 is used for the detection of modulators that modulates the ability of CARD-14 to bind to Bol-10 and stimmlates phosphorylation of Bol-10 or activation of nuclear factor-kappa B (NF-kB). The CARD-14 is useful for regulating growth and cell death and useful for the treatment of autoimmune disorders (e.g., systemic lupus erythematosus), neurological disorders e.g., Alzheimer's and Parkinson's disease, inflammatory disorders, haematological disorders and parkinson's disease, inflammatory disorders, haematological disorders strokes, immune disorders (e.g., annowne disorders (e.g., crohn's disease, allergic rhinitis), cell signalling disorders and certain viral and bacterial infections.
An isolated caspase recruitment domain polypeptide useful for regulating growth and cell death and useful for the treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ALTALDEETLWEMMESHRHRIVRCICPSRLTPYLROAKVLCOLDEEEVLHSPRLTNSAMR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 ALTALDEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMR 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; caspase recruitment domain; CARD-11; Bc1-10; NF-kappaB;
apoptosis; hyperproliferative disorder; autoimmune; neurological;
inflammatory disorder; viral infection; stress-related response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "cAMP- and cGMP-dependent protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Casein kinase II phosphorylation site" 168..171 /note= "Casein kinase II phosphorylation site" 175..183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGHLLDLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFSNFS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human caspase recruitment domain, CARD-11 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 560; DB 22;
100.0%; Pred. No. 1.9e-64;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coil domain"
                                                                                                             Disclosure; Fig 2A-2C; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "CARD domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU01207 standard; Protein; 1147 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100..102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162..165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1139 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Simi
Matches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU01207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU01207
```

site"

site"

"Casein kinase II phosphorylation

"N-myristoylation site"

site"

"Casein kinase II phosphorylation

"Casein kinase II phosphorylation site"

"N-myristoylation site"

```
/note= "N-myriscogramma." | Note= "N-myriscogramma." | Note= "Protein kinase C phosphorylation site" | Note= "Note= "
                                                                                                                                                                                                                 872..875
/note= "casein kinase II phosphorylation site"
/note= "cuanylate kinase (GUK) domain"
                                                                                                                                                                                                                                                                                                                                                                               .929
.e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "Casein kinase II phosphorylation site"
1120..1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Casein kinase II phosphorylation site"
/note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Tyrosine kinase phosphorylation site"
1050..1055
                                                                                           .850
.e= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "N-myristoylation site"
.088..1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2000; 2000WO-US32716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Cas
1010..1018
                                                    .828
                                                                                                                  /note= "C
853..858
                  .819
                                                                                                                                                                                                                                                                                                .900
                                                                                                                                                                                                                                                                                                                                          .922
                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                         'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                              note=
                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-367809/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAS05389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200140468-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                  Modified-site
                                                        Modified-site
                                                                                                Modified-site
                                                                                                                                     Modified-site
                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-FEB-2000;
10-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-DEC-1999;
18-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bertin J;
                                                                                                                                                                                                                                                               Domain
THE STATE OF THE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="N-glycosylation site"
779..782
70.00 "Gasein kinase II phosphorylation site"
787..789
                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Protein kinase C phosphorylation site"
471..474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .581
e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .689
.e- "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ...695
ce= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..767
te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                          . 292
:e- "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..479
te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .510
.e= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..728
.e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 558..560
/note= "Protein kinase C phosphorylation site"
                                                                                                                                                            "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                        "Casein kinase II phosphorylation site"
                                       "Casein kinase II phosphorylation site"
                                                                             site"
  note= "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Glycosaminoglycan attachment site"
                                                                                                                                                                                                                                                                                                                       "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                               /note= "cAMP- and cGMP-dependent protein
                                                        .195
e- "Tyrosine kinase phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Case... .. 698..703

^^note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    587..592
/note= "N-myristoylation site"
634..637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .766
e= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..475
te= "N-glycosylation site"
                                                                                                                     "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                    phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "N-myristoylation
                                                                                                                                                                                                    "Amidation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "MAGUK domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "PDZ domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "SH3 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .779
                                                                                                                                                                               . 285
                                                                                                                                                                                                                       . 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..683
                                                                                                                                         . 245
                                                                                                                                                                                                                                                                                                                                            .432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         635..748
                      182..185
                                                                                                  . . 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
508..51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
635..11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note=
                                                                                                                                                                                                                                            note=
                                                                                                                                                                                                                                                                                                                             'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note=
                                                                                                                         'note=
                                                                                                                                                                "note=
                                                                                                                                                                                                                                                                                   note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note=
                                                                                 'note-
                                                                                                                                                                                                                                                                                                                                              129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                    Modified-site
                                                          Modified-site
                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                  Modified-site
                                                                                                                                       Modified-site
                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
```

```
The present sequence represents novel human caspase recruitment domain, CARD-11. The polynucleotide encoding this sequence was isolated from a human T-cell cDNA library. Also described are sequences for CARD-9 and CARD-10 (AAU01205, AAU01206) and rat CARD-9 (AAU01204). CARD-9, CARD-10 and CARD-11 interact with Bol-10 which is thought to activate nuclear factor (NF) kappaB and apoptosis. The sequences of the invention can be used for treating a disorder associated with abnormal levels of apoptosis by modulating the expression or activity of CARD-9, CARD-10, or CARD-11. They can be used for the treatment of hyperproliferative disorders (e.g. cancer), autoimmune disorders (e.g. systemic lupus erythematosus), neurological disorders (e.g. Alzheimer's disease), inflammatory disorders (e.g. crohos disease), and viral infection (e.g. HIV). The CARD polypeptide, polynucleotide and an antibody which selectively binds to CARD can be used in screening and detection assays (e.g. chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteins, CARD-9, CARD-10, as immunogens, and in screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel caspase recruitment domain (CARD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful as targets for therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 9; Fig 14A-14C; 145pp; English.
99US-0168780.
2000US-0507533.
2000US-0513904.
2000US-0685791.
                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM PHARM INC
```

site"

site"

```
..644
te= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "N-myristcy_____681.684
fnote= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Protein kinase C phosphorylation site"
869..872
/note= "Casein kinase II phosphorylation site"
                                                                                              . 441
te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mote= "Protein kinase C phosphorylation site"
   "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                               "Glycosaminoglycan attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Casein Ainer."
754..756
/note= "Protein kinase C phosphorylation
                                                                                                                                                               .481
.e= "Casein kinase II phosphorylation
                                                                                                                                                                                                        .513
.te= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                  . 573
te- "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                            ..605
te= "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..693
ce= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..751
te= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          757
e= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     784 -
s= "Protein kinase C phosphorylation
                                                     415
-- "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                        ...560
te= "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .870
te= "Protein kinase C phosphorylation
           ..334
te= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                           "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                  /hote= "Caselu Alunco.
733..739
/note= "Tyrosine kinase phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .1032
e= "Guanylate kinase (GUK) domain"
                                                                                       "Leucine zipper homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .766
e= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "N-myristoylation site"
                                                                                                                                                                                                "N-myristoylation site"
                                                                                                                                                                                                                                                                                                           "N-myristoylation site'
                                                                                                                                                                                                                                                                                                                                       .598
e= "N-glycosylation site"
                                                                                                                                                      "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "N-glycosylation site"
                                            "Tropomyosin domain"
                                                                                                                  .
.1032
rem "MAGUK domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ....
4..772
^+e= "SH3 domain"
                                                                                                                                                                                                                                                                                    /note= "P:
565..570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "N
714..717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "P
809..814
                                                                                                                                                                                     ..492
                                                                           ..447
                                                                                                                                           472..475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                  note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
                                               /note=
                                                                                        /note=
                                                                                                             'note=
                                                                                                                                                        'note=
                                                                                                                                                                                                                                             'note=
                                                                                                                                                                                                                                                                'note=
                                                                                                                                                                                                                                                                                                            note=
                                                                                                                                                                                                                                                                                                                                                      'note=
                                                                                                                                                                                                                                                                                                                                                                                                'note=
                                                                                                                                                                                                                                                                                                                                                                                                                    'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R 3 0
             Modified-site
                                                      Modified-site
                                                                                                 Modified-site
                                                                                                                                         Modified-site
                                                                                                                                                                Modified-site
                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                   Domain
                                                                            Region
                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Domain
   ö
             The
mapping, tissue typing), predictive medicine (prognostic assays, monitoring clinical trials, and therapy (treatment and prophylaxis). The CARD polypeptide may be used to screen for drugs that bind to and/or modulate it. CARD sequences are potential targets for regulating inflammation, cancer, NF kappaB signalling, stress related response and apoptosis in human disease. A host cell containing a polynucleotide encoding CARD can be used to create transpenic animals.
                                                                                                                                 Gaps
                                                                                                                                                      65
                                                                                                                                                                  DEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGHLL
                                                                                                                                                                                                                                                                                                                                                             Human; caspase recruitment domain; CARD-10; Bcl-10; NF-kappaB; apoptosis; hyperproliferative disorder; autoimmune; neurological; inflammatory disorder; viral infection; stress-related response.
                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 295
te= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .296
e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              site"
                                                                                                           Length 1147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..207
te= "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .115
ce- "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 245
te= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Protein kinase C phosphorylation
                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human caspase recruitment domain, CARD-10 polypeptide.
                                                                                                          Query Match 48.2%; Score 270; DB 22; Best Local Similarity 51.5%; Pred. No. 4.3e-26; Matches 51; Conservative 22; Mismatches 26;
                                                                                                                                                                                              /note= "Case... ... 309..314
/^orte= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Coiled coil domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Amidation site'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Casein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "CARD domain"
                                                                                                                                                                                                                                                                           ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                         AAU01206 standard; Protein; 1032
                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .123
                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note≃
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6...9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note=
                                                                                                                                                                                                                                                                                                                    (first
                                                                                     1147 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modifled-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                    12-SEP-2001
                                                                                        Seguence
                                                                                                                                                                                                                                                                                               AAU01206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                      9
                                                                                                                                                                                                                   71
                                                                                                                                                                                                99
                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                      g
  888888888888
                                                                                                                                                                                                ò
                                                                                                                                                      ò
```

site"

site"

site"

site"

site"

99

DLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQP

99

δ

9

```
from a human skin cDNA library. Also described are novel human sequences from a human skin cDNA library. Also described are novel human sequences for CARD-10. The polynucleotide encoding this sequence as sequences of the care and the control of the care and the control of the care and the care and the care and the care and the care as a sequence of the invention can be used for treating a disorder associated with abnormal levels of apoptosis by modulating the expression or activity of CARD-9, CARD-10, or CARD-11. They can be used for the treatment of hyperproliferative disorders (e.g. cancer), autoimmune disorders (e.g. systemic lupus errythematosus), neurological disorders (e.g. Alzhehmer's disease), inflammatory disorders (e.g. crohn's disease), and viral infection (e.g. HIV). The CARD polypeptide, polynucleotide and an antibody which selectively binds to CARD can be used in screening and an antibody which selectively binds to CARD can be used in screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and detection assays (e.g. chromosomal mapping, tissue typing), predictive medicine (prognostic assays, monitoring clinical trials, and therapy (treatment and prophylaxis). The CARD polypeptide may be used to screen for drugs that bind to and/or modulate it. CARD sequences are potential targets for regulating inflammation, cancer, NF-kappab signalling, stress-related response and apoptosis in human disease. A host cell containing a polynucleotide encoding CARD can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel caspase recruitment domain (CARD) proteins, CARD-9, CARD-10, CARD-11, useful as targets for therapy, as immunogens, and in screening and detection assays -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present sequence represents novel human caspase recruitment
.885
e= "Casein kinase II phosphorylation site"
                                                                                                     ..949
.te= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                /note= "Protein Kinase C phosphorylation site"
1028..1031
                                                                                                                                                                                                                                                             "Casein kinase II phosphorylation site"
                                                    "N-myristoylation site"
                                                                                                                                                          "N-myristoylation site"
                                                                                                                                                                                          "N-myristoylation
                                                                                      "Amidation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 9; Fig 10A-10C; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2000; 2000WO-US32716
                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0507533
2000US-0513904
                                                                                                                                                                                            /note= "N-m
1022..1024
                                                                                                                                                                                                                                ρι
.ακ..1031
/note= "Γ
                                                                                                                                                                                                                                                                                                                                                                                                     99US-0168780
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0685791
                                                                                                                                                          /note= "N-m
1021..1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          create transgenic animals.
                   /note= "C
893..898
                                                                    ..918
                                                                                                                   /note= |
981 986
                                                        'note=
                                                                                        'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-367809/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1032 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAS05388
                                                                                                                                                                                                                                                                                                WO200140468-A2
 Modified-site
                                                                                                       Modified-site
                                                                                                                                                                          Modified-site
                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                               Modified-site
                                  Modified-site
                                                                                                                                         Mod1fied-site
                                                                                                                                                                                                                                                                                                                                                                                                     03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                       18-FEB-2000;
25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-OCT-2000;
                                                                                                                                                                                                                                                                                                                                  07-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bertin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The
```

```
The invention relates to an isolated plakoglobin interacting polypeptide (I). (I) is useful as a medicament and in the manufacture of a medicament for treating plakoglobin related diseases, such as skin carcinoma or an acantholytic disease, and to screen compounds that interfere with the interaction of the polypeptide with plakoglobin related diseases include basal cell carcinoma, squamous cell carcinoma, extramammary Paget's disease, Naxos disease, heart diseases, skin blistering and acantholytic diseases such as subcorneal acantholysis, Grover's disease, Hailey's disease or Darier's disease, and ectodermal dysplasia/Skin fragility syndrome. AAU73245-AAU73254 represent novel human plakoglobin interacting protein amino acid sequences and related sequences of the invention.
                                                                                                                                                                                                                                         Human; plakoglobin; cytostatic; osteopathic; dermatological; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide, useful for treating skin carcinoma or acantholytic diseases such as Grover's and Darier's disease, comprises a protein interacting with human plakoglobin and involved in transduction of plakoglobin related signal to nucleus -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGHLL 65
                                                                                                                                                                                                                                                        plakoglobin related disease; skin carcinoma; acantholytic disease; basal cell carcinoma; squamous cell carcinoma; Maxos disease; extramanmany Paget's disease; heart disease; skin blistering; subcorneal acantholysis; Grover's disease; Hailey Hailey's disease; Darier's disease; ectodermal dysplasia; skin fragility syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 246; DB 23;
Pred. No. 5.6e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQP 99
                                                                                                                                                                                                         Human plakoglobin interacting protein #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vanlandschoot A;
                                                                                                    AAU73247 standard; Protein; 1032 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Figure 3; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-MAY-2001; 2001WO-EP04872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-MAY-2000; 2000EP-0201668
                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 48.9 es 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bonne S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-062246/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1032 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAS98203
                                                                                                                                                                                                                                                                                                                                                                                                 WO200185933-A2.
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                       12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                     15-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Van Roy F,
                                                                                                                                      AAU73247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99
                                                                                                                      δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
              g
```

ö

ó

Gaps

..

Length 1032; Indels 0

43.9%; Score 246; DB 22; 48.9%; Pred. No. 5.6e-23;

21; Mismatches

Conservative

46;

Matches 6 23

o o

Query Match Best Local Similarity

```
q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                          Rat; caspase recruitment domain; CARD-9; Bcl-10; NF-kappaB; apoptosis; hyperproliferative disorder; autoimmune; neurological; inflammatory disorder; viral infection; stress-related response.
                                                                                                                                                                                                                                       "CAMP- and cGMP-dependent protein kinase phosphorylation pite"
                                                                                                                                                                                                                                                                                                                                                                                                /note= "cAMP- and cGMP-dependent protein kinase
phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           451..453
/note= "Protein kinase C phosphorylation site"
483..486
                                                                                                                                                                                                                                                                                                                         .365
ce= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           428
e= "Casein Kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     431..433
/note= "Protein kinase C phosphorylation site"
451..453
                                                                                                                                                                                                        "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                       "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                    .141
te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                              231..233
/note= "Protein kinase C phosphorylation site"
267..270
                                                                                                                                                                                                                                                                                                                                                                                                                              267..270
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            .305
te= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .364
te= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Casein kinase II phosphorylation site"
                                                                                                                                                         'note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                              "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                             "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                             "Protein kinase C phosphorylation site"
                                                                                                                                                                                       "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                 ..183
te= "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cysteine rich repeat homology region"
                                                                                                                                                                                                                                                                                                                                                                         /note= "Indole-3-glycerol phosphate synthase homology region"
                                                                            recruitment domain, CARD-9 polypeptide.
                                                                                                                                                                                                                                                                                                                  ..416
re- "Coiled coil domain"
                                                                                                                                                                        "CARD domain"
                                                                                                                                         Location/Qualifiers
                             AAU01204 standard; Protein; 536 AA
                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "C
                                                                                                                                                                                                                                                                                                                                                                                                                                             285..338
                                                                                                                                                                                                                                                                                      ..140
                                                                                                                                                                                                                                                                                                                                                                                        228..231
                                                                                                                                                                                                                      /note=
92..95
/note=
                                                                                                                                                                                                       /note=
23..26
                                                                                                                                                                                                                                                                      95..98
/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note=
                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                               'note=
                                                                                                                                                                                                                                                                                               'note=
                                                                                                                                                                                                                                                                                                             "note"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note=
                                                                                                                                                                                                6..18
                                                                                                                                                                                                                                                      95..97
                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note-
                                                                                                                                                                         'note-
                                                                                                                                                                                        note-
                                                                                                                                          Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                Modified-site
                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Addified-site
                                                            12-SEP-2001
                                                                            Rat caspase
                                                                                                                         Rattus sp
                                             AAU01204;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                                                                                  Region
                     AAU01204
```

```
The present sequence trepresents movel that caspase Fectivithment domain, CARD-9. The polynucleotide encoding this sequence was isolated from a rat neuronal cDNA library. Also described are novel solated from a rat neuronal cDNA library. Also described are novel caspanes for CARD-9, CARD-10 and CARD-11 interact with Bel-10 which is thought to activate nuclear factor (NF)-kappaB and apoptosis. The sequences of the invention can be used for treating a disorder associated with abnormal levels of apoptosis by modulating the expression of activity of CARD-9, CARD-10, or CARD-11. They can be used for activity of CARD-9, CARD-10, or CARD-11. They can be used for cartivity of CARD-9, CARD-10, or CARD-11. They can be used for cortaction and viral infection (e.g. HIV). The CARD polypeptide, alsorders (e.g. Alzheimer's disease), inflammatory disorders (e.g. Alzheimer's disease), inflammatory disorders (e.g. crohn's disease), and viral infection (e.g. thry). The CARD con be used in screening and detection assays (e.g. chromosomal mapping, tissue typing), predictive medicine (prognostic assays, monitoring clinical crimials, and therapy (treatment and prophylaxis). The CARD polypeptide may be used to screen for drugs that bind to and/or modulate it. CARD can be used to screen for drugs that bind to and/or modulate it. CARD sequences are potential targets for regulating inflammation, cancer, NF-kappaB signalling, stress-related response and apoptosis in human disease. A host cell containing a polynucleotide encoding CARD can be used to create transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel caspase recruitment domain (CARD) proteins, CARD-9, CARD-10, CARD-11, useful as targets for therapy, as immunogens, and in screening and detection assays -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGHLL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SERVALESFRVKLISVIDPSRITPYLRQCKVLNPDDEEQVLSDPNLVIRKRKVGVLL 65
                                                                                                                                                                                         /note= "N-glycosylation site"
526..529 .
/note= "Casein kinase II phosphorylation site"
531..534
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                    514..516
/note= "Protein kinase C phosphorylation site"
'note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present sequence represents novel rat caspase recruitment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 217; DB 22;
; Pred. No. 1.5e-19;
17; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFS 104
                                                                                                                            "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; Fig 1A-1B; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 Match 38.8%;
Local Similarity 45.5%;
hes 45; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0507533.
2000US-0513904.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0168780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2000; 2000WO-US32716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0685791
                                                                                                                                                           ..527
                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-367809/38
N-PSDB; AAS05386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 536 AA;
                                                                                                                                                                                                                                                                                                                                                                                      WO200140468-A2
                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-DEC-1999;
18-FEB-2000;
25-FEB-2000;
                                 Modified-site
                                                                                              Modified-site
                                                                                                                                                           Modified-site
                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bertin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The
```

ö

ö

```
antipositatic; antiparties such as 'yeother's properties, antiparties, antiparties, antiparties, antiparties, antiparties, antiparties, antiparties, antiparties, antiparties, immunosuppressant; ordiant; thrombolytic; coagulant; vasotropic; antidulabetic: hypotensive; dermatological; immunosuppressive; antidiabetic: hypotensive; dermatological; immunosuppressive; antidiabetic: hypotensive; dermatological; antifungal; antirheumatic; antidinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OREX associated disorder. The nucleic acids can be used to express OREX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
                                                                                                                                                                                                                                                                   vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiiviral; antibacterial; antifungal; antirheumatic; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                               antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder, osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                 Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                               Human ORFX ORF831 polypeptide sequence SEQ ID NO:1662.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 1326; 5507pp; English.
                                            AAB41067 standard; Protein; 174 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-2000; 2000WO-US08621
                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thrombosis; contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shimkets RA, Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-602362/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAC75276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200058473-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                              08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-OCT-2000
                                                                                               AAB41067;
RESULT 7
                    AAB41067
```

```
(referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN27552 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders realated to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; inflectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention describes substantially purified human proteins
                                                                                                                                                               71 NDDECWNVLEGFRVTLTSVIDPSRITPYLRQCKVLNPDDEEQVLSDPNLVIRKRKVGVLL 130
                                                                                      Gaps
                                                                                                                           6 DEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGHLL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
                                                                                      ö
                                                   Length 174;
                                                                                      Indels
                                                                                      39;
                                                                                                                                                                                                                          DLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFS 104
                                                   DB 21;
                                                 Score 209; DB 21;
Pred. No. 3.5e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human ORFX protein sequence SEQ ID NO:21546.
                                                                                      16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID 21546; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                        ABP10782 standard; Protein; 174
                                                   37.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000; 2000US-206132P. 29-AUG-2000; 2000US-228716P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAY-2001; 2001WO-US10836
                                                                      44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                24-JUN-2002 (first entry)
                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leach MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-106308/14.
                                                   Query Match
Best Local Similarity
               174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             myasthenia gravis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABN26534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200192523-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-DEC-2001.
                                                                                        44;
                                                                                                                                                                                                                                                                                                                                                                               ABP10782;
               Sequence
                                                                                          Matches
                                                                                                                                                                                                        99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The
                                                                                                                                                                                                                                                                                                  RESULT 8
                                                                                                                                                                                                                                                                                                                      ABP10782
ID ABP
x os
                                                                                                                                                             QQ
                                                                                                                                                                                                        δλ
                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                             δŏ
                                                                                                                                                                                                                                                                                                                      hypertension;
```

```
ö
                                                                                                                                    the printed
            arthritis, autoimmune thyroiditis, myasthenia gravis, graft.versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an Oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                              N.B. The sequence data for this patent did not form part of the printer specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
 diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
                                                                                                                                                                                                                                                                                                                           primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                       6 DEFILWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGHLL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ٦,
ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamamoto
                                                                                                                                                                                                                                    37.3%; Score 209; DB 23; Length 174; 44.4%; Pred. No. 3.5e-19; Live 16; Mismatches 39; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saito K,
, Otsuki '
                                                                                                                                                                                                                                                                                                                                                                                            DLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; SEQ ID 18328; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nishikawa T, Hayashi K, Sa
T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human protein sequence SEQ ID NO:18328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB95617 standard; Protein; 366 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000JP-0241899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-318749/34.
                                                                                                                                                                                                                                                    Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                   174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isoqai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP1074617-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ishii S,
                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB95617;
                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ota T,
                                                                                                                                                                                                                                                                                                                                                                        99
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB95617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                        qq
ŏ
```

```
ö
           complementary strand of a polymucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polymucleotide which comprises a 3'-end sequence. Where the complementary to a ligonucleotide which comprises a 1'-end sequence, where the combination of the 5'-end sequence 1s selected from those defined in the specification. The primers are useful for synthesising polymucleotides, particularly full-length cDNAs. The primers are useful for synthesising polymucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs as 11'-length cDNAs. The primers allow obtaining of the full-length AAH13618 and AAH13631 cAAH13618 represent human cDNA sequences; AAB92446 to AAH13632 represent toligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                             6 DEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGHLL 65
                                                                                                                                                                                                                                                                                                                                                                            6 NDDECWNVLEGFRVTLTSVIDPSRITPYLRQCKVLNPDDEEQVLSDPNLVIRKRKVGVLL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; caspase recruitment domain; CARD-9; Bcl-10; NF-kappaB; apoptosis; hyperproliferative disorder; autoimmune; neurological; inflammatory disorder; viral infection; stress-related response.
 an oligonucleotide comprising a sequence complementary to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "CAMP- and cGMP-dependent protein kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                ..
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.38..141
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Indole-3-glycerol phosphate synthase
                                                                                                                                                                                                                                                                                                 Length 366;
                                                                                                                                                                                                                                                                                              ; Score 209; DB 22; Length 3; Pred. No. 1e-18; 16; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human caspase recruitment domain, CARD-9 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                          DLLKTRGKNGALAFLESLKFHNPDVYTLVTGLQPDVDFS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..416
te= "Coiled coil domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "CARD domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU01205 standard; Protein; 536
                                                                                                                                                                                                                                                                                               37.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                              44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..213
                                                                                                                                                                                                                                     of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176..183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92..95
/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95..97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95..98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23..26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86.
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                  366 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU01205;
                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
00000000000000000x0
                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

homology region"

```
The present sequence represents novel human caspase recruitment domain, CARD-9. The polynuclectide encoding this sequence was isolated from a human megakaryocyte cDNA library. Also described are novel human sequences for CARD-10 and CARD-11 interact with Bcl-10 and rat CARD-9 (AAU01204). CARD-9, CARD-10 and CARD-11 interact with Bcl-10 which is thought to activate nuclear factor (NF) kappaB and apoptosis. The sequences of the invention can be used for treating a disorder associated with abnormal levels of apoptosis by modulating the expression or activity of CARD-9, CARD-10, or CARD-11. They can be used for the treatment of hyperproliferative disorders (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteins, CARD-9, CARD-10, as immunogens, and in screening
                                                                                                                                                   /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"
228..231
/note= "cAMP- and cGMP-dependent protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "N-myristoylation site"
531..534
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                            /note= "Casein Kinase .- , 425..428
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                  .433
:e= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                           "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                               "Casein kinase II phosphorylation site"
                                                                                                                                                                                 .366
.e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                          ..452
te- "Protein kinase C phosphorylation site"
                                                                             "Casein kinase II phosphorylation site"
                                                                                                                                "Protein kinase C phosphorylation site"
                                                   "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                          "Protein kinase C phosphorylation site'
                                                                                                       "Cysteine rich repeat homology region"
                                                                                                                                                                                                                                                                                                                                                    "N-myristoylation site"
                                                                                                                                                                                                                                                                                                  "N-myristoylation site"
                           phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel caspase recruitment domain (CARD) CARD-11, useful as targets for therapy,
                                                                                                                                                                                                                                                                                                                                                                                                      "N-glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; Fig 5A-5B; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-FEB-2000; 2000US-0507533.
25-FEB-2000; 2000US-0513904.
10-OCT-2000; 2000US-0685791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2000; 2000WO-US32716
                                                                                                                                                                                                                                                                                                                                                                                                                                            ..532
                                                                                                                                                                                                                                                                                                                                                                                         ..527
                                                                                                                                                                                                                                                                                                               .462
                                                                                                                                                                                                                                                                                                                                                               ..486
                                                                  ..270
                                                                                            .338
                                                                                                                 .305
                                                                                                                                             336
                                                                                                                                                                                                                                                                                    453..458
                                                                                                                                                                                                                                                                                                                                        ..486
                                                                                                                                                                                                                                                                                                                                                                                                                  529
                                       231..233
                                                                                                                                                                                                                                                                                                                                                       /note= |
483..486
                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
527..53
                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                    /note-
                                                                                                                                                                                                                                                                                                                             /note-
                                                                                                                                                                                                                                                                                                                                                                                                       /note=
526..5
                                                                              /note=
                                                                                                         /note=
                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                               'note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and detection assays -
                                                                                                                                   /note=
                                                       'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-367809/38.
N-PSDB; AAS05387.
                                                                                                                                                                                                                                                                                                                 460.
                                                                                                                                                                                   363,
                                                                                                                                                                                                                                                                                                                                         481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200140468-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
    Modified-site
                                        Modified-site
                                                                  Modified-site
                                                                                                                    Modified-site
                                                                                                                                              Modified-site
                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bertin J;
                                                                                             Region
```

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide
a
cancer), autoimmune disorders (e.g. systemic lupus erythematosus), neurological disorders (e.g. Alzheimer's disease), inflammatory disorders (e.g. crohn's disease), and viral infection (e.g. HIV). The CARD polypeptide, polynucleotide and an antibody which selectively binds to CARD can be used in screening and detection assays (e.g. chromosomal mapping, tissue typing), predictive medicine (prognostic assays, monitoring clinical trials, and therapy (treatment and prophylaxis). The CARD polypeptide may be used to screen for drugs that bind to and/or modulate it. CARD sequences are potential targets for regulating inflammation, cancer, MP-kappab signalling, stress-related response and apopptosis in human disease. A host cell containing a polynucleotide encoding CARD can be used to create transgenic animals.
                        disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; plakoglobin; cytostatic; osteopathic; dermatological; cardiant; plakoglobin related disease; skin carcinoma; acantholytic disease; basal cell carcinoma; squamous cell carcinoma; squamous cell carcinoma; squamous cell carcinoma; naxos disease; extramammary paget's disease; heart disease; skin blistering; subcorneal acantholysis; Grover's disease; Hailey-Hailey's disease; Darier's disease; ectodermal dysplasia; skin fragility syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acantholytic
                                                                                                                                                                                                                                                                                                                                                                                                          SINDECWNVLEGERVILTSVIDPSRIIPFILGCKVLNPDDEEQVLSDPNLVIRKRKVGVLL 65
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                   DEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGHLL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptide, useful for treating skin carcinoma or acantholytidisease such as Grover's and Darier's disease, comprises a protein interacting with human plakoglobin and involved in transduction of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated plakoglobin interacting polype (I). (I) is useful as a medicament and in the manufacture of a medicament for treating plakoglobin related diseases, such as skin carcinoma or an acantholytic disease, and to screen compounds that
                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                      Length 536;
                                                                                                                                                                                                                                                                                                      37.3%; Score 209; DB 22;
44.4%; Pred. No. 1.7e-18;
iive 16; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |:|: | | :||||||: : | :| ||| || || DILQRTGHKGYVAFLESLELYYPQLYKKVTGKEPARVFS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DELKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human plakoglobin interacting protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vanlandschoot A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plakoglobin related signal to nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 42-43; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU73245 standard; Protein; 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAY-2001; 2001WO-EP04872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-MAY-2000; 2000EP-0201668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Van Roy F, Bonne S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-062246/08.
N-PSDB; AAS98201.
                                                                                                                                                                                                                                                                                                                           Local Similarity
es 44; Conserv
                                                                                                                                                                                                                                                                       536 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200185933-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU73245;
                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΟY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
            ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence is the human CIPER protein. The invention relates to protein acts as a positive regulator of apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10 during CD95 signalling. The invention provides methods for identifying apoptosis signalling pathway inhibitors and activators, and methods and compositions for screening compounds which will modulate the interactions of the various compositions which will modulate the interactions of the various compositions and DREP-1). RICK, and the CIDE family of activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening assays for agents, useful in the diagnosis, prognosis or treatment of disease associated with excess cell growth and dysregulation of apoptosis. Complexes containing RICK and CLARP can be used in drug screening assays to identify inhibitor molecules blocking CD95-mediated apoptosis, overexpression of ARC in an in vitro cell system can be used to identify inhibitors of the enzymatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RICK; mouse; RIP-like interacting CLARP kinase; apoptosis regulator; ARC; caspase-10; CD95 signalling; apoptosis signalling pathway; CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation; gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS; aplastic anaemia; ischaemic injury; toxin-induced liver disease;
                The plakoglobin related diseases include basal cell carcinoma, squamous cell carcinoma, extramamnary paget's disease, Naxos disease, heart diseases, skin blistering and acantholytic diseases such as subcorneal acantholysis, Grover's disease, Halley-Halley's disease or Darier's disease, and ectodermal dysplasia/skin fragility syndrome. AAU73254 represent novel human plakoglobin interacting protein amino acid sequences and related sequences of the invention.
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Compositions for identifying apoptosis signalling pathway inhibitors useful for treating diseases -
interfere with the interaction of the polypeptide with plakoglobin
                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                  Length 237;
                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                            17.9%; Score 100; DB 23; L
51.4%; Pred. No. 0.00014;
ive 10; Mismatches 7;
                                                                                                                                                                                                                                                                                                               65 LDLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQP 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 20b; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY59412 standard; Protein; 233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inohara N, Koseki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human CIPER protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US09183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0069023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                        Query Match
Best Local Similarity 51.49
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000-072163/06
                                                                                                                                                                         237 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAZ48767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09955134-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nunez G,
                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY59412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CIPER.
                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                    AAY59412
                                                                                                                                                                                                                                                                                                                                                                                                                                                         888888888888
                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                 q
```

```
4
activity of caspase-8. Identification of ARC-like inhibitory compounds may be useful for gene therapy treatment of disease with increased cell death in muscle tissue and cardiac disorders. Therapeutic compositions of CIDEs can be used and cardiac disorders, and toxin-induced liver disorders, aplastic anaemia, ischaemic injury, and toxin-induced liver disorders, aplastic anaemia, ischaemic injury, and toxin-induced liver affinity chromatography media, and for diagnostically measuring RICK levels. A specific inhibitor of an essential step in the biochemistry of apoptosis is needed. RICK interaction with intracellular factors such as CLARP and FADD appears to be essential for apoptosis, inhibitors of RICK binding to intracellular apoptosis factors are potential drug candidates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence is the mouse CIPER protein. The invention relates to the human RICK (RIP-like interacting CLARP kinase) protein. The RICK protein acts as a positive regulator of apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10 during CD95 signalling. The invention provides methods for identifying apoptosis signalling pathway inhibitors and activators, and methods and compositions for screening compounds which will modulate the interactions of the various compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RICK; mouse; RIP-like interacting CLARP kinase; apoptosis regulator; ARC; caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway; CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation; gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS; aplastic anaemia; ischaemic injury; toxin-induced liver disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Compositions for identifying apoptosis signalling pathway inhibitors useful for treating diseases -
                                                                                                                                                                                                                                                                                                                                         4 ALDEETLWEM----MESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAM 59
                                                                                                                                                                                                                                                                                                                                                               .;
8
                                                                                                                                                                                                                                                               14.5%; Score 81; DB 21; Length 233; 36.5%; Pred. No. 0.045;
                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                    32;
                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 20d; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY59413 standard; Protein; 233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                   RAGHLLDLLKTRGKNGAIAFLESLK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                      87
                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                                                            ||| ||| |: :|| :| | :|| :: |
RAGKLLDYLQENPK-GLDTLVESIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse CIPER protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Koseki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US09183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inohara N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-072163/06.
                                                                                                                                                                                                                                                                                 Local Similarity
les 31; Conserv
                                                                                                                                                                                                                           233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAZ48768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9955134-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY59413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>ن</u>
                                                                                                                                                                                                                               Seguence
                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nunez
                                                                                                                                                                                                                                                                                                                                                                                                                   09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CIPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                        64
                                                                                                                                                                                                                                                                                                  tches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY59413
       ŏ
                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                 δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Op
```

```
and DREP-1). RICK, and the CIDE family of activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening assays for agents, useful in the diagnosis, prognosis or treatment of disease associated with excess cell growth and dysregulation of apoptosis. Complexes containing RICK and CLARP can be used in drug screening assays to identify inhibitor molecules blocking Or95-mediated apoptosis. Overexpression of ARC in an in vitro cell system can be used to identify inhibitors of the enzymatic activity of caspase-8. Identification of ARC-like inhibitory compounds may be useful for gene therapy treatment of disease with increased cell death in muscle tissue and cardiac disorders. Therapeutic compositions of CIDEs can be used to treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia, ischaemic injury, and toxin-induced liver of disease. AntiRICK antibodies can be used as reagents for the preparation or affinity chromatography media, and for diagnostically measuring RICK levels. A specific inhibitor of an essential step in the biochemistry of apoptosis is needed. RICK interaction with intracellular factors such as CLARP and FADD appears to be essential for apoptosis, inhibitors of RICK binding to intracellular apoptosis factors are potential drug candidates.
                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 ALDEETLWEM----MESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAM 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                         .;
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 14745; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                   Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                       33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster polypeptide SEQ ID NO 14745.
                                                                                                                                                                                                                                                                                                                                                                                     DB 21;
                                                                                                                                                                                                                                                                                                                                                                                13.9%; Score 78; DB 21
35.3%; Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB62651 standard; Protein; 845 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||| ||| ||| |:
RAGKLLDYLQ-ENPRGLDTLVESIR 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84
                                                                                                                                                                                                                                                                                                                                                                                                                       14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RAGHLLDLLKTRGKNGAIAFLESLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2000; 2000US-191637P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ľ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                               233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ABL06754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB62651;
                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB6265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

```
Š,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunostimulating complex; iscom; glycoside; lipid; antigen presentation; vaccine; cholera toxin Al subunit; CTA1; protein A D-region dimer; DD; OVA peptide; chimeric.
                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
     and
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  2 LTALDEETLWE----MMESHR-----HRIVRCICPSRLTP--YLRQAKVLCQLDEEEV 48
useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                Length 845;
                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                 sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36;
                                                                                                                                                                                                                                                                                                   DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 LHSPRLTNSAMRAGHL---LDLLKTRGKNGAIAFLESLKFH
                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                          Pred. No. 6.7;
                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                12.6%; Score 70.5; 30.7%; Pred. No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "Encoded by TGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Encoded by TAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by TAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by TGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       by TAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     by TGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Encoded by TAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Encoded by TAG'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE22544 standard; Protein; 1266 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   py
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     γ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ρλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ρλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  þy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric - Staphylococcus aureus.
Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Encoded
                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTA1-OVA-DD fusion protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 30.79
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 59
                                                                                                                                                                                                                                                       845 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE22544;
                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
AAE22544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NO CONTROL OF THE PROPERTY OF 
     00000000000xx
                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                     δλ
```

TAA" TGA" /note= "Encoded by TGA" 1198 /note= "Encoded by TGA" Misc-difference 1220 /note= "Encoded by TAG" 739 note- "Encoded by TGA" 'note= "Encoded by TGA" 'note= "Encoded by TAA" by TGA" by TGA" by TGA" by TAG" by TGA" by TAA" by TGA" by TAG' by TAG" by TAG" by TAA" note- "Encoded by TAA" by TAA" by TAG" by TAG" ρλ þу ρλ ρλ ρλ ρλ 'note- "Encoded by 'note= "Encoded by 'note- "Encoded 'note= "Encoded note= "Encoded 'note= "Encoded 'note= "Encoded note- "Encoded note= "Encoded note- "Encoded 'note= "Encoded 'note= "Encoded 'note- "Encoded note- "Encoded 'note= "Encoded note= "Encoded note= "Encoded note= "Encoded 'note- "Encoded 'note= "Encoded 'note= "Encoded /note= "Encoded 'note- "Encoded 'note= "Encoded 'note- "Encoded 'note= "Encoded 'note- "Encoded 'note= "Encoded 'note= Misc-difference 1144 Misc-difference 1191 Misc-difference 438 Misc-difference 489 Misc-difference 676 Misc-difference 367 Misc-difference 386 Misc-difference 392 Misc-difference 398 Misc-difference 417 Misc-difference 472 Misc-difference 517 Misc-difference 853 Misc-difference 906 Misc-difference 467 Misc-difference 

The invention relates to an immunogenic complex comprising one glycoside and one lipid, integrated into an iscom complex or matrix and one antigen which is integrated into the iscom complex or coupled on to or mixed with the iscom complex or iscom matrix complex, also comprising an enzyme. The immunogenic complex is used for providing iscom complexes on to which a receptor expressed on a cell capable of antigen presentation. The complex may also be used as an immunogenic matrix complex compression on a lipid onto which antigens, enzymes and/or peptides or glycoside, a lipid onto which antigens, enzymes and/or peptides or grotelins, which specifically bind to a receptor expressed on a cell capable of antigen presentation have been coupled. The invention is used as vaccine. The present sequence is cholera toxin Al subunit (CTAI)-OVA An immunogenic complex for use as immunostimulating complexes (iscoms) or matrixes comprises a glycoside and a lipid integrated into the 1092 GLVDASDFETSVMAGLENKSGKKCINFCHSHRIOSSLMVISHLITLFLTRGNXXVVLMLD 1151 ------RHRIVRCICPSRLTPYLRQAKVLCQLD- 44 -----EEEVL------HSPRLTNSAMRAGHLLDLLKTRGKNGAIAFLE 81 41; Kaastrup DB 23; Length 1266; Indels Loewenadler B, 37; Pred No. 12; ; Mismatches Score 70.5; Search completed: January 22, 2003, 08:52:10 Job time : 22.8535 secs /note= "Encoded by TGA" /note= "Encoded by TGA" Mc Mowat A, Example 2; Fig 7; 64pp; English. 17; 12.6%; 01-OCT-2001; 2001WO-SE02117 29-SEP-2000; 2000SE-0003538 protein of the invention. Conservative 3 TALDEETLWEMMESH----χ, Misc-difference 1235 Dalsgaard 2002-372091/40. Query Match Best Local Similarity Matches 25; Conserv 1266 AA; (ISCO-) ISCONOVA N-PSDB; AAD35585 WO200226255-A1 34-APR-2002 Lycke N, Sequence complex 45 g δy δ

э, Э,

THIS PAGE BLANK (USPTO)

```
US-09-069-023-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-069-023-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31;
Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
Pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2, Appli
2, Appli
13, Appli
13, Appli
18, Appl
60, Appl
59, Appl
15, Appl
15, Appl
15, Appl
142, Appl
142, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Appl
Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 36, App.
                                                                                                                  January 22, 2003, 08:52:30; Search time 7.33468 Seconds (without alignments) 429.229 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Sequence 18, Sequence 61, Sequence 60, Sequence 15, Sequence 15, Sequence 15, Sequence 142, Sequence 73, Sequence 72, Sequence 72, Sequence 72, Sequence 72, Sequence 72, Sequence 28, Sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33, 1
236,
                                                                                                                                                                                                                               1 ALTALDEETLWEMMESHRHR......PDVYTLVTGLQPDVDFSNFS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
               5.1.3
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-069-023-36
US-09-069-023-38
US-08-029-023-38
US-08-042-72-2
US-08-942-761-2
US-08-942-761-2
US-08-147-4948-13
US-08-16-2968-61
US-08-16-2968-61
US-08-16-2968-61
US-08-16-2968-61
US-08-16-2968-61
US-08-16-2968-15
US-09-16-2968-17
US-09-16-2968-17
US-08-16-2968-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-557-034-33
US-09-564-805-236
                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                       262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
               GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                           US-09-767-215-2_COPY_10_116
560
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                    - protein search, using sw model
                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                               length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match
                                                                                                                                                                                                                                                                                                                                                                                               sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB
Maximum DB
                                                                                      protein
                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Result
```

```
Sequence 7, Appli
Sequence 5, Appli
Sequence 9, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4908, Ap
Sequence 3032, Ap
Sequence 20, Appli
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 36, Application US/09069023A

Sequence 36, Application US/09069023A

Patent No. 6348573

GENERAL INFORMATION:
APPLICANT: INDEX, Gabriel
APPLICANT: Inchez, Gabriel
APPLICANT: Roseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
CURRENT APPLICATION NUMBER: US/09/069,023A

NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 36
LINGTH: 233
                                                                                                                                                                                                                                                    Sequence 11, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 38, Application US/09069023A
Patent No. 6348573
GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Inchara, Nachiro
APPLICANT: Nunez, Gabriel
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REPERENCE: UM-033A
CURRENT APPLICATION NUMBER: US/09/069,023A
CURRENT APPLICATION NUMBER: US/09/069,023A
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 ALDEETLWEM----MESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAM 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32; Indels
                  US-08-749-902-5
US-08-504-048-9
US-09-342-647-2
US-09-055-097-3
US-08-652-971-4
US-08-991-258A-4
US-08-991-953A-4
US-08-991-34-001C-3032
US-09-134-001C-3032
US-09-134-001C-3032
US-09-134-05-04-13
US-08-702-153-4
US-08-702-153-4
US-08-702-153-4
US-08-702-153-4
US-08-897-719-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.5%; Score 81; DB 4; 36.5%; Pred. No. 0.006; tive 14; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | | | | | | : | | : | | | RAGKLLDYLQENPK-GLDTLVESIR 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAGHLLDLLKTRGKNGAIAFLESLK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
     TYPE: PRT
CORGANISM: Homo sapiens
US-09-069-023-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
```

```
δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 TALDEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAG 62
                                                                                                                                                                                4 ALDEETLWEM----MESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAM 59
                                                                                                                                                                                                        11.9%; Score 66.5; DB 1; Length 497; 26.1%; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Duhamel, Gerald E.
APPLICANT: Elder, Robert
TITLE OF INVENTION: Nucleotide Sequences and Methods for
TITLE OF INVENTION: Detection of Serpulina Hyodysenteriae
NUMBER OF SEQUENCES: 5
                                                                                             13.9%; Score 78; DB 4; Length 233; 35.3%; Pred. No. 0.015; tive 14; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,492
FILING DATE:
CLASSIFICATION: 424
ATTONNEY/AGENT INPORMATION:
NAME: ROWALCHYK, Ratherine M.
REGISTRATION NUMBER: 36,848
REFERENCE/POCKET NUMBER: 9338.25US01
TELECOMMULICATION INFORMATION:
TELECOMMULICATION:
TELECOMMULICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               392 ----LLIYREKTNASIVLKDAVSFLMHENDIY 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 HLLDLLKTRGK-NGAIAFLESLKF--HNPDVY 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSE: Merchant & Gould
STREET: 3100 No. 5698394west Center
CITY: Minneapolis
STATE: M
COUNTRY: USA
ZIP: 55402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                   60 RAGHLLDLLKTRGKNGAIAFLESLK 84
                                                                                                                                                                                                                                                                                             64 RAGKLLDYLQ-ENPRGLDTLVESIR 87
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08252492 Patent No. 5698394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 497 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 26.18
Matches 24; Conservative
                                                                                                    Ouery Match
Best Local Similarity 35.39
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-252-492-2
               TYPE: PRT
CRGANISM: Mus musculus
US-09-069-023-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                             US-08-252-492-2
LENGTH: 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                           g
```

RESULT 4

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 TALDEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08942761
Patent No. 6068843
GENERAL INFORMATION:
APPLICANT: Duhamel, Gerald E.
APPLICANT: Blder, Robert
ATTLE OF INVENTION: Nucleotide Sequences and Methods for TITLE OF INVENTION: Detection of Serpulina Hyodysenteriae
                                      GERREAL INFORMATION:
APPLICANT: Duhamel, Gerald E.
APPLICANT: Duhamel, Robert
TILLE OF INVENTION: Nucleotide Sequences and Methods for
TITLE OF INVENTION: Detection of Serpulina Hyodysenteriae
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5869630west Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/727,126
FILING DATE: 08-OCT-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 66.5; DE; Pred. No. 1.8; 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          392 ----LLIYREKTNASIVLKDAVSFLMHENDIY 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 HLLDLLKTRGK-NGAIAFLESLKF--HNPDVY 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9338.25US01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 6068843west Center
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08,252,492
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kowalchyk, Katherine M.
REGISCRATION NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 39,38.255
TELECOMMUNICATION:
Sequence 2, Application US/08727126
Patent No. 5869630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.9%;
26.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       612-332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 497 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-727-126-2
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                               STREET: 3100 No. SCITY: Minneapolis STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 24; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55402
                                                                                                                                                                                                                                                                                COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
US-08-942-761-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
```

4

```
FILING DATE: June 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J.
REGISTRATION NUMBER: 24,175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19; Conservative
                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Cleveland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 GLOPDVDF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 NLNPDLQY 72
                                                                                                                                                                                                                                                                                                                                                                                        00
                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
US-08-427-497E-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-341-843B-13
                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL:
                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :| : |: | || : : :| :| :| :| 342 TVIDADALYLMFESTLNELNNFI---TPPHIYEFEKLTQINHIEVLENPYQA------ 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 TALDEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 11.9%; Score 66.5; DB 3; Length 497; Best Local Similarity 26.1%; Pred. No. 1.8; Matches 24; Conservative 18; Mismatches 33; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Lemmon, Vance
TITLE OF INVENTION: A Method for Characterizing the
TITLE OF INVENTION: A Method for Characterizing the
TITLE OF INVENTION: Nucleotide Sequence
TITLE OF INVENTION: The Nucleotide Sequence
TITLE OF INVENTION: The Nucleotide Sequence
TITLE OF INVENTION: Characterized Thereby
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fay, Sharpe, Beall, Fagan,
ADDRESSEE: Minnich & McKee
STREET: 1100 Superior Avenue
STREET: Suite 700
CITY: Cleveland
STATE: Ohio
medium TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/942,761
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COFERATING SICTION DATA:
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/341,843B
FILING DATE: NO. 5872225ember 18, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
MEDIUM TYPE: storable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            392 ----LLIYREKTNASIVLKDAVSFLMHENDIY 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 HLLDLLKTRGK-NGAIAFLESLKF--HNPDVY 91
                                                                                                                                                                                                                                                                                                                                           9338.250S01
                                                                                                                                                              CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/252,492
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KOWAICHYK, KATHERINE M.
REGISTRATION NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 9338.25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEPHONE: 612-332-5001
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
FENCTH: 497 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/08341843B Patent No. 5872225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Compaq Prolinea 5100e OPERATING SYSTEM: DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 497 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 44114-2518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-341-843B-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-942-761-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

```
41 CQLDEEEVLH-SPRLTNSAMRAGHLLDLLKTRGKNGAIAFLE----SLKFHNPDVYTLVT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.7%; Score 65.5; DB 2; Length 98; 27.9%; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Method for Characterizing the Nucleotide Sequence of LICAM and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18, Application US/08427497E
Patent No. 5969124
GENERAL INFORMATION: Vance
APPLICANT: Lemmon, Vance
TITLE OF INVENTION: Nucleotide Sequence of LIC;
Patent No. 5969124
TITLE OF INVENTION: the Nucleotide Sequence
TITLE OF INVENTION: Characterized Thereby
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                            ORGANISM: mouse
INDIVIDUAL ISOLATE: 8 day old mouse brain
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          member of the immunoglobulin
superfamily with binding domains
similar to fibronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neural adhesion molecule L1 is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Fay, Sharpe, Beall, Fagan, ADDRESSEE: Minhich & McKee
STREET: 1100 Superior Avenue
STREET: Suite 700
REFERENCE/DOCKET NUMBER: CWR 2 149-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582
TELERX: (216) 241-1666
TELEX: (216) 980162
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            LIBRARY: lamda GT 10 and lamda GT11 CLONE: synthesis of several clones PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: amino acids
HYPOTHETICAL: irrelevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS: Tacke, R.
AUTHORS: Scherer, H.
AUTHORS: Teplow, D.
AUTHORS: Fruh, K.
AUTHORS: Schachner, M.
```

ä

```
Sequence 60, Application US/08506296B
Sequence 60, Application US/08506296B
Sequence 60, Sala265
GENERAL INFORMATION:
APPLICANT: Phillips, Greg
APPLICANT: Cunningham, Bruce A.
APPLICANT: CLOSSIN, Kathryn L.
TITLE OF INVENTION: NEURITE OUTGROWTH-PROMOTING POLYPEPTIDES
TITLE OF INVENTION: CONTAINING FIBRONECTIN TYPE III REPEATS AND METHODS OF USE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
Patent No. 6313265
GENERAL INFORMATION:
APPLICANT: Phillips, Greg
APPLICANT: Cunningham, Bruce A.
APPLICANT: Crossin, Kathryn L.
TITLE OF INVENTION: NEURITE OUTGROWTH-PROMOTING POLYPEPTIDES
TITLE OF INVENTION: CONTAINING FIBRONECTIN TYPE III REPEATS AND METHODS OF USE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 CQLDEEEVLH-SPRLTNSAMRAGHLLDLLKTRGKNGALAFLE----SLKFHNPDVYTLVT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.7%; Score 65.5; DB 4; Length 209; 27.9%; Pred. No. 0.69; tive 12; Mismatches 26; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: The Scripps Research Institute
STREET: 10550 No. 6313265th Torrey Pines Road, TPC-8
                                                                                                                                                                                                   ADDRESSEE: The Scripps Research Institute
STREET: 10550 No. 6313265th Torrey Pines Road, TPC-8
                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/506,296B
FILING DATE: 24-JUL-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 24-JUL-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: FILLING, Thomas
REGISTRATION UNDABER: 34,163
REFERENCE/DOCKET NUMBER: TSRI
TELECOMMUNICATION. INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (619) 554-2937
TELEFAX: (619) 554-6312
INFORMATION FOR SEQ ID NO: 61:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 11.7%
Best Local Similarity 27.9%
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-506-296B-61
                                                                                                                                                                                                                                                                                                               ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: La Jolla
STATE: California
                                                                                                                                                                                                                                            CITY: La Jolla
STATE: California
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 GLQPDVDF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 NLNPDLQY 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-506-296B-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 CQSDTSLLLHWQPPLSHNGVLTGYLLSYHPVEGESKEQLFFNLSDPELRTHN-----LT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 COLDEEEVLH-SPRLTNSAMRAGHLLDLLKTRGKNGAIAFLE----SLKFHNPDVYTLVT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.7%; Score 65.5; DB 2; 27.9%; Pred. No. 0.22; tive 12; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: mouse
INDIVIDUAL ISOLATE: 8 day old mouse brain
IMMEDIATE SOURCE:
LIBRARY: lamda GT 10 and lamda GT11
CLONE: synthesis of several clones
PUBLICATION INFORMATION:
AUTHORS: Moos, M.
AUTHORS: Scherer, H.
AUTHORS: Teplow, D.
                             COUNTRY: U.S.A.
ZIF: 44114-2518
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
MEDIUM TYPE: storable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neural adhesion molecule L1 is a
member of the immunoglobulin
superfamily with binding domains
similar to fibronectin
                                                                                                                                                                                                                                                                                                                                                                                                                           CWR 2 149-3-1
                                                                                                                                                                                SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NAME: US/08/427,497E
FILING DATE: APIL1 24, 1995
CLASSIFICATION 3435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/904,991
FILING DATE: June 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J.
REGIERROCE/COCKET NUMBER: 24,175
REFERROCE/COCKET NUMBER: CWR 2 149-3-
FILECOMMUNICATION INFORMATION:
TELEFONE: (216) 241-1666
TELEFAX: (216) 280162
TELEFAX: (216) 241-1666
TELEFAX: (216) 980162
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                         COMPUTER: Compaq Prolinea 5100e OPERATING SYSTEM: DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: amino acids
HYPOTHTICAL: irrelevant
ANTI-SENSE: no
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schachner, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VOLUME: 334
ISSUE:
PAGES: 701-702
PAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 GLQPDVDF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 NLNPDLQY 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-427-497E-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS:
AUTHORS:
TITLE: Ne
TITLE: me
TITLE: su
TITLE: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ογ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
```

3,

ZIP: 92037 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

US-08-506-296B-61 ; Sequence 61, Application US/08506296B

RESULT 8

ë,

```
192 MRGCRHSGVRIIIPPRKAP--QPTRVTCRYLGKDKLAHPPPLSEGEALASRILEMAPHGA 249
                                                                                                                                                                                                                                                     41 CQLDEEEVLH-SPRLTNSAMRAGHLLDLLKTRGKNGAIAFLE----SLKFHNPDVYTLVT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 MESHRHRIVRCICPSRLTPYLRQAKVLCQ-LDEEEVLHSPRLTNSAMRAGHLLDL---- 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Application US/09031485

Patent No. 5824306

GENERAL INFORMATION:
APPLICANT: Tang, Liang
APPLICANT: Blehm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
ORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
                                                                                                                                   DB 4; Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 409;
                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,485
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DARBER: US/08/847,429
FILING DATE: 24-APR-1997
ATTORNEEY/AGENT INFORMATION:
                                                                                                                                 11.7%; Score 65.5; DE 27.9%; Pred. No. 1.8; tive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 11.7%; Score 65.5; DI Best Local Similarity 25.0%; Pred. No. 1.9; Matches 22; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
PRFFRENCE/DOCKET NUMBER: HW-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: HW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                // TOPOLOGY: linear
MOLECULE TYPE: protein
// FRAGMENT TYPE: C-terminal
US-08-506-296B-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 409 amino acids
                                                                                                                                                      Best Local Similarity 27.99
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-09-031-485-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
      amino acid
                           linear
                                                                                                                                                                                                                                                                                                               96 GLQPDVDF 103
                                                                                                                                                                                                                                                                                                                                                        118 NLNPDLQY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-031-485-15
                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                               δλ
                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δλ
                                                                                                                                                                                                                           δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: Phillips, Greg
APPLICANT: Cunningham, Bruce A.

APPLICANT: Cunningham, Bruce A.

APPLICANT: CUNNING BROWN L.

TITLE OF INVENTION: CONTAINING FIBRONECTIN TYPE III REPEATS AND METHODS OF USE NUMBER OF SEQUENCES: 77

CORRESPONDENCE ADDRESS:

ADDRESSEE: The Scripps Research Institute
STREET: 10550 No. 6313265th Torrey Pines Road, TPC-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 CQLDEEEVLH-SPRLTNSAMRAGHLLDLLKTRGKNGAIAFLE----SLKFHNPDVYTLVT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 24-JUL-1995
CLASSIFICATION: 514
                                         PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
11.7%; Score 65.5; DB 4;
Best Local Similarity 27.9%; Pred. No. 1.2;
Matches 19; Conservative 12; Mismatches 26;
                                                                                                                                                                        NAME: Fitting, Thomas
REGISTRATION NUMBER: 34.163
REFERENCE/DOCKET NUMBER: TSRI 488.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 554-2937
TELEFAX: (619) 554-6312
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
                                                                                   APPLICATION NUMBER: US/08/506,296B
FILING DATE: 24-JUL-1995
CLASSIFICATION: 514
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 59, Application US/08506296B Patent No. 6313265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 554-2937
TELEPAX: (619) 554-2937
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
                                                                                                            FILING DATE: 24-JUL-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: FILLING, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         397 amino acids
                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-506-296B-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   La Jolla
1: California
1RY: U.S.
COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ||: :
165 NLNPDLQY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 GLQPDVDF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
US-08-506-2968-59
                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: STATE:
```

g õ

```
14 MESHRHRIVRCICPSRLTPYLRQAKVLCQ-LDEEEVLHSPRLTNSAMRAGHLLDL---- 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tang, Liang
Blehm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
PROTEINS, NUCLEIC ACID MOLECULES, AND
UMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.7%; Score 65.5; DB 3; Length 409; illarity 25.0%; Pred. No. 1.9; Conservative 12; Mismatches 33; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible OPERATING SYSTEM: Windows 95 SOFTWARE: WordPerfect for Windows, Version 7.0
                                                                                                                                                         COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: Windows 95
SOFTWARE: WORDPERFECT for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,474
FILING DATE: 24-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INPORMATION:
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Carol Talkington Verser, Ph.D. Heska Corporation
Carol Talkington Verser, Ph.D.
Heska Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,034
FILING DATE: 21-Apr-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1825 Sharp Point Drive CITY: Fort Collins STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250 KFLGPVILEVPHFASLRGREREIVILRS 277
                                                                                                                                                                                                                                                                                                                                                                                                                                       HW-5-C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 ------LKTRGKNGAIAFLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                         NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5-C
TELECOMMUNICATION INFORMATION:
TELEBHONE: 970/493-7272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-09-557-034-15
Sequence 15, Application US/09557034
Patent No. 6365569
GENERAL INFORMATION:
                                               STREET: 1825 Sharp Point Drive CITY: Fort Collins STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               409 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 22; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
    ADDRESSEE:
ADDRESSEE:
                                                                                                                                          80525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-065-474-15
                                                                                             STATE: CC
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ج
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 MRGCRHSGVRIIIPPRKAP--OPTRVICRYLGKDKLAHPPPLSEGEALASRILEMAPHGA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 MESHRHRIVRCICPSRLTPYLRQAKVLCQ-LDEEEVLHSPRLTNSAMRAGHLLDL---- 67
                                                                                                                                                                                                                                     GENERAL INFORMATION. Liang
APPLICANT: Blehm, E. Scot
APPLICANT: Blehm, E. Scot
APPLICANT: Blehm, E. Scot
TITLE OF INVENTION: DISPEILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: DISPEILARIA NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Colins
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-09-065-474-15
US-09-065-474
Sequence 15, Application US/09065474
Patent No. 6063599
GENERAL INFORMATION:
APPLICANT: Tang, Liang
APPLICANT: Tang, Liang
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/847,429A
FILLING DATE: 24.APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
11.7%; Score 65.5; DB
Best Local Similarity 25.0%; Pred. No. 1.9;
Matches 22; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 KFLGPVILEVPHFASLRGREREIVILRS 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 KFLGPVILEVPHFASLRGREREIVILRS 277
                82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435 ATTORNEY AS ATTORNEY/AGENT INFORMATION:
NAME: VERSEr, Carol Talkington REGISTRATION NUMBER: 37.459
REFERENCE/DOCKET NUMBER: HW-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/489-7272
TELEPHONE: 970/484-9505
                                                                                                                                                                    Sequence 15, Application US/08847429A
Patent No. 5827692
                   ---LKTRGKNGAIAFLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 409 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 409 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-847-429A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8052
                                                                                                                                                         US-08-847-429A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                       ò
                                                                  g
```

21;

```
.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 MESHRHRIVRCICPSRLTPYLRQAKVLCQ-LDEEEVLHSPRLTNSAMRAGHLLDL---- 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-065-474-142

Sequence 142, Application US/09065474

Faction No. 6063965

Faction No. 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 25.0%; Pred. No. 1.9;
Matches 22; Conservative 12; Mismatches 33; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: Worldberfect for Windows, Version 7.0

CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/09/065,474

FILING DATE: 24-APR-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAMME: VERSEX, Carol Talkington

REGISTRATION NUMBER: 37,459

REFERENCE/DOCKET NUMBER: 37,459

REFERENCE/DOCKET NUMBER: 37,459

TELECHMUNICATION INFORMATION:

TELECHMUNICATION INFORMATION:

TELEFRAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 142:

SEQUENCE CHARACTERISTICS:

LENGTH: 422 amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: ALLO ACID ACID
                       ATORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REGISTRATION INFORMATION:
TELEPHONE: 970/493-7272
TELEPAX: 970/493-7272
TELEFAX: 970/494-9505
INFORMATION FOR SEO ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 409 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: amino acid;
; TOPOLOGY: linear;
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-557-034-15
APPLICATION NUMBER: 09/065,474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               250 KFLGPVILEVPHFASLRGREREIVILRS 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: Protein
US-09-065-474-142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

THIS PAGE BLANK (USPTG)

Sequence 236, App

9 US-09-992-598-236

344

11.0

61.5

20

```
January 22, 2003, 08:49:35; Search time 4.31452 Seconds (without alignments) 500.428 Million cell updates/sec
                                                                                                                                                                                                                                                                                                       US-09-767-215-2_COPY_10_116
560
1 ALTALDEETLWEMMESHRHR......PDVYTLVTGLQPDVDFSNFS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1: /cgn2_6/ptodata/2/pubpa/USOB_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpa/USOB_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpa/USOB_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpa/USOT_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpa/USOT_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpa/USOT_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpa/USOB_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpa/USOB_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpa/USOB_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpa/USOB_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpa/USOB_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpa/USOB_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122226 seqs, 20178551 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                   Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

																	•		
Description	Sequence 16, Appl			Sequence 18, Appl	Sequence 8, Appli	Sequence 10, Appl	Sequence 2, Appli	Sequence 20, Appl	Sequence 4, Appli	Sequence 4454, Ap	Sequence 200, App	Sequence 27, Appl	Sequence 229, App	Sequence 230, App	Sequence 7, Appli	Sequence 285, App	Sequence 4, Appli	Sequence 3, Appli	Sequence 11, Appl
B ID	9 US-10-032-159A-16	10 US-09-767-215-2	10 US-09-767-215-5	9 US-10-032-159A-18	9 US-10-032-159A-8	9 US-10-032-159A-10	9 US-10-032-159A-2	9 US-10-032-159A-20	9 US-10-032-159A-4	9 US-09-738-626-4454	12 US-10-078-929-200	9 US-10-024-918-27			9 US-10-058-820-7	9 US-09-712-363-285	9 US-10-058-820-4	9 US-10-058-820-3	10 US-09-910-150-11
% Query Watch Length DB	139	1004	1138	92	1247	92	366	366	72	763	431	1260	433	433	100	461	476	553	926
% Query Match	100.0	100.0	100.0	86.4	48.2	45.9	37.3	37.3	28.2	12.1	12.0	11.7	11.2	11.2	11.2	11.2	11.2	11.2	11.2
Score	260	260	260	484	270	257	209	209	158	67.5	49	65.5	63	63	62.5	62.5	62.5	62.5	62.5
Result No.	1	7	m	4	ហ	9	7	80	6	10	11	12	13	14	15	16	17	18	19

RESULT 2 US-09-767-215-2

```
RESULT 5
US-10-032-159A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-032-159A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ōλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                   δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 ALTALDEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMR 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 ALTALDEETLWEWMESHRRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMR 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ALTALDEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ALTALDEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 560; DB 10; Length 1004; 100.0%; Pred. No. 4.4e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1138;
                                GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF;
FILE REFERENCE: 07334-142001
CURRENT APPLICATION NUMBER: US/09/767,215
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 60/181,159
PRIOR FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-09-767-215-5
; Sequence 5, Application US/09767215
; Sequence 5, Application US/09767215
; Patent No. US20020081636A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-142001
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 60/181,159
; PRIOR FILING DATE: 2000-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 AGHLLDLIKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFSNFS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AGHLLDLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFSNFS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 560; DB 10;
100.0%; Pred. No. 5.1e-56;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18, Application US/10032159A Patent No. US20020164703A1 GENERAL INFORMATION: APPLICANT: Pawlowski, Krzysztof APPLICANT: Reed, John C.
Sequence 2, Application US/09767215
Patent No. US20020081636A1
                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
COCCANISM: Homo sapiens
US-09-767-215-5
                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-032-159A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1138
                                                                                                                                                                                                                                                                                                                                        US-09-767-215-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                            õ
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 DEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGHLL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 EETLWEMMESHRHRIVRCICPSRLTPYLROAKVLCOLDEEEVLHSPRLTNSAMRAGHLLD 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EETLWEMMESHRHRIVRCICPSRLIPPYLRQAKVLCQLDEEEVLHSPRLTNSAWRAGHLLD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 8, Application US/10032159A; Sequence 8, Application US/10032159A; Sequence 8, Application US/10032159A; Patent No. US20020164703A1; General Information: Read, John C. APPLICANT: Pawlowski, Adam C. APPLICANT: Gedalk, Adam C. TITLE OF INVENTION: ENCODING NUCLEIC ACIDS, AND METHODS OF USE FILE REFERENCE: P-LJ 5100; CURRENT APPLICATION NUMBER: US/10/032,159A; CURRENT FILING DATE: 2000-12-19; PRIOR APPLICATION NUMBER: US 60/257,457; PRIOR PLING DATE: 2000-12-21; NUMBER OF SEQ ID NOS: 37; SOFTWARE: FastSEQ for Windows Version 4.0
APPLICANT: Godzik, Adam
TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,
TITLE OF INVENTION: EARD-DOMAIN CALLS, AND METHODS OF USE
TITLE OF INVENTION: BNCODING NUCLEIC ACIDS, AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/10/032,159A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 60/257,457
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 92
LENGTH: PRT
CREATER PRT

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9; Length 1247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.2%; Score 270; DB 9; L
51.5%; Pred. No. 1e-22;
tive 22; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 86.4%; Score 484; DB 9; 1
Best Local Similarity 100.0%; Pred. No. 1.1e-48;
Matches 92; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 DLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 LLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQ 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/10032159A
Patent No. US20020164703A1
GENERAL INFORMATION:
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Reed, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 51.59
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
US-10-032-159A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-032-159A-18
```

```
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 KNGAIAFLESL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | :||||||
62 HKGYVAFLESL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-738-626-4454
                                                                                                                                                                                                                                              US-10-032-159A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-032-159A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-032-159A-4
                                                                                                                                                                                       LENGTH: 366
                                                                                                                                                                 SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                 οqα
                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                     7 EETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGHLLD 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 DEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGHLL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PAWLOWSKI, KZZYSZLOF
APPLICANT: Reed, John C.
APPLICANT: Reed, John C.
APPLICANT: Reed, John C.
APPLICANT: Reed, John C.
TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,
TITLE OF INVENTION: ENCODING NUCLEIC ACIDS, AND METHODS OF USE
FILE REFERENCE: P-LJ 5100
CURRENT APPLICATION NUMBER: US 60/22,159A
CURRENT FILING DATE: 2001-12-19
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,
TITLE OF INVENTION: ENCODING NUCLEIC ACIDS, AND METHODS OF USE
FILE REPERENCE: P-LJ 5100
CURRENT APPLICATION UNBER: US/10/032,159A
RIOR APPLICATION NUMBER: US 60/257,457
PRIOR PAPLIA DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 366;
                                                                                                                                                                                                                                                                                                       Length 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence 20 Application US/10032159A
patent No. US20020164703A1
GENERAL INFORMATION:
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Reed, John C.
APPLICANT: Reed, John C.
APPLICANT: TREE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,
TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.3%; Score 209; DB 9; I
44.4%; Pred. No. 2.1e-16;
tive 16; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 DLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.9%; Score 257; DB 9;
ilarity 53.3%; Pred. No. 1.2e-22;
Conservative 20; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 LLKTRGKNGAIAFLESLKFHNPDVYTLVTG 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 2, Application US/10032159A ; Patent No. US20020164703A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-159A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-032-159A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-032-159A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-032-159A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 DEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGHLL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 MMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGHLLDLLKTRG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/10032159A
Patent No. US20020164703A1
Sequence 4, Application US/10032159A
Patent No. US20020164703A1
Sebreral Information:
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Reed, John C.
TITLE OF INVENTION: EMCODING NUCLEIC ACIDS, AND METHODS OF USE
FILE REFERENCE: P-LJ 5100
CURRENT APPLICATION NUMBER: US/10/032,159A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 60/257,457
PRIOR APPLICATION NUMBER: US 60/257,457
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
TITLE OF INVENTION: ENCODING NUCLEIC ACIDS, AND METHODS OF USE CURRENT APPLICATION NUMBER: US/10/032,159A
CURRENT APPLICATION NUMBER: US/10/032,159A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 60/257,457
NUMBER OF SEC 1D NOTE: 200-12-21
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                        37.3%; Score 209; DB 9; Length 366; 44.4%; Pred. No. 2.1e-16; Live 16; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.2%; Score 158; DB 9; Length 72;
49.3%; Pred. No. 1.9e-11;
iive 9; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 DLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4454, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGANA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO:
APPLICANT: HAYASHI, MIKIRO
APPLICANT: CCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 44.48
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
```

```
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sandal, Molline
APPLICANT: Meyers, Blake
APPLICANT: Odell, Joan T.
APPLICANT: Meyers, Blake
APPLICANT: Meyers, Blake
APPLICANT: Meyers, Blake
APPLICANT: Meyers, Blake
APPLICANT: Weng, Zude
TITLE OF INVENTION: Stress Response
TITLE OF INVENTION: Stress Response
TITLE OF INVENTION: Stress Response
FILE REFERENCE: BB1357 US NA
CURRENT APPLICATION NUMBER: US/10/078,929
CURRENT APPLICATION NUMBER: 09/566,394
PRIOR APPLICATION NUMBER: 60/133042
PRIOR FILING DATE: 1999-05-07
PRIOR PILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133427
PRIOR APPLICATION NUMBER: 60/133437
PRIOR FILING DATE: 1999-05-11
PRIOR PELLING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133436
PRIOR FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: 60/133436
PRIOR FILING DATE: 1999-06-11
PRIOR FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | : :: | ::|: | ::|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- | :-|- 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 QAKVLCQLDEEEVLHSPRLTNSAMRAGHLLDLLKTRGKNGAIAF---LESLKFHNPDVYT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 12.1%; Score 67.5; DB 9; Length 763; Best Local Similarity 30.4%; Pred. No. 9.1; Matches 21; Conservative 13; Mismatches 28; Indels
                                                                                                                                                                                                      FILE REFERENCE: 249-125
CURRENT APPLICATION NOVEL POLYNUCLECTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Corynebacterium glutamicum US-09-738-626-4454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 200, Application US/10078929 Patent No. US20020152497A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Miao, Guo-Hua
Falco, Saverio Carl
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Rafalski, Antoni
                                                                                                                                          IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sakai, Hajime
                                                                                                                                                                                    OZAKI, AKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 LVTGLQPDV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           496 EVTGL-PDI 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-078-929-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                            APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

```
APPLICANT: Schense, Jason
APPLICANT: 21sch, Andreas
APPLICANT: 21sch, Andreas
APPLICANT: 21sch, Andreas
APPLICANT: 1sch, Andreas
APPLICANT: Hall, Heike
TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE ENGINEERING
FILE REFERENCE: CIT 2606 CIP
CURRENT APPLICATION NUMBER: US/10/024,918
CURRENT FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 33
SOFWARE: Patentin version 3.1
SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COTATION: (516)..(604)
COTHER INFORMATION: the sixth Ig-like domain of the cell adhesion molecule L1
US-10-024-918-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ώ
,
                                                                                                                                                                                                                                       ;
9
                                                                                                                                                                                                                                                                                                                                                                                                           248 EGSTYEILAAH---IWRCACKARGLTDDQATKLYVATDGRSRLCPPLPPGYLGNVVFTAT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                 7 EETLWEMMESHRHRIVRCICP-----SALTP-----YLRQAK-VLC 41
                                                                                                                                                                                                                                                                                                                                                                              42 QLDEEEVLHSPRLTNSAMRAGHLLDLLKTRGKNGAIAFLESLKFHNPDVYTLVTG----L 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 CQLDEEEVLH-SPRLTNSAMRAGHLLDLLKTRGKNGAIAFLE----SLKFHNPDVYTLVT 95
                                                                                                                                                                                                                                       36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1260;
                                                                                                                                                                                         Length 431;
                                                                                                                                                                                                                                     45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9;
                                                                                                                                                                                         DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 229, Application US/09771161A
Patent No. US20020110811A1
GENERAL INFORMATION:
APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION UMBER: US/09/771,161A
CURRENT FILLING DATE: 2001-01-26
                                                                                                                                                                                                                                17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 11.7%; Score 65.5; I Best Local Similarity 27.9%; Pred. No. 29; Matches 19; Conservative 12; Mismatches
                                                                                                                                                                                         Score 67;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 77, Application US/10024918; Patent No. US/2002018718A1
GENERAL INFORMATION: APPLICANT: APPLICANT: Hubbell, Jeffrey
                                                                                                                                                                                       12.0%;
24.6%;
NUMBER OF SEQ ID NOS: 208
SOFTWARE: Microsoft Office 97
SEQ ID NO 200
LENGTH: 431
                                                                                                                                                                                                                                     Conservative
                                                                                                             ; ORGANISM: Ipomoea batatas
US-10-078-929-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Mus Musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 SPNLNINSWT 370
                                                                                                                                                                                       Ouery Match
Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 QPDVDFSNFS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ||: :
981 NLNPDLQY 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 GLQPDVDF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-09-771-161A-229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-024-918-27
```

S

```
Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   οy
                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 EKQKMYMVME-----YCVCGMQEMLDSVPEKRFPVCQAHGYFCQLIDGLEYLHSQGIV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 EKQKMYMVME-----YCVCGMQEMLDSVPEKRFPVCQAHGYFCQLIDGLEYLHSQGIV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 HKDIKPGNL--LLTTGGTLKISDLGVAEALHPFAADDTCRTSQGSPAFOPPEIANGLDTF 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 HKDIKPGNL--LLTTGGTLKISDLGVAEALHPFAADDTCRTSQGSPAFQPPEIANGLDTF 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NSAMRAGHLLDLLKTRG--KNGAIAFLESL-------KFHNPDV----- 90
                                                                                                                                                                                                                                                                                                                                                                                                                        6 DEETLWEMMESHRHRIVRCIC-----PSRLTPYLRQAKVLCQL-DEEEVLHSPRLT 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 DEETLWEMMESHRHRIVRCIC-----PSRLTPYLRQAKVLCQL-DEEEVLHSPRLT 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58;
                                                                                                                                                                                                                                                                                                                           Query Match 11.2%; Score 63; DB 10; Length 433; Best Local Similarity 21.0%; Pred. No. 15; Matches 30; Conservative 19; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.2%; Score 63; DB 10; Length 433; 21.0%; Pred. No. 15; tive 19; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR PILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NOS: 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 NSAMRAGHLLDLLKTRG--KNGAIAFLESL----
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR PELING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR PRIOR APPLICATION NUMBER: 135619
PRIOR PILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGFKVDIWSAGVTLYNITTGLYP 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 SGFKVDIWSAGVTLYNITTGLYP 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----YTLVTGLQP 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----YTLVTGLQP 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 21.0%
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-230
                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-09-771-161A-229
                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ОР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

5,

THIS PAGE BLANK (USPTU)

```
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

January 22, 2003, 08:49:35 ; search time 8.19758 Seconds (without alignments) 1254.807 Million cell updates/sec Run on:

US-09-767-215-2\_COPY\_10\_116 560 1 ALTALDEFTLWEMMESHRHR......PDVYTLVTGLQPDVDFSNFS 107 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result		* Query			SUMMARIES	
No.	Score	Match	Length	DB	ID	Description
щ	73	13.0		7	S55671	hypothetical prote
7	73	13.0		~	н97280	ų
m	72.5	12.9		~	S59644	sister chromatid c
4	7.1	12.7		~	T33012	hypothetical prote
Ŋ	σ.	٠.		~	D72349	$\sim$
9	ζ.			~	T50952	
7	67.5			~	T26673	hypothetical prote
œ	ζ.	12.1		7	E86922	
6	29			~	T13018	hypothetical prote
10	66.5			ď	AB0269	
11	9			7	D95365	
12	ď.	11.7		~	H70947	hypothetical prote
13	5	11.7		7	E83849	
14	65.5	11.7	Н	-	S05479	neural cell adhesi
15	₹.	11.5		N	E69264	pyruvate formate-1
16	4	11.5		7	H83493	hypothetical prote
17	64.5	11.5		7	875969	
18	₹.	11.5		~	T39654	ical
13	64	11.4	221	7	A41333	ത
20	64	11.4		~	T33951	hypothetical prote
21	64	11.4		7	AB3375	beta-(1->2)glucan
22	64	11.4	7	-	S27802	zinc finger protei
23	ø	11.4	~	7	T19450	hypothetical prote
24		11.3		~	H72623	_
25	۳.	11.3		-	YRHUB6	œ
56	63	11.2		7	A30227	hypothetical prote
27	63	11.2		7	_	0
28	63	11.2		7	213	iron(III) dicitrat
59	63	11.2		7	E71136	threonine synthase

hypothetical prote	alanine-tRNA ligas	type I site-specif	type I site-specif	hypothetical prote	GTP-binding regula	chorismate mutase	probable oxidoredu	protein disulfide-	N-acetylglucosamin	hypothetical prote	hypothetical prote	neural cell adhesi	flagellar motor co	probable phosphoes	molybdopterin bios
S57142	H70411	T44802	T09459	G83824	S13221	E82570	B70697	S69181	T31673	T01239	T15890	S36126	G97127	A89124	H64402
7	7	7	~	7	7	~	~	7	7	~	N	~	~	Н	0
728	867	1025	1025	195	356	373	461	513	1036	1111	1168	1259	259	271	298
11.2	11.2	11.2	11.2	11.2	11.2	11.2	11.2	11.2	11.2	11.2	11.2	11.2	11.1	11.1	11.1
63	63	63	63	62.5	62.5	62.5	62.5	62.5	62.5	62.5	62.5	62.5	62	62	62

## ALIGNMENTS

```
Dypothetical protein E10 - equine herpesvirus 2
C;Species: equine herpesvirus 2
C;Species: equine herpesvirus 2
C;Species: equine herpesvirus 2
C;Date: 27-oct-1995 #sequence_revision 03-Nov-1995 #text_change 24-Nov-1999
C;Accession: S55671
R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
T;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
A;Title: The DNA sequence of equine herpesvirus 2
A;Reference number: S5594; MUID:95302501; PMID:7783207
A;Accession: S55671
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Nolecule type: DNA
A;Status: DNA
A;Residues: 1-210 <TEL>
A;Cross-references: GSU200824; NID:96995172; PIDN:AAC13865.1; PID:96995250
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995; Superfamily: equine herpesvirus 2 hypothetical protein E10
```

	5,
	Gaps
	30;
Length 210;	Indels
;	24;
13.0%; Score 73; DB 2; I 29.5%; Pred. No. 2.5;	13; Mismatches
Query Match 13.0%; Score 73; DB 2; I Best Local Similarity 29.5%; Pred. No. 2.5;	atches 28; Conservative 1
UШ	~

Matche	s 28;	Matches 28; Conservative 13; Mismatches 24; Indels 30; Gaps	3; Mism	atches	24;	Indels	30;	Gaps	
	5 LDEETLWEM	5 LDEETLWEM	MESHRHR:	IVRCICPSR	LTPYI	TPYLRQAKVLCQLDEEEVL :    :  :		L 49	
Db 1	6 LTEED:	16 LTEEDIWDVERLCLEELRVLLVSHLKSHKHLDHLRAKKILSREDAEEV- 63	HLKSHKH-		-LDHI	RAKKILSRI	EDAEE	. 63	
Qy 2	O HSPRL	50 HSPRLTNSAMRAGHLLDLLKTRGKNGAIAFLESLK 84	KNGAIAFL	ESLK 84					

# Op

64 -SSRAT-SRSRAGLLVDMCQDHPR-GFQCLKESCK 95

Nydroxyethylthiazole kinase ThiM/ThiK (FS1) CAC3095 [imported] - Clostridium acetobut Cispecies: Clostridium acetobutylicum Cispecies: Clostridium acetobutylicum (Cispecies: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 30-Sep-2001 Cispecies: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #sequence\_revision 14-Sep-2001 #sequence are in the sequence are in the sequence are in the sequence are in the sequence are considered in the sequence and Comparative Analysis of the Solvent-Producing Bacterium A;Reference number: A96900; MUD:21359325; PMID:21359325 A;Accession: H97280 A;

A; Residues: 1-265 <KUR>
A; Residues: 1-265 <KUR>
A; Cross-references: GB: AE001437; PIDN: AAK81035.1; PID: 915026160; GSPDB: GN00168
A; Experimental source: Clostridium acetobutylicum ATCC824
C; Genetics:

A;Gene: CAC3095 C;Superfamily: phosphomethylpyrimidine phosphate kinase

```
A; Map position: 4
A; Introns: 7/2; 32/1; 114/3; 165/3; 202/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.4%;
28.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.1%;
30.0%;
                                                                                                      12.7%;
23.9%;
                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: NCSP: B24P7.70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: T50952
                                                                                               Query Match
Best Local Simi
Matches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
D72349
                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Op
                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Reference number: 221731
A; Reference number: 221731
A; Accession: T38603
A; Accession: T38603
A; Accession: T38603
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Accession: T38603
A; Residues: 1-1583 <DE2>
A; Residues: 1-1583 <DE3
A; Residues: 1-1583 <DE3
A; Residues: 1-1583 <DE3
A; Residues: 1-1583 <BE3
A; Residues: 1-1583 <BE3
A; Reference number: 222478
A; Reference number: 22478
A; Reference number: 222478
A; Reference number: 222478
A; R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sister chromatid cohesion molecule Mis4p - fission yeast (Schizosaccharomyces pombe) C; Species: Schizosaccharomyces pombe C; Species: Schizosaccharomyces pombe C; Date: 14-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 18-Feb-2000 C; Accession: 738603; 743392; S59644 C; Accession: 738603; T43392; S59644 B; Date Library, July 1995 Bubmitted to the EMBL Data Library, July 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: AF047658; PIDN: AAC04418.1; GSPDB:GN00022; CESP:K03H6.2
A; Experimental source: strain Bristol N2; clone K03H6
                                                                            4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O'Species: Caenorhabdatis elegans
C'Species: Cabon, A.
Submitted to the EMBL Data Library, February 1998
A'Speciption: The sequence of C. elegans cosmid K03H6.
A'Specience number: 221263
A'Species: Netlaminary; translated from GB/EMBL/DDBJ
A'Species: DNA
A'Nolecule type: DNA
A'Residues: 1-265 <WAMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1091 LTKAGTATLME------IVPCLCSLFTRLNDYERLKKIVVSCLKSLEEARHS---ENN 1139
                                                                                                                                                                                          23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LTALDEETLWEMMESHRHRIVRCICP--SRLTPYLRQAKVL--CQLDEEEVLHSPRLTNS 57
                                                                            Gaps
                                                                                                                                            20 RIVRCICP--SRLTPYLRQAKVLCQL---DEEEVLHSPRLTNS-----AMRAGHLLD-L 67
                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.9%; Score 72.5; DB 2; Length 1583; 29.0%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : | : | | : | 1140 FQKMVRLIDLIGLESRYGDLNRINDDWKHSLDFISPECDDAYVILLG 1186
   DB 2; Length 265;
                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 AMRAGHLLDLLKTRGKNGAI-----AFLESLKFHNP---DVYTLVTG 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: mis4; SPAC31A2.05c
A;Map position: 1
A;Introns: 33/1; 98/2; 543/3; 699/3; 1294/2; 1339/3; 1558/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39;
                                                                        29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein K03H6.2 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 12.9%; Score 72.5; DE
Best Local Similarity 29.0%; Pred. No. 31;
Matches 31; Conservative 14; Mismatches
Query Match 13.0%; Score 73; DB 3 Best Local Similarity 23.8%; Pred. No. 3.3; Matches 20; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                          TDLFYKNGYIEWFKLEKIDNPNTH 208
                                                                                                                                                                                                                                                                                             68 LKTRGKNGAIAFLESLKFHNPDVY 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: CESP: K03H6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Genetics
                                                                                                                                                                                                                                                                                                                                                                     185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                    ò
```

```
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu submitted to the Protein Sequence Database, July 2000
A;Reference number: 225286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-522 <ARN
A, Cross-references: GB: AE001739; GB: AE000512; NID: g4981176; PIDN: AAD35747.1; PID: g498
A, Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D.H.; Hic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A;Reference number: A72200; MUID:99287316; PMID:10360571
                                                                                                                                                                                                                                                                                                                                                                                                   conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: D72349
E;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickston, K.E.; Clayton, R.A.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Neurospora crassa
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C;Accession: T50952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348 EPLWKLTDEER-SFVRVYHPGKVTYINLEKDALLRAREEGILLSPEEINLHPEKHTMVAG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                          8 ETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTN-----SAMRAG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
                                                     24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: TW0663
C;Superfamily: Pyrococcus horikoshii hypothetical protein PH0466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-270 <SCH>
A; Cross-references: EMBL:AL389890; GSPDB:GN00116; NCSP:B24P7.70
A; Experimental source: BAC clone B24P7; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----HLLDLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFSNF 106
                                                                                                                                                                                                                                                      69 FVAKKAFFDSGYIFEFFYDAYLALWKGGLEAEMRNLKYRYPDYEVWVTG 117
                                                                                                        11 WEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLD--EEEVLHSPRLTNSAMR-
                                                                                                                                                                                                                    -----AGHLL-----DLLKTRGKNGAIAFLESLKFHNPDVYTLVTG 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transposase related protein [imported] - Neurospora crassa N,Alternate names: protein \rm B24P7.70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41;
                                                     40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
  5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 69.5; DB
Pred. No. 18;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.5; D
No. 13;
                                                     19; Mismatches
  DB
Score 71;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
```

	- Arabidopsis thaliana a (mouse-ear cress) Levision 13-Aug-1999 #text_change 22-Oct-1999 1 Staveren, M.; Dirkse, W.; Stiekema, W.; Bancro ance Database, July 1999 1 Staveren, M.; Dancro ance Database, July 1999 1 Columbia; BAC clone FBL21 1 1221/3; 1289/2; 1330/3; 1399/3 1 Score 67; DB 2; Length 1446; 18; Pred. No. 1.1e+02;	Vative 1 SHRHRIVRCI     : : :       : : :   SIRYPSIKCT DLLKTRGKNG       :   PVQKTLDNHA GLQPD 100 GLQCD 100 GLQCD 879	ABOUT 10 ABOLGG C; Species: Yersinia pestis C; Species: Yersinia pestis C; Species: Yersinia pestis C; Date: 02-Nov-2001 C; Species: Yersinia pestis C; Date: 02-Nov-2001 C; Accession: ABOLGG B; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M. denor-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G. il, M.: Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel A; Title: Genome sequence of Yersinia pestis, the causative agent of plague. A; Reference number: ABOLGG A; Reference number: ABOLGG A; Status: preliminary A; Molecule type: DNA A; Residues: 1-521 <krr> A; Cross : references: GB: AL590842; PIDN: CAC91014.1; PID: 915980208; GSPDB: GN00175 C; Genetics: A; Conservative 14; Mismatches 46; Indels 39; Gaps 6; Best Local Similarity 25.0%; Pred. No. 37; Batches: 33; Conservative 14; Mismatches 46; Indels 39; Gaps 6; A; H. I. III III IIIIIIIIIIIIIIIIIIIIIIII</krr>
Matches 24; Conservative 11; Mismatches 26; Indels 19; Gaps 4;  Qy 29 RLTPYLRQAKV	TEESULT 7 Tees and the protein Y38E10A.w - Caenorhabditis elegans C; Species: C; Accession: T26673 R; Wallis, J. R; Ralliary; Caenorhabditis elegans by Pidn: Caenorhabditis elegans A; Residues: 1315 cwlt.> A; Cross references: EMBL: AllO484; PIDN: CAB54414.1; CESP: Y38E10A.w C; Genetics: A; Genetics: Clone Y38E10A.w A; Resen: CESP: Y38E10A.w A; Marcons: 112/1; 172/2 C; Superfamily: Caenorhabditis elegans hypothetical protein Y38E10A.w	Owery Match Best Local Similarity 26.8%; Pred. No. 16;  Matches 30; Conservative 15; Mismatches 40; Indels 27; Gaps 5;  Qy 14 MESHRHRIVRCICPSRL-TPYLRQAKVLCQLDEEVLHSPRLTNSAMRAGHLLD 66  18 LAENRPEFQQAIADSPLFTAYMKLLKRQAELSPRILSALSAISSIVRSHLPA 70  Qy 67 LLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFSN 105	RESULT 8 E86922 E86922 Cryptobacterium leprae Rricole, S.T.; Eiglimeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hamlin, N.; Holroyd, R., Deviso, 1007-1011, 2001 A.Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R., A., Reference number: A86909; MUID:21128732; PMID:11234002 A.Accession: E86922 A.Accession: E86923 A

3

Gaps

11;

Indels

27;

Length 448;

.; ;;

DB

× ø

```
Userial Carlo Substantian inclusion in precursor. Incluse in cure and cure and cure and cure and cure and cure mouse)
C; Species; IN of sequence revision 10-Sep-1999 #text_change 10-Sep-1999
C; Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
C; Date: 10-Sep-1999 #sequence revision 10-Sep-1999
C; Date: 10-Sep-1999 #sequence revision 10-Sep-1999
R; Moos, M.; Tacke, R.; Scherer, H.; Teplow, D.; Frueh, K.; Schachner, M.
A; Title: Neural adhesion molecule L1 as a member of the immunoglobulin superfamily winth A; Reference number: S05479; MUD: 88318924; PMID: 3412448
A; Accession: S05479
A; Molecule type: mRNA
A; Residues: 1-1260 < MOO>
A; Cross-references: EMBL: X12875; NID: 953336; PIDN: CAA31368.1; PID: 953337
A; Cross-references: EMBL: X12875; NID: 953336; PIDN: CAA31368.1; PID: 953337
A; Mote: part of this sequence, including the amino end of the mature protein, was con R; Rathlen, F. G.; Wolff, J. M.; Frank, R.; Bonhoeffer, F.; Rutishauser, U.
Cell Biol. 104, 343-353, 1987
A; Title: Membrane qlycoproteins involved in neurite fasciculation.
A; Reference number: A60850; MUD: 87109457; PMID: 3805123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: Î-496 <STO>
A;Cross-references: GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BAB05316.1; GSPDB:G
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Dacession: E83840
C;Dacession: E83840
C;Dacession: E83840
C;Arcession: E83840
C;Arcession: E83840
C;Arcession: E83840
C;Species: Date: Dec-2000 #text_change 15-Jun-2001
C;Arcession: E83840
C;Species: Date: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      spore germination protein BH1597 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 20-28, XX',31-36 <RAT>
R;Kohl, A.; Giese, K.P.; Mohajeri, M.H.; Montag, D.; Moos, M.; Schachner, M.
Submitted to the EMBL Data Library, December 1991
Submitted to the EMBL Data Library, December 1991
A;Peference number: $22167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 LDEETLWEMMESHRHRIVRCICPSR-LTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGH 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 LTPYL-RQAKVLCQLDEE-----EVLHSPRLTNSAMRAGHLLDLLKTRGKNGAIAFLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell adhesion molecule L1 precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pred. No. 45;
20; Mismatches
                                                                                                                               12; Mismatches
                                                                       40;
           Score 65.5;
Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: spore germination protein gerBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 65.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 LKFHNPDVYTLVTGLQ---PDVDFS 104
                      11.7%;
31.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.7%;
27.1%;
Query Match
Best Local Similarity 31.5%.
Ma+ches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||:
|||09 LLDV----KNGA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                          92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 LLDLLKTRGKNGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: BH1597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                               δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
D95366
Nable Carborates (ubiquinone) (EC 1.6.5.3) chain G NuoG2 [imported] - Sinorhizobium m C; Species: Slockizobium meliloti
C; Species: Slockizobium meliloti
C; Species: Slockizobium meliloti
C; Species: Slockizobium meliloti
C; Decession: D95365
R; Barentt, M. J.; Fisher, R. F.; Jones, T.; Komp, C.; Abola, A. P.; Barloy-Hubler, F.; Bows
R; Brancht, M. J.; Fisher, R. F.; Jones, T.; Komp, C.; Abola, A. P.; Barloy-Hubler, F.; Bows
R; Brancht, M. J.; Fisher, R. F.; Jones, T.; Komp, C.; Abola, A. P.; Barloy-Hubler, Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A; Title: Nucleotide sequence and predicted functions of the entire sinorhizobium melilot
A; Reference number: A95262; MuID: 21396509; PMID: 11481432
A; Status: preliminary
A; Molecule Lype: DNA
A; Residues: 1-853 < KND
A; Status: preliminary
A; Molecule Lype: DNA
A; Residues: 1-853 < KND
A; Status: preliminary
A; Molecule Lype: DNA
A; Residues: 1-853 < KND
A; Status: preliminary
A; Molecule Lype: DNA
A; Residues: 1-853 < KND
A; Status: preliminary
A; Molecule Lype: DNA
A; Residues: 1-853 < KND
A; Status: preliminary
A; Molecule Lype: DNA
A; Residues: 1-853 < KND
A; Status: preliminary
A; Molecule Lype: DNA
A; Residues: 1-853 < KND
A; Status: preliminary
A; Molecule Lype: DNA
A; Residues: 1-853 < KND
A; Residues: 1-853 < KND
A; Status: preliminary
A; Molecule Lype: DNA
A; Residues: 1-853 < KND
A; Molecule Spi. Bolion
A; Molecule Public P; Vandenbol, M: Vorholter; F.J.; Weldersphel, N: Vorholter; Rybiorian meliloti.
A; A; Title: The composite genome of the legume symbionic A; Molecules: annotation
C; Genetics:
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C. Accession: H70947
R. Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Hamlin, N.; Holroyd, S.; Artitle: Daciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MUID:98295987; PMID:9634230
A.Accession: H70947
A.Status: pre-liminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-448 <COL>
A. Residues: 1-448 <C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species: Mycobacterium tuberculosis
;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                 ETL--LVLDHQHRSTR-LQASLFTPDSSEYQRLATRLEQLSHQLQQAPHPIPATSVPEMA 236
                                                                                                                                          94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein Rv3170 - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                            --CQLDEEEVLHSPRLTNSAMRAGHLLDLLKTRGKN----GAIAFLESLKFHNPDVYTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 RLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGHLLDLLKTRGKNGAIAFL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 853; 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.8%; Score 66; DB 30.8%; Pred. No. 76; iive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 30.8°
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                            TGLQPDVDFSNF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -- FMQDNDFSLF 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: Rv3170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                          ò
                                                                                                                                                                                                                                        QQ
                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Op
```

5;

21; Gaps

Indels

21; DB 2;

Length 496;

neural

```
Poytuate formate-lyase activating enzyme (act-1) homolog - Archaeoglobus fulgidus C; Species: Arcession: E69264
R; Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson. F; Flaischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Nature 390, 364-370, 1997
A.Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C. R.; Venter, J.C.
A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A; Recession: E6926; MUID:98049343; PMID:9389475
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-320 <a href="https://docs.org/linkness/references: GB:AE001098; GB:AE000782; NID:92689421; PIDN:AAB91111.1; PID:9265052 C; Superfamily: conserved hypothetical protein MJ0808
A;Accession: $22167
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Rosidues: 1-165, L',167-189, 'E',191-281, 'S',283-395, 'S',397-514, 'APEKNPVDV',524, 'GEGNE
A;Cross-references: EMBL:X63511
C;Genetics:
A;Introns: 26/1; 31/1; 66/2; 133/1; 174/1; 231/1; 268/2; 330/1; 374/1; 422/1; 459/2
A;Note: the list of introns may be incomplete
C;Superfamily: neural cell adhesion molecule L; fibronectin type III repeat homology; if C;Reywords: alternative splicing; cell adhesion; duplication; glycoprotein; transmembran F;1-19/Domain: signal sequence #status predicted <SIG>F;20-1260/Product: neural cell adhesion molecule #status experimental <MAT>F;20-1260/Product: immunoglobulin homology <IRMM1>F;20-1260/Domain: immunoglobulin homology <IRMM2>F;31-592/Domain: immunoglobulin homology <IRMM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 EMMESHRHRIVRCIC----PSRLTPY-LRQAKVLCQLDEEEVL----HSPRLTNSAMRA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 CQLDEEEVLH-SPRLTNSAMRAGHLLDLLKTRGKNGAIAFLE----SLKFHNPDVYTLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 11.5%; Score 64.5; DB 2; Length 320; Best Local Similarity 22.9%; Pred. No. 34; Matches 24; Conservative 25; Mismatches 39; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 GHLLDLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFSNF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.7%; Score 65.5; DB 1; 27.9%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: January 22, 2003, 08:54:27 Job time: 11.1976 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 27.9%
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 GLQPDVDF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            981 NLNPDLQY 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

THIS PAGE BLANK (USPTO)

;

```
5.1.3
Compugen Ltd.
version - 2003 (
GenCore
Copyright (c) 1993
```

protein search, using sw model OM protein January 22, 2003, 08:49:35; Search time 4.1707 Seconds (without alignments) 1064.082 Million cell updates/sec Run on:

US-09-767-215-2\_COPY\_10\_116 560

1 ALTALDEETLWEMMESHRHR......PDVYTLVTGLQPDVDFSNFS 107 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

112892

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	-																																	
	Description		mus m	Q9bx17 homo sapien	mus m	Q9bwt7 homo sapien	rattu	~	рр				P56914 rhizobium m	O53320 mycobacteri	Q13586 homo sapien	mus n	_		macac	Q96rt8 homo sapien	Q55470 synechocyst	-		P34706 caenorhabdi	P17643 homo sapien	_	Q15831 homo sapien		067323 aquifex aeo	P22454 caenorhabdi	3 zea n	$\sim$	3 rattu	•
SUMMARIES	ID	24	CARE_MOUSE	CARB_HUMAN	CARA_MOUSE	CARA_HUMAN	CAR9_RAT	CAR9_HUMAN	BCLA_HUMAN	BCLA_RAT	BCLA_MOUSE	MIS4_SCHPO	NUG2_RHIME	AOFH_MYCTU	STM1_HUMAN	CAML_MOUSE	TPO_CANFA	V022_FOWPV	GCP5_MACFA	GCP5_HUMAN	Y514_SYNY3	AGMR_PSEAE	RIFF_AMYMD	SDC3_CAEEL	TYR1_HUMAN	CAO2_MOUSE	ST11_HUMAN	YJ89_YEAST	SYA_AQUAE	GBA2_CAEEL	PDI_MAIZE	OGT1_HUMAN	OGT1_RAT	CAML_RAT
	DB	-	H	-	Н	П	-	П	-	1	-	H	1	Н	Н	-4	Н	-	-	+-1	Н	<del>, ,</del>		7	Н	Н		-	٦	-		-	Н	Н
	Length DB	1004	666	1147	1021	1032	536	536	233	233	233	1583	853	454	685	1260	352	578	725	1024	554	221	260	2150	537	681	433	728	867	356	513	1036	1036	1259
di	Query	0	83.9	æ	45.0	43.9	38.8	37.3	14.5	14.5	13.9	12.9		11.7	-	11.7	~	11.6	~	-	11.5	~	~	11.4	11.3	11.3	11.2	11.2	11.2	11.2	11.2	11.2	11.2	11.2
	Score	260	470	270	252	246	217	209	81	81	78	72.5	S	65.5			9	65	65	9	64.5	64	64	64	63.5	۳.	63	63	9			62.5	62.5	62.5
	Result No.	1	7	m	4	Ŋ	9	7	80	Φ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

Q21268 caenorhabdi Q58234 methanococc P12830 homo sapien O60513 h beta-1,4- P07147 mus musculu Q99424 homo sapien P20715 xenopus lae O70361 mus musculu P28828 mus musculu P40855 homo sapien O62640 sus scrofa	
YMSO_CAEEL MOAA_METJA CAD1_HUMAN B4G4_HUMAN TYRL_MOUSE CAO2_HUMAN PER3_MOUSE PYFW_MOUSE PYFW_MOUSE PYFW_MOUSE PYFW_MOUSE GGFT_METJA	
ппппппппппппппппппппппппппппппппппппппп	
290 298 882 344 537 681 1113 1452 299 359	
111111111111111111111111111111111111111	
62 62 62 61.5 61.5 61.5 61.5 61.5	
88888884444444444486786788888888844444444	

## ALIGNMENTS

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- TISSUE SPECIFICITY: Expressed in placenta. Also detected in HeLa
-!- SIMILARITY: Dut not in the other cancer cell lines tested.
-!- SIMILARITY: CONTAINS I CARD DOMAIN.
-!- SIMILARITY: CONTAINS I PDZ/DHR DOMAIN.
-!- SIMILARITY: CONTAINS I GUANYLATE KINASE-LIKE DOMAIN.
-!- CAUTION: Supposed to contain a SH3 domain which is not detected by PROSITE, Pfam or SMART.
                                                                         15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 14 (CARD-containing MAGUK protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Activates NF-kappaB via Bcl10 and IKK. Stimulates the
phosphorylation of Bcl10.
-!- SUBUNIT: CARD14 and Bcl10 bind to each other by CARD-CARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J., "Carmal, a CARD-containing binding partner of Bc110, induces Bc110 phosphorylation and NF-Repaga activation."; FEBS Lett. 496:121-127(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.; FEBS Lett. 505:198-198(2001).
                                                                                                                                                                                                                                                                                                                 MEDLING-21192234; PubMed=11278692; Bertin J., Wang L., Guo Y., Jacobson M.D., Poyet J.-L., Srinivasula S.M., Merriam S., Distefano P.S., Alnemri E.S.; "CARDII and CARDI4 are novel caspase recruitment domain (CARD)/membrane-associated guanylate kinase (MAGUK) family members that interact with Bc110 and activate NF-kappaB."; J. Biol. Chem. 276:11877-11882(2001).
                                                                                                                                                                                                                       Euteleostomi;
                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                       PRT; 1004 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=21255663; Pubmed=11356195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-740 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Cervix, and Colon;
                                       STANDARD;
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

    (Carma 2).
    CARD14 OR CARMA2.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interaction.
                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                     CARE_HUMAN
Q9BXL6; Q9BVB5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERRATUM.
                    CARE_HUMAN
RESULT 1
```

```
Query Match
                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9BXL7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
CARB_HUMAN
                                                                                                                                                                                                                                                                                                                                                               Matches
 Pb
                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δλ
                                                                                                                                                                                                                                                                                                                               ô
 removed. Usage by and for commercial ent (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 14 (Bcl10-interacting MAGUK protein
                                                                                                                                                                                                                                       DYEASEPLFKAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTD
                                                                                                                                                                                                                                                 GYKRLLQDLEAK -> SRARPLLSPGLLMGTVAAGGVTQAD
                                                                                                                                                                                                                                                             FTSPRRCRSTLGWASALSWADVKRSAHL (IN REF. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ဍ
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                    1 ALTALDEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMR 60
                                                                                                                                                                                                                                                                                                                                                                10 ALTALDEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMR 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Benito A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Binpl, a MAGUK family member linking protein kinase C activation Bcll0-mediated NF-kappa B induction."; J. Biol. Chem. 276:30589-30597(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Activates NF-kappaB via Bcll0 and IKK.
-!- SUBUNT: CARD14 and Bcll0 bind to each other by CARD-CARD interaction (By similarity).
-!- SUBCELLULAR LCCATION: Cytoplasmic (By similarity).
-!- SUBCELLULAR LCCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                       Length 1004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21391892; Pubmed=11387339;
McAllister-Lucas L.M., Inohara N., Lucas P.C., Ruland J., Be
Li Q., Chen S., Chen F.F., Yamaoka S., Verma I.M., Mak T.W.,
Nunez G.,
                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            70 AGHLLDLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFSNFS 116
                                                                                                                                                                                                                                                                                  7469BBB56BE06073 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                61 AGHLLDLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFSNFS 107
                                                                                                                                                                                           CARD. COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                       ; Score 560; DB 1;
; Pred. No. 3.5e-52;
0; Mismatches 0;
                                                                                                                                   PROSITE; PS50209; CARD; 1.
PROSITE; PS60865; GUANYLATE_KINASE_1; FALSE_NEG.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PDZ; 1.
                                                                                                                                                                                                                            GUANYLATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               999 AA
                                         EMBL; AF322642; AAG53403.1; -.
EMBL; AY032927; AAK54453.1; -.
EMBL; BC018142; AAH18142.1; -.
EMBL; BC001326; AAH01326.1; ALT_INIT.
INTERPRO; IPR000619; Guanylate_kin.
INTERPRO; IPR01478; PDZ.
SNART; SM00072; GUKC; 1.
SMART; SM00228; PDZ; 1.
modified and this statement is not remo
entities requires a license agreement (
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                          AAH01326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 82-743 FROM N.A.
                                                                                                                                                                                                                                                                                   1004 AA; 113299
                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                           107
409
658
990
671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-10090;
                                                                                                                                                                                           128
128
568
858
619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARD14 OR BIMP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.
                                                                                                                                                                                  Coiled coil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARE_MOUSE
                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          099KF0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARE_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                     g
 ò
                                                                                                                                                                                                                                                                                                                                                       õ
```

```
between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·
0
                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration
-!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
-!- SIMILARITY: CONTAINS 1 GUANYLATE KINASE-LIKE DOMAIN.
-!- CAUTION: Supposed to contain a SH3 domain which is not detected by PROSITE, Pfam or SMART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 11 (CARD-containing MAGUK protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 LTALDEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 LTALDEEMLWDMLESHRCRIVQSICPSRLTPYLRQAKVLGQLDEEELLHSSRFTNSAMRV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE-2125663; PubMed=11356195;

MEDLINE-2125663; PubMed=11356195;

MEDLINE-2125663; PubMed=11356195;

Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.;

"Carmal, a CARD-containing binding partner of Bcll0, induces Bcll0
phosphorylation and NF-kappaB activation.";

FEBS Lett. 496:121-127(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21192234; PubMed=11278692; Bettin J., Wang L., Guo Y., Jacobson M.D., Poyet J.-L., Shertin J., Rardiam S., Distefano P.S., Alnemri E.S.; "CARDII and CARDI4 are novel caspase recruitment domain CARDI4 are sscotiated quanylate kinase (WAGUK) family members that interact with Bcll0 and activate NF-kappaB."; J. Biol. Chem. 276:11877-11882(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GUANYLATE KINASE.
QAQQQLLA -> HLLEDHRS (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 GHLLDLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFSNFS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARD. COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR00619; Guanylate_kin.
InterPro; IPR001478; PDZ.
Pfam; PF00595; PDZ; 1.
PROSITE; PS502095; CARD; 1.
PROSITE; PS500856; GUANYLATE_KINASE_1; FALSE_NEG.
PROSITE; PS50062; GUANYLATE_KINASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 470; DB 1;
Pred. No. 1.6e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1147 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113496 MW;
                                                                                                                                                                                                                                                                                                                                                  EMBL; AF363457; AAK60137.1; -. EMBL; BC004692; AAH04692.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.9%;
85.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107
411
655
986
743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             999 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

    (Carma 1).
    CARD11 OR CARMA1.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15
125
572
854
736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARB_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
DOMAIN
COMAIN
```

m

```
Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Sim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Carma 3)
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the between the Swiss Institute of Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                            -1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- TISSUE SPECIFICITY: Detected in adult peripheral blood leukocytes, thymus, spleen and liver. Also found in promyelocytic leukemia HL-60 cells, chronic myelogenous leukemia K562 cells, Burkitt's lymphoma Raji cells and colorectal adenocarcinoma SW480 cells. Not detected in HeLa Si, Molt-4, A549 and G431 cells. Not detected in HeLa Si, Molt-4, A549 and G431 cells.
-!- SIMILARITY: CONTAINS I CARD DOMAIN.
-!- SIMILARITY: CONTAINS I PDZ/DHR DOMAIN.
-!- SIMILARITY: CONTAINS I GUANYLATE KINASE-LIKE DOMAIN.
-!- CAUTION: Supposed to contain a SH3 domain which is not detected by PROSITE, Pfam or SMART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 10 (Bcl10-interacting MAGUK protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGHLL 65
                        , Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.; t. 505:198-198(2001).
                                             -!- FUNCTION: Activates NF-kappaB via Bc110 and IKK. Stimulates the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                            phosphorylation of Bcl10.
SUBUNIT: CARDII and Bcl10 bind to each other by CARD-CARD
interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.2%; Score 270; DB 1; Length 1147; 51.5%; Pred. No. 5.1e-21; Live 22; Mismatches 26; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 442 COILED COIL (POTENTIAL).
673 748 PDZ.
966 1133 GUANYLATE KINASE.
808 P -> L (IN REF. 2).
1147 AA; 132641 MW; 913A4B015D2B36CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARD. COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50209; CARD; 1.
PROSITE; PS00856; GUANYLATE_KINASE_1; FALSE_NEG.
PROSITE; PS50052; GUANYLATE_KINASE_2; FALSE_NEG.
PROSITE; PS50106; PDZ; FALSE_NEG.
Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1021 AA.
                                                                                                                                                                                                                                                                                                                                                                Genew; HGNC:16393; CARD11.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                    EMBL; AF322641; AAG53402.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 51.5
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103
442
748
1133
808
                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00228; PDZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARDIO OR BIMP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARA_MOUSE
P58660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Bimpl)
                                    FEBS Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                        Gaide O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute.

The European Bioinformatics Institute.

The European Bioinformatics institutes are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a alicense agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21292987; PubMed=11259443; Wang L., Guo Y., Huang W.-J., Ke X., Poyet J.-L., Manji G.A., Mang M.-D., Guo Y., Huang M.-J., Ke X., Poyet J.-L., Manji G.A., Bertin J.; Merriam S., Glucksmann M.A., Distefano P.S., Alnemri E.S., Bertin J.; "CARD10 is a novel caspase recruitment domain/membrane-associated guanylate kinase family member that interacts with Bcl10 and activates
                                                                                                                                  -i. TISSEE SPECIFICITY: Highly expressed in kidney, heart followed by brain, lung, liver, skeletal muscle and testis.
-i. SIMILARITY: CONTAINS 1 CARD DOWAIN.
-i. CAUTION: Supposed to contain a SH3, a PDZ and a guanylate kinase-like domain. But none of these 3 domains are detected by PROSITE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARA_HUMAN STANDARD; PRT; 1032 AA.
09BW77; Q9UGR5; Q9VGR6; Q9Y3H0;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 10 (CARD-containing MAGUK protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 DEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGHLL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Benito A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.0%; Score 252; DB 1; Length 1021; 51.1%; Pred. No. 3.8e-19;
MEDLINE=21391892; PubMed=11387339; MCAllister-Lucas L.M., Inohara N., Lucas P.C., Ruland J., Be Li Q., Chen S., Chen F.F., Yamaoka S., Verma I.M., Mak T.W., Nunez G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4811A09BDB8F792C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NF-kappa B.";
J. Biol. Chem. 276:21405-21409(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1021 AA; 114413 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF363456; AAK60136.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50209; CARD; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115
450
565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam or SMART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARD10 OR CARMA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
```

i.n no

as its content is

non-profit institutions as long

modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

EMBL, AY028896; AAK26165.1; -.
EMBL, AX032928; AAK54454.1; -.
EMBL, AL049851; CAB63075.1; ALT\_SEQ.
EMBL, AL049851; CAB63076.1; ALT\_SEQ.
EMBL, AL023315; CAB42832.1; ALT\_SEQ.
PROSITE; PS50209; CARD; 1.

ö

Gaps

.; 0

; Score 246; DB 1; Length 1032; ; Pred. No. 1.7e-18; 21; Mismatches 27; Indels

43.9%; Score 246;

48.98;

Query Match
Best Local Similarity 48.9%

qq

ò

115946

Q -> R (IN REF. 4). K -> K Q (IN REF. 4; CAB63075). R -> L (IN REF. 4). WW: 8377319AB82A0949 CRC64;

CARD.
COILED COIL (POTENTIAL)
POLY-SER.

1115 456 574 574 289 917

23 11 138 45 567 57 289 28 917 91 932 AA;

CONFLICT

Coiled DOMAIN DOMAIN DOMAIN

CONFLICT

SEQUENCE

DEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGHLL 65 

|:|: ||| | ||||:|:|:||:||:|| || 83 DILRCRGKRGYEAFLEALEFYYPEHFTLLTGQEP 116 66 DLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQP 99

qq

```
RX BUDINE-2019/165; PubMed=10591208;

RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,

RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,

Radguley C., Balley J., Barlow R.F., Bates K.N., Beasley O.P.,

Burrill W.D., Burring J. Barlow R.P., Bates K.N., Beasley O.P.,

Radguley C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,

Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,

RA Glery J. Corby N.R., Coville G.J., Cox A.V., Davis J., Davson E.,

RA Glery J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,

RA Hall R.E., Hall-Tamlyn G., Heathcort R.W., Ho S., Mortinore B.J.

RA Hall R.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,

Ratin G.K., Langford C.E., Leversham M.A., Lloyd C., Lloyd D.M.,

RA Martyn I.D., Washredhi Wohammadi M., Matthews L.H., Mccann O.T.,

RA Martyn I.D., Washredhi Wohammadi M., Matthews L.H., Mccann O.T.,

RA Martyn I.D., Washredhi Wohammadi M., Matthews L.H., Mccann O.T.,

RA Martyn I.D., Washredhi Wohammadi M., Matthews L.H., Mccann O.T.,

RA Scott C.E., Spragon L., Steward C.A., Sulston J.E., Sanith M.L.,

RA Scott C.L., Hubbard T., Steward C.A., Sulston J.E., Wilming L.,

RA Millams E., Williams S., Wulliams S., Kavuski K., Sasalt Y., Aoki N., Milley D.L.,

RA Minoshima S., Kavaski K., Yoshila Y., Milley D.L.,

RA Minoshima S., Kavaski K., Yoshila Y., Mattery S., Sinth M.L.,

RA Borman A., Shipuya K., Yoshilaxi Y., Aoki N., Milley D.L.,

RA Bontan A., Shipuya K., Yoshilaxi Y., Aoki N., Willey D., Milley D.,

RA Bon Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Zoo D.,

RA Bon S., Ola Y., Wang C., White J., Williams D., Wu H., Yao Z.,

RA Bon M., Zhang G., Chinsos S., White J., Williams D., Wu H., Yao Z.,

RA Crodes M., Du Z., Fulton L., Goshu D., Graves T., Hawkins J.,

RA Crodes M., Du Z., Fulton L., Goshu D., Graves T., Hawkins J.,

RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,

RA McDermid H.E., Johnson A., Watte B., WatterSton R., Wilkinson P., Bodentein P., Watter M., Wat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interaction. They both participate in a complex with MaLT1, where MALT1 binds to Bell0 (By similarity).

SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

TISSUE SPECIFICTY: Detected in adult heart, kidney and liver; lower levels in intestine, placenta, muscle and lung. Also found in fetal lung, liver and kidney.

SIMILARITY: CONTAINS I CARD DOMAIN.

CAUTION: Supposed to contain a SH3, a PDZ and a guanylate kinase-like domain. But none of these 3 domains are detected by PROSITE,
                     Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J., Carmal, a CARD-containing binding partner of Bc110, induces Bc110 phosphorylation and NF-kappaB activation."; FEBS Lett. 496:121-127(2001).
                                                                                                                                                      Jaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.;
FEBS Lett. 505:198-198(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: Activates NF-kappaB via Bc110 and IKK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The DNA sequence of human chromosome 22.";
                                                                                                                                                                                                                                                 MEDLINE=20057165; PubMed=10591208;
MEDLINE=21255663; PubMed=11356195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 402:489-495(1999).
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                   SRRATUM.
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                         Bertin J., Guo Y., Wang L., Srinivasula S.M., Jacobson M.D., Poyet J.-L., Merriam S., Du M.-Q., Dyer M.J.S., Robison K.E., Distefano P.S., Alnemri E.S.;
"CARD9 is a novel caspase recruitment domain-containing protein that interacts with Bcl10/CLAP and activates NF-kappa B.";
J. Biol. Chem. 275:41082-41086(2000).
-!- FUNCTION: Activates NF-kappaB via Bcl10 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SUBUNIT: Self-associates. CARD9 and Bcl10 bind to each other by CARD-CARD interaction (By similarity).
-i- SUBCELGUAR LOCATION: Cytoplasmic (By similarity).
-i- SIMILARITY: CONTAINS 1 CARD DOMAIN.
                                                                                    15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 9 (rCARD9)
                                                PRT;
                                                                                                                                                                                                                                                                                                                                                STRAIN=Sprague-Dawley;
MEDLINE=20576268; PubMed=11053425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF311288; AAC28791.1; -. InterPro; IPR001315; CARD. PROSITE; PS50209; CARD; 1.
                                                STANDARD;
                                                                                                                                                                                                           Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                CAR9_RAT
RESULT 6
                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ref.4 sequence differs from that shown due to various
```

gene identification problems.

Pfam or SMART.

CAUTION:

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Wishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara M., Hosolri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yammoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T.; Nakamura Y., Nagahari K., Masuho Y., Nabo human cDNA sequencing project."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bertin J., Guo Y., Wang L., Srinivasula S.M., Jacobson M.D., Poyet J.-L., Merriam S., Du M.-Q., Dyer M.J.S., Robison K.E., Distefano P.S., Alnemri E.S.; "CARD9 is a novel caspase recruitment domain-containing protein that lineracts with Bcll0/CLAP and activates NF-kappa B."; J. Biol. Chem. 275:41082-41086(2000).
                                                                                                                                                        6 DEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGHLL 65
                                                                                                                                                                            Strausberg R.; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases. -:- FUNCTION: Activates NF kappaB via Bcil0. -:- SUBUNIT: Self-associates. CARD9 and Bcil0 bind to each other by
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                            ;
0
                                                                                            Length 536;
                                                                                                                            37; Indels
              CARD.
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
6F33089CB7E6BAC9 CRC64;
                                                                                                                                                                                                                       66 DLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFS 104
                                                                                            DB 1;
                                                                                           38.8%; Score 217; DB 1. 45.5%; Pred. No. 1e-15;
                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
25-JUN-2002 (Rel. 41, Last annotation update)
CARD9.
                                                                                                                                                                                                                                         536 AA
                                                                                                                          17; Mismatches
                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-20576268; PubMed-11053425;
              98 CV
277 CC
420 CC
62631 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-492 FROM N.A.
                                                                                                                            45; Conservative
                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE-Retinoblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
              6
117
303
4
536 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalla; Eutheria;
                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Muscle;
Coiled coil.
DOMAIN
                                                                                                                                                                                                                                                                                                                                    CAR9_HUMAN
Q9H257; Q9H
                                              DOMAIN
SEQUENCE
                                                                                            Query Match
                                 DOMAIN
                                                                                                                                                                                                                                                                                                                   CAR9_HUMAN
                                                                                                                            Matches
 KW
FT
FT
SO
                                                                                                                                                                                       g
                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                   q
```

```
ö
 entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99214546; PubMed-10187771;
Thome M., Martinon F., Hofmann K., Rubio V., Steiner V., Schneider P., Mattmann C., Tschopp J.;
Equine herpesvirus-2 E10 gene product, but not its cellular homologue, activates NF-kappaB transcription factor and c-Jun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation) (Rel. 41, Last annotation update)
13/ICH-1 prodomain homologous E10-11ke regulator) (CIPER) (CARD-
containing molecule enhancing NFkappaB) (Cellular homolog of vCARMEN)
(CCARMEN) (Mammalian CARD-containing adapter molecule E10) (mE10)
(Cellular-E10) (CARD-like apoptotic protein) (hCLAP).
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Koseki T., Inohara N., Chen S., Carrio R., Merino J., Hottiger M.O., Nabel G.J., Nunez G.;
"CIPER, a novel NF kappaB-activating protein containing a caspase recruitment domain with homology to Herpesvirus-2 protein ElO.";
J. Biol. Chem. 274:9955-9961(1999).
                                                                                                                                                                                                                                                                                                                                                                   6 DEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGHLL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHE-218
                                                                                                                                                                                                                                         LSSGEPPEKER -> PAGLPGIGAVC (IN REF. 3).
6EB1835315B83DE5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Willis T.G., Jadayel D.M., Du M.-Q., Peng H., Perry A.R.,
Abdul-Rauf M., Price H., Karran L., Majekodunmi O., Wlodarska I.,
Pan L., Crook T., Hamoudi R., Isaacson P., Dyer M.J.S.;
"Bcll0 is involved in t(1:14)(p22:q32) of MALT B cell lymphoma and
mutated in multiple tumor types.";
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., VARIANT FOLLICULAR LYMPHOMA GLU-210 DEL, MESOTHELIOMA ILE-52, AND VARIANTS GERM CELL TUMOR GLY-58 AND
                                                                                                                                                                                                                                                                                                Score 209; DB 1; Length 536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2] SEQUENCE FROM N.A., AND MUTAGENESIS OF LEU-41 AND GLY-78
                                                                                                                                                                                        COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
N -> S (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          |:|: | | :|||||||: : | :| | || || || DILQRTGHKGYVAFLESLELYYPQLYKKVTGKEPARVFS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                      66 DLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFS 104
                                                                                                                                                                                                                                                                                                             7.5e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 AA.
                                                                                                                                                                                                                                                                                                           44.4%; Pred. ...
tive 16; Mismatches
              or send an email to license@isb-sib.ch)
                                           EMBL; AF311287; AAG28790.1; -.
EMBL; AK024001; BAB14766.1; ALT_FRAME.
EMBL; BC008877.1; -.
GGNew, HGNC:16391; CARD9.
INTERPYO, IPR001315; CARD.
PROSITE: PS50209; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99214545; PubMed=10187770;
                                                                                                                                                                        CARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Lymphoma;
MEDLINE=99142601; Pubmed=9989495;
                                                                                                                                                                                                                                                            62267 MW;
                                                                                                                                                                                                                                                                                            37.3%;
                                                                                                                                                                                                                                                                                                                                44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                        98
277
419
12
492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                            536 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              3est_Local Similarity
                                                                                                                                                                        6
1117
332
12
482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                        Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BCLA_HUMAN
095999;
                                                                                                                                                                                                         DOMAIN
CONFLICT
                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                          DOMAIN
                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BCLA_HUMAN
                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
δλ
                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
```

```
c-i- FUNCTION: Promotes apoptosis, pro-caspase-9 maturation and activation of NF-kappaB via NIK and IKK. May be an adapter protein between upstream TNFRI-TRADD-RIP complex and the downstream NIK-IKAP complex.

IKK-IKAP complex.

--- SUBGNIT: Self-associates by CARD-CARD interaction and forms a tight complex with MALTI. Interacts with other CARD-proteins such as CARD9, CARD10, CARD11 and CARD14. Binds caspase-9 with its C-terminal domain. Interacts with TRAF2 and BIRC2/C-IAP2.

--- SUBGELLULAR LOCATION: Cytoplasmic. Appears to have a perinuclear, compact and filamentous pattern of expression. Also found in the nucleus of several types of tumor cells.

--- TISSUE SPECIFICITY: Ubiquitous.

--- PTM: Phosphorylated. Phosphorylation results in dissociation from TRAF2 and binding to BIRC2/C-IAP2.

--- PTM: Phosphorylated. Phosphorylation results in dissociation from TRAF2 and binding to BIRC2/C-IAP2.

--- DISEASE: Involved in a t(1:14)(p22:q32) chromosomal translocation recurrent in low-grade MALT lymphoma (Mucosa-associated lymphoid tissue). Although the BcIllO/THH translocation leaves the coding region of BCL10 intact, frequent BCL10 mutations could be
                                       SEQUENCE FROM N.A., AND MUTAGENESIS OF LEU-28; LEU-41; ILE-46; LEU-47; GLU-53 AND ILE-55.
MEDLINE-99214590; PubMed=10187815;
Yan M., Lee J., Schilbach S., Goddard A., Dixit V.M.;
"mEl0, a novel caspase recruitment domain-containing proapoptotic molecule.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANTS MESOTHELIOMA SER-5; GLN-45; GLN-58; SER-93; VAL-153; GLU-213
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND VARIANTS MALT LYMPHOMA SER-5; GLU-16; GLU-31; ARG-57; LXS-64; GLU-101; PRO-134; ALA-168; SER-174; GLU-213 AND
                                                                                                                                                                              MEDLINE-99292766; PubMed=10364242; Srinivasula S.M., Ahmad M., Lin J.-H., Poyet J.-L., Fernandes-Alnemit T., Tsichlis P. N., Alnemit E.S.; "CLAP, a novel caspase recruitment domain-containing protein in the tumor necrosis factor receptor pathway, regulates NF-kappaB activation and apoptosis."; Biol. Chem. 274:17946-17954 (1999).
                                                                                                                                                                                                                                                                                                                                             Costanzo A., Guiet C., Vito P., "c-E10 is a caspase-recruiting domain-containing protein that interacts with components of death receptors signaling pathway and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apostolou S., de Rienzo A., Murthy S.S., Jhanwar S.C., Testa J.R., "Absence of BCL10 mutations in human malignant mesothelioma.";
Cell 97:684-686(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yul D., Yoneda T., Oono K., Katayama T., Imaizumi K., Tohyama M.;
"Interchangeable binding of Bcll0 to TRAF2 and cIAPs regulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-99251581; PubMed-10319863;
Zhang Q., Siebert R., Yan M., Hinzmann B., Cui X., Xue L.,
Rakestraw K.M., Naeve C.W., Beckmann G., Weisenburger D.D.,
Sanger W.G., Noworny H., Vesely M., Callet-Bauchu E., Salles G.,
Dixit V.M., Rosenthal A., Schlegelberger B., Morris S.W.;
"Inactivating mutations and overexpression of BCL10, a caspase recruitment domain-containing gene, in MALT lymphoma with
t(1:14)(P22:93-932).";
                                                                                                                                                                                                                                                                                                                                                                                      activates nuclear factor kappaB.";
J. Biol. Chem. 274:20127-20132(1999).
                                                                                                                                    Biol. Chem. 274:10287-10292(1999)
N-terminal kinase.";
J. Biol. Chem. 274:9962-9968(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [8]
PHOSPHORYLATION.
MEDLINE-21359851; PubMed-11466612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND PHE-218.
MEDLINE-99308628; Pubmed-10380921;
                                                                                                                                                                                                                                                                                                                              MEDLINE=99329013; PubMed=10400625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oncogene 20:4317-4323(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              apoptosis signaling
                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                TISSUE-Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARG-57;
ILE-230.
                                                                                                                                                                                                                                                                                     [9]
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
                                DISEASE: Defects in BCL10 are involved in various types of cancer. SIMILARITY: Contains 1 CARD domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTIG=VAR_013224.
S -> F (IN GERM CELL TUMOR, MESOTHELIOMA
MD OTHER CANCER CELL LINES).
/FTIG=VAR_013225.
attributed to the Ig somatic hypermutation mechanism resulting in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apoptosis; Chromosomal translocation; Anti-oncogene; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         // -> I (IN MALT LYMPHOMA).
/FIIG-VAR_013226.
L->A: ABOLISHES CELL DEATH-INDUCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTId=vAR_013222.
MISSING (IN FOLLICULAR LYMPHOMA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A -> S (IN MALT LYMPHOMA AND MESOTHELIOMA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FTIG=VAR_013212.
C -> R (IN MALT LYMPHOMA).
/FTIG=VAR_013213.
R -> G (IN GERM CELL TUMOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> E (IN MALT LYMPHOMA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MESCYHELLOMA).

/FTd=VAR_013208.

V -> E (IN MALT LYMPHOMA).
/FTd=VAR_013209.

/FTd=VAR_013210.

K -> E (IN MALT LYMPHOMA).
/FTd=VAR_013210.

T -> I (IN MESCYHELIOMA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /FTId-vAR_013218.

S -> P (IN MALT LYMPHOMA).

/FTId-vAR_013219.

M -> V (IN MESOTHELIOMA).

/FTId-vAR_013220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /FIId=VAR_013217.
D -> E (IN MALT LYMPHOMA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R -> K (IN MALT LYMPHOMA).
/FTId=VAR_013216.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S (IN MALT LYMPHOMA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTId=VAR_013214.
R -> Q (IN MESOTHELIOMA).
/FTId=VAR_013215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T -> A (IN MALT LYMPHOMA)./FTId=VAR_013221.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S (IN MESOTHELIOMA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTId=VAR_013223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MESOTHELIOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ٨
                                                                                                                                                                                                                    EMBL; AJ006288; CAA06955.1; --
EMBL, AF057700; AAD18800.1; --
EMBL, AF100338; AAD16428.1; --
EMBL, AF127386; AAD32597.1; --
EMBL, AF124395; AAD33597.1; --
EMBL, AF105066; AAF06894.1; --
EMBL, AF082283; AAD34918.1; --
EMBL, AF097732; AAD24918.1; --
                nucleotide transitions
                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001315; CARD. Pfam; PF00619; CARD; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00114; CARD; 1.
PROSITE; PS50209; CARD;
                                                                                                                                                                                                                                                                                                                                                                Genew; HGNC:989; BCL10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disease mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174
                                                                                                                                                                                                                                                                                                                                                                                603517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
```

4

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified annothis statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                   4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Embryonic brain;
MEDLINE-20219157; PubMed-10753917;
WEDLINE-20219157; PubMed-10753917;
Yoneda T., Imaizumi K., Maeda M., Yui D., Manabe T., Katayama T.,
Sato N., Gomi F., Morihara T., Mori Y., Miyoshi K., Hitomi J.,
Ugawa S., Yamada S., Okabe M., Tohyama M.;
Regulatory mechanisms of TRAF2-mediated signal transduction by BC110,
a MALT lymphoma-associated protein.
J. Biol. Chem. 275:11114-11120(2000).
I- FUNCTION: Promotes apoptosis, pro-caspase-9 maturation and
activation of NF KappaB via NIK and IKK. May be an adapter protein
between upstream TNFR1-TRADD-RIP complex and the downstream NIK-
 ABOLISHES NF-KAPPA-B ACTIVATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IKK-IKAP complex (By similarity).
SUBUNTI: Self-associates by CARD-CARD interaction and interacts with other CARD-proteins such as CARD9, CARD10, CARD11 and CARD14.
Binds caspase-9 with its C-terminal domain (By similarity).
Interacts with TRAF2 and BIRC2/c-IAP2.
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                  4 ALDEETLWEM----MESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAM 59
                                                                                                                                                                                                                                                                                                                       G->R: ABOLISHES NF-KAPPA-B ACTIVATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
B cell lymphoma/leukemia 10 (B-cell CLL/lymphoma 10) (Bcl-10) (R-CD1) (RCD).
                               ABOLISHES CELL DEATH-INDUCING
                                                                  I->A: ABOLISHES CELL DEATH-INDUCING
                                                                                               L->A: ABOLISHES CELL DEATH-INDUCING
                                                                                                                                  E->A: ABOLISHES CELL DEATH-INDUCING
                                                                                                                                                                 I->A: ABOLISHES CELL DEATH-INDUCING
                                                                                                                                                                                                                                  Score 81; DB 1; Length 233;
                                                                                                                                                                                                                                                                 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Cytoplasmic (By similarity). PTM: Phosphorylated (By similarity). SIMILARITY: Contains 1 CARD domain.
                 HOMO/HETERO-DIMERIZATION
                                                                                                                                                                                                                                               0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 AA
                                                                                                                                                                                                                                                                   14; Mismatches
                                                                                                               CAPABILITY
                                                                                                                                                                                   CAPABILITY
                                                                                 CAPABILITY
                                                                                                                                                  CAPABILIT
                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                       ||| ||| |: | :||::
| RAGKLLDYLQENPK-GLDTLVESIR 87
                                                                                                                                                                                                                                                                                                                                                                    RAGHLLDLLKTRGKNGAIAFLESLK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB016069; BAA88822.1; -
                                                                                                                                                                                                                                  14.5%;
36.5%;
                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                               41
                                                                46
                                                                                                                                53
                                                                                                                                                               55
                                                                                                                                                                                                 78
                                                                                               47
                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-10116;
                               41
                                                                46
                                                                                             47
                                                                                                                              53
                                                                                                                                                               55
                                                                                                                                                                                                 78
                                                                                                                                                                                                                                                                 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BCLA_RAT
Q9QYN5;
                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                     Local
                                                                                                                                  MUTAGEN
                                                                                                                                                                 MUTAGEN
                                                                                                                                                                                                 MUTAGEN
MUTAGEN
                                 MUTAGEN
                                                                MUTAGEN
                                                                                                 MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                  09
                                                                                                                                                                                                                                                               Matches
q
                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                  Q
```

InterPro; IPR001315; CARD.

```
SEQUENCE FROM N.A. MEDLINES-92214545; PubMed=10187770; MEDLINES-92214545; PubMed=10187770; Koseki T., Inohara N., Chen S., Carrios R., Merino J., Hottinger M.O., Nabel G.J., Nunez G.; "CIPER, a novel NF kappaB-activating protein containing a caspase recruitment domain with homology to Herpesvirus-2 protein E10."; J. BAD1. Chem. 274:9955-9961(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thome M., Martinon F., Hofmann K., Rubio V., Steiner V., Schneider P.,
Mattman C., Tschopp J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annocation update)
15-JUN-2002 (Rel. 41, Last annocation update)
16-JUN-2002 (Rel. 41, Last annocation update)
17-JUN-2002 (Rel. 41, Last annocation (Rel-10) (CED-3/ICH-1 prodomain homologous E10-like regulator) (MCIPER) (CARD-containing molecule enhancing NFkappaB) (Cellular homolog of vCARMEN)
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Equine herpesyirus-2 El0, but not its cellular homologue, activates NF-KB transcription factor and c-jun N-terminal kinase."; J. Biol. Chem. 274:9962-9968(1999).
                                                                                                                                                                                                                      4 ALDEETLWEM----MESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAM 59
                                                                                                                                                                                                                                          SLTEEDLIEVKKDALENLRVYLCEKIIAERHFDHLRAKKILSREDTEEI--SCR-TSSRK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

Willis T.G., Jadayal D.M., Du M.-Q., Peng H., Perry A.R.,

Willis T.G., Jadayal D.M., Du M.-Q., Peng H., Perry A.R.,

Abdul-Rauf M., Price H., Karran L., Majekodumn O., Wlodarska I.,

Pan L., Crook T., Hamoudi R., Isaacson P., Dyer M.J.S.;

Ballo is involved in t(1.14)(p22;q32) of MALT B cell lymphoma and

cell 96:35-45(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yan M., Lee J., Schilbach S., Goddard A., Dixit V.M.;
"mEl0, a novel caspase recruitment domain-containing proapoptotic
nolecule.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (mE10)
                                                                                                                                                                              8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CCARMEN) (Mammalian CARD-containing adapter molecule E10) (r(Cellular-E10) (c-E10) (CARD-like apoptotic protein) (mCLAP) BCL10 OR CIPER OR CLAP.
                                                                                                                                         Length 233;
                                                                                               SEQUENCE 233 AA; 25999 MW; B43274B4B825FC7D CRC64;
                                                                                                                                                                              32;
                                                                                                                                       14.5%; Score 81; DB 1; 36.5%; Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                         233 AA
                                                                                                                                                                              Mismatches
              SMART; SM0114; CARD; 1.
PROSITE; PS50209; CARD; 1.
Apoptosis; Anti-oncogene; Phosphorylation.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. 274:10287-10292(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=99214546; PubMed=10187771;
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE-Embryo;
MEDLINE-99214590; PubMed=10187815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=99292766; PubMed=10364242;
                                                                                                                                                                                                                                                                                                                         ||| ||| |: | | | :||:: | RAGKLLDYLQENPK-GLDTLVESIR 87
                                                                                                                                                                                                                                                                                                60 RAGHLLDLLKTRGKNGAIAFLESLK 84
                                                                                                                                                                              14;
                                                                                                                                                                              31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
Pfam; PF00619; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                              BCLA_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         molecule.
                                                                                                                                       Query Match
                                                                                                                                                             Best Local
                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                       STRAIN=972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
                                                                                                                                                                          Strausberg R.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Promotes apoptosis, pro-caspase-9 maturation and activation of NF-KappaB via NIK and IKK. May be an adapter protein between upstream TNFR1-TRADD-RIP complex and the downstream NIK-
                                                                                                                                                                                                                                                                                IKK-IKAP complex (By similarity).
SUBUNIT: Self-associates by CARD-CARD interaction and interacts with other CARD-proteins such as CARD9, CARD10, CARD11 and CARD14.
Binds caspase-9 with its C-terminal domain. Interacts with TRAF2 and BIRC2/c-IAP2 (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
INTSSUE SPECIFICITY: Highly expressed in heart, brain, spleen, lung, liver, skeletal muscle, kidney and testis. Detected in developing brain, olfactory epithelium, tongue, whisker follicles, salivary gland, heart, lung, liver and intestinal epithelia of Prim: Phosphorylated (By similarity).
Srinivasula S.M., Ahmad M., Lin J.-H., Poyet J.-L.,
Fernandes-Alnemri T., Tsichlis P.N., Alnemri E.S.;
"CLAP, a novel caspase recruitment domain-containing protein in the
tumor necrosis factor receptor pathway, regulates NF-kappaB activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 ALDEETLWEM----MESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAM 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 SLTEEDLTEVKKDALENLRVYLCEKIIAERHFDHLRAKKILSREDTEEI--SCR-TSSRK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C0539BC97102DBB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 78; DB 1,
Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1583 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sister chromatid cohesion protein mis4. MIS4 OR SPAC31A2.05C. Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apoptosis; Anti-oncogene; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Contains 1 CARD domain.
                                                                                        and apoptosis.";
J. Biol. Chem. 274:17946-17954(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 RAGHLLDLLKTRGKNGAIAFLESLK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||| ||| || || RAGKLLDYLQ-ENPRGLDTLVESIR 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AJ006289; CAA06956.1; -. EMBL; AF057701; AAD15801.1; -. EMBL; AF100339; AAD16429.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF127387; AAD32598.1; -. AF134396; AAD39148.1; -. BC024379; AAH24379.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 AA; 25948 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.9%;
35.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001315; CARD.
Pfam; PF00619; CARD; 1.
SMART; SM00114; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS50209; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 13.99
Best Local Similarity 35.33
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI:1337994; Bcl10
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIS4_SCHPO
Q09725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
MIS4_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOUTH THE SERVICE OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
```

```
RA WOOd V., Gwilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A.,
RA Sqouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Collins M., Connor R., Diewarth S., Huchel B.J., Hudt S., Ages G.,
RA Holroyd S., Honsby T., Hewarth S., McDonald S., McLean J.,
RA James K., Jones L., Jones M., Laather S., McDonald S., McLean J.,
RA Oliver K., O'Nell S., Pearson D., Quall M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Sauders R., Steper S., Stevens K.,
RA Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aerr R., Robben J., Grymonprez B.,
Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller H., Rainhardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Dominguez A., Revuelta J.L., Mcreno S., Armstrong J., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT Wither 41581-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: CHROMATID COHESION MOLECULE REQUIRED FOR EQUAL SISTER CHROMATID SEPARATION IN ANAPHASE. MAY FORM A STABLE LINK BETWEEN CHROMATIDS IN S PHASE THAT IS SPLIT RATHER THAN REMOVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUNCTATE FASHION THROUGHOUT THE CELL CYCLE. INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
SIMILARITY: CONTAINS 5 HEAT REPEATS.
                                                                                                                                                                       Furuya K., Takahashi K., Yanagida M.; "Faithful anaphase is resured by Mis4, a sister chromatid cohesion molecule required in S phase and not destroyed in G1 phase."; Genes Dev. 12:3408-3418(1998).
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB016866; BAA7479.1; -. PROSITE; PS50077; HEAT_REPEAT; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
POTENTIAL.
HEAT 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HEAT
HEAT
HEAT
HEAT
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21848401; Pubmed=11859360;
                                                                                                                                                      MEDLINE=99026114; PubMed=9808627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z50113; CAA90463.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      653
784
1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1472
808
847
884
                              Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1097
1179
1583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      633
                                                            NCBI_TaxID=4896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANAPHASE.
```

C8CF2F1D5C3E9271 CRC64;

180203 MW;

AA;

```
Complete
                                                                                          METAL
METAL
                                                METAL
METAL
                                                                     METAL
METAL
                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                   AOFH_MYCTU
                              METAL
                                        METAL
                                                                                                                                                                                                                                                                                                                         RESULT 13
ŏ
                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There is no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                             9
                                                                                                                                                                                                                                                                                                                                                                                                      1091 LTKAGTATLME-----IVPCLCSLFTRLNDYERLKKIVVSCLKSLEEARHS---ENN 1139
                                                2 LTALDEETLWEMMESHRHRIVRCICP--SRLTPYLRQAKVL--CQLDEEEVLHSPRLTNS 57
                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Sinorhizobium.
                             23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00643; COMPLEX1_75K_3; 1. Oxidoreductase; NAD; Ubiquinone; Iron-sulfur; 4Fe-4S; Plasmid;
         Length 1583;
                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
NADH dehydrogenase I chain G 2 (EC 1.6.5.3) (NADH-ubiquinone oxidoreductase chain G 2).
NUGG2 OR RAO828 OR SMA1523.
Rhizobium meliloti (Sinorhizobium meliloti).
                                                                                                     Putnoky P., Jady B., Chellapilla K.P., Barta F., Kiss E.; "Rhizobium meliloti carries two sets of nuo genes."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                             Indels
                                                                                           96
                                                                                          58 AMRAGHLLDLLKTRGKNGAI-----AFLESLKFHNP---DVYTLVTG
         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF01568; Molýdop_binding; 1.
TE; PS00198; 4FE4S_FEREDOXIN; 2.
TE; PS00641; COMPLEX1_75K_1; FALSE_NBG.
TE; PS00642; COMPLEX1_75K_2; 1.
TE; PS00643; COMPLEX1_75K_3; 1.
                                                                                                                                                                853 AA
       12.9%; Score 72.5; C
29.0%; Pred. No. 11;
ive 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR001450; 4Fe48_ferredoxin.
Interpro; IPR000283; Complex1_75K.
Interpro; IPR001041; Ferredoxin.
Pfam: PF00037; fer4; 1.
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21396509; PubMed-11481432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00111; fer2; 1.
PF00384; molybdopterin; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ245399; CAB51635.1; -.
                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                            Plasmid pSymA (megaplasmid 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AE007270; AAK65486.1;
                             Conservative
                                                                                                                                                                 STANDARD;
        Query Match
Best Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                        NCBI_TaxID-382;
                                                                                                                                                               NUG2_RHIME
P56914;
                                                                                                                                                                                                                                                                                                                        STRAIN-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF0
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
PROSITE;
                                                                                                                                                      NUG2_RHIME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam;
                                                                   g
                                                                                           δλ
                                                                                                             qq
```

```
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E., III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Ouall M.A., Rahandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Putative flavin-containing monoamine oxidase Rv3170 (EC 1.4.3.-).
Rv3170 OR MT3259 OR MTV014.14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Whole genome comparison of Mycobacterium tuberculosis clinical
                                                                                                                                                            (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- COFACTOR: FAD (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.
                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           470 RLVSTLKEGRSVTLLVSVDLLRSPLARKTLEQLGNLLQLLRLLGKEPSLQFL 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 RLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGHLLDLLKTRGKNGAIAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K -> R (IN REF. 1).
T -> L (IN REF. 1).
T -> L (IN REF. 1).
T -> I (IN REF. 1).
S -> G (IN REF. 1).
R -> C (IN REF. 1).
R -> C (IN REF. 1).
R -> G (IN REF. 1).
C -> C (IN REF. 1).
C -> C
                                (2FE-2S)
(2FE-2S)
(2FE-2S)
(2FE-2S)
(2FE-2S)
(4FE-4S)
(4FE-4S)
(4FE-4S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        454 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.8%; Pred. ...
                                                                                                                                                                                                      IRON-SULFUR
IRON-SULFUR
IRON-SULFUR
                                IRON-SULFUR (IRON-SULFUR (IRON-SULFUR (
                                                                                                                                                                                                                                                                                                                                                                                          IRON-SULFUR
IRON-SULFUR
                                                                                                                                                                      IRON-SULFUR
                                                                                                                                                                                                                                                                                                                                                     IRON-SULFUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.8%; Score 66; 30.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98295987; PubMed=9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5-DEC-1998 (Rel. 37, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                34
455
483
483
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
11001
10001
10001
10001
10001
10001
10001
10001
10001
10001
10001
10001
10001
10001
10001
10001
10001
10001
10001
10001
10001
10000
10001
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  laboratory strains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     853 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 16; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1773;
                                         STRAIN-H37Rv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AOFH_MYCTU
053320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
```

ö

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation-the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 LDEETLWEMMESHRHRIVRCICPSR-LTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGH 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parker N.J., Begley C.G., Smith P.J., Fox R.M.; "Molecular cloning of a novel human gene (D11S4896E) at chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLYCOSYLATION, PHOSPHORYLATION, SUBCELLULAR LOCATION, AND TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21356314; PubMed-11463338; Williams R.T., Manji S.S.M., Parker N.J., Hancock M.S., Van Stekelenburg L., Eid J.-P., Senior P.V., Kazenwadel J.S., Shandala T., Saint R., Smith P.J., Dziadek M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Manji S.S., Parker N.J., Williams R.T., van Stekelenburg L., Pearson R.B., Dziadek M., Smith P.J.; "STIMI: a novel phosphoprotein located at the cell surface."; Biochim. Biophys. Acta 1481:147-155(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.7%; Score 65.5; DB 1; Length 454; 31.5%; Pred. No. 15; Live 12; Mismatches 27; Indels II:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002937; Amino_oxidase.
InterPro; IPR00205; NAD_binding.
Pfam; PF01593; Amino_oxidase; 1.
PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00757; AMINEOXDASEF.
Hypothatical protein; Oxidoreductase; Flavoprotein; FAD; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAD (ADP PART) (POTENTIAL).
6C1AEB97FB2F435F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-UUN-2002 (Rel. 41, Created)
15-UUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        685 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stromal interaction molecule 1 precursor STIM1 OR GOK.
                                                                                                                                                                                                                                                                                                                                                                                                    Tuberculist, Rv3170; -.
InterPro; IPR000759; Adrndx_reductase.
InterPro; IPR001613; Amineoxid_f1.
                                                                                                                                                                                                                                                                        EMBL; AL021646; CAA16635.1; ALT_INIT.
EMBL; AE007139; AAK47598.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20461006; PubMed=11004585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Placenta, and Fetal liver; MEDLINE-97079692; PubMed-8921403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY, AND SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49136 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomics 37:253-256(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 31.5
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 LLDV----KNGA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 LLDLLKTRGKNGA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                      P27338; 1GOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      454 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                        TIGR; MT3259; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region 11p15.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STM1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIND
      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDT TDD DDT DD
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .,
α
                                                                                                                                                     FUNCTION: Possible adhesion molecule with a role in early hematopoiesis by mediating attachment to stromal cells. Influences the survival and/or proliferation of B cell precursors. Binding to cells requires Mn(II) (By similarity).

SUBGELLULAR LOCATION: Type I membrane protein. Cell surface
                                                                                                                                                                                                                                                                       primary cells and tumor cell lines.
--- PTM: Glycosylated.
--- PTM: Phosphorylated predominantly on Ser residues.
--- DISEASE: Defects in STIM1 may cause rhabdomyosarcoma and rhabdoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98021968; PubMed-9377559; Sabbloni S., Barbanti-Brodano G., Croce C.M., Negrini M.; GOK: a gene at 11pl5 involved in rhabdomyosarcoma and rhabdoid tumor development.";
"Identification and characterization of the STIM (stromal interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 EETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRA---- 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART, SM00454; SAM, 1.
PROSITE; PS50105; SAM_DOMAIN; 1.
Cell adhesion; Anti-oncogene; Transmembrane; Coiled coil; Signal; Glycoprotein; Phosphorylation.
          molecule) gene family: coding for a novel class of transmembrane proteins.";
                                                                                                                                                                                                                                                          -!- TISSUE SPECIFICITY: Ubiquitously expressed in various human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
STROMAL INTERACTION MOLECULE
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0AB512CA8D68A7A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COILED COIL (POTENTIAL). PRO/SER-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 --GHLLDLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVD 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      591 DKAHSLMELSPSAPPGGSPHLDSSRSHSPS-----SPDPD 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1260 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 65.5;
Pred. No. 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYS-RICH.
                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 1 SAM DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLU-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAM
                                                                                                                                            57:4493-4497(1997).
                                        Biochem. J. 357:673-685(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77492 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.7%;
24.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U52426; AAC51627.1; -. Genew; HGNC:11386; STIM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 605921; -.
InterPro; IPR001660; SAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234
685
200
200
343
336
336
629
685
685
1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         685 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                              Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214
235
132
238
270
362
600
672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAML_MOUSE
ID CAML_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                       DISEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIĞNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
TISSUE-Brain;

MEDLINE-88318924; PubMed=3412448;

MEDLINE-88318924; PubMed=341248;

MEDLINE-88318824; PubMed=3412488;

MEDLINE-88318824; PubMed=3412488;

MEDLINE-88318824; PubMed=3412488;

MEDLINE-88318824; PubMed=3412488;

MEDLINE-88318824; PubMed=3412488;

MEDLINE-88318824; PubMed=3412488;

MEDLINE-883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DR HSSP, P20241; 1CPB.

BR MGD; MGI:96721; Licam.

DR InterPro: IPR003961; FN_III.

DR InterPro: IPR003961; Fn_III.

DR InterPro: IPR003965; Ig_MHC.

InterPro: IPR003506; Ig_MHC.

DR InterPro: IPR003506; Ig_MHC.

DR Pfam: PF00041; fn3; 4.

DR PRINTS. PR000601; FNTYPBIII.

SMART; SM00060; FN3; 3.

SMART; SM00060; FN3; 3.

SMART; SM00408; IG_Like; 1.

NR SMART; SM00408; IG_Like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CELL ATTACHMENT SITE (POTENTIAL). CELL ATTACHMENT SITE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEURAL CELL ADHESION MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
POTENTIAL.
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 3.
IG-LIKE C2-TYPE DOMAIN 4.
IG-LIKE C2-TYPE DOMAIN 4.
IG-LIKE C2-TYPE DOMAIN 5.
IG-LIKE C2-TYPE DOMAIN 5.
IG-LIKE C2-TYPE DOMAIN 5.
IG-LIKE C2-TYPE DOMAIN 5.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 3.
                 01-077-1989 (Rel. 12, Created)
01-077-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Neural cell adhesion molecule L1 precursor (N-CAM L1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY
BY
BY
BY
                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                            LICAM OR CAMLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NI WOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
```

```
٠.
ش
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                              41 CQLDEEEVLH-SPRLTNSAMRAGHLLDLLKTRGKNGAIAFLE----SLKFHNPDVYTLVT 95
                                                                                                                      (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                       26; Indels 11;
                                                          POTENTIAL)
                                                                       (POTENTIAL)
                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                    (POTENTIAL)
                                                                                                 (POTENTIAL)
                                                                                                            ( POTENTIAL)
                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                            (POTENTIAL
                                                                                                                                                                                                                                                                                            Length 1260;
                                                                                                                                                                                                                                                                      22BE57001CB2A538 CRC64;
                                                                                                                                                                                                                                                                                             Score 65.5; DB 1;
Pred. No. 47;
           N-LINKED GLCNAC.
                                                                                                                                                                                                                                                                                                                      12; Mismatches
 SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: January 22, 2003, 08:53:24
Job time: 7.1707 secs
                                                                                                                                                                                                                                                                                               11.78;
27.98;
                                                                                                                                                                                                                                                                      140968
                                                                                                                                                                                                                                                                                                                       19; Conservative
                                                                                                                                                                                                                     1022
1030
1073
1107
590
1000
1000
2002
2045
4433
4438
4438
504
705
707
824
824
                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                             96 GLQPDVDF 103
                                                                                                                                                                                                                                                                                                                                                                                                                    981 NENPDLOY 988
                                                                                                                                                                                               CARBOHYD
CARBOHYD
                                                                                    CARBOHYD
                                                                                                            CARBOHYD
                                                                                                                         CARBOHYD
                                                                                                                                    CARBOHYD
                                                                                                                                                 CARBOHYD
                                                                                                                                                             CARBOHYD
                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                               Query Match
                                   CARBOHYD
                                                CARBOHYD
                                                             CARBOHYD
                                                                        CARBOHYD
                                                                                                 CARBOHYD
                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                        Matches
 g
                                                                                                                                                                                                                                                                                                                                                                                              ò
```

THIS PAGE BLANK (USPTO)

OM protein

Run on:

Sequence:

```
Q9nai9 caenorhabdi
Q9ylu6 pristionchu
Q9cda4 mycobacteri
Q8swy2 drosophila
Q9ncp8 drosophila
Q9vas2 drosophila
Q9vas9 thermoplasm
Q93a18 clostridium
                                                                                                      OSSTR UDDAGE DATE OF STREET OF STREE
                                                                                                                                                                                                                                                                                                     O9w1q6 drosophila
O9s434 myxococcus
O69441 legionella
O30119 archaeoglob
 Q67683 groundnut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 DEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGHLL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 EEDALWENVECNRHMLSRYINPAKLTPYLRQCKVIDEQDEDEVLNAPMLPSKINRAGRLL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohara O., Nagase T., Kikuno R., Okumura K.; "The nucleotide sequence of a long cDNA clone isolated from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 48.2%; Score 270; DB 4; Length 1171; Local Similarity 51.5%; Pred. No. 2.9e-22; es 51; Conservative 22; Mismatches 26; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1171 AA; 134966 MW; FA567ABBC8A703FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   spleen.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK074049; BAB84875.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   QBTES3;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
FLJ00120 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1171 AA
                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
           090NA19
09Y1U6
09Y1U6
09SWYZ
09NCP8
09SXZAZ
097AL9
091E29
091E29
091E29
091HT2
091HT2
091HT2
091HT3
09EEF7
09EEF7
09EEF7
09EEF7
09EEF7
09EEF7
09EEF7
                                                                                                                                                                                                                                                                                                                                         030119
112
112
113
113
114
115
116
117
117
117
117
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=SPLEEN;
NCBI_TaxID=9606
                                                                                                                               NON_TER
SEQUENCE
67.5
67.5
67.5
67.5
67.5
67.5
                                                                                                                                                                                                                                                                                                     65
64.5
64.5
                                                                                                                     67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8TES3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
 Q8TES3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   099PQ2
                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q99pq2 mus musculu
Q66677 equine herp
Q97el5 clostridium
Q9yln5 equine herp
O61218 caenorhabdi
Q9v466 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O9wzdl thermotoga
O95zc3 leishmania
O9btq5 homo sapien
O96h24 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8vdx5 mus musculu
Q8tdn1 homo sapien
Q9ddu9 xenopus lae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q96et5 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8tes3 homo sapien
                                                                              January 22, 2003, 08:49:36; Search time 16.6828 Seconds (without alignments) 1321.544 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9p3s8 neurospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                              US-09-767-215-2_COPY_10_116
560
1 ALTALDEETLWEMMESHRHR......PDVYTLVTGLQPDVDFSNFS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                          671580
          GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                 671580 segs, 206047115 residues
                                                                                                                                                                                                                                                                                                                            summaries
                                                          - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8TES3
Q95PQ2
Q66PD2
Q97EL5
Q97JN5
Q97JN6
Q9WZD1
Q9WZD1
Q96FD2
Q96FD5
Q96FD5
Q96FD5
Q96FD5
Q96FD5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9DDU9
Q9P3S8
                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                        sp_fung1:*
sp_human:*
sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_virus:*
sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 su
                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                 seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                 sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1112
112
112
113
114
113
113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                                                                            sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length DB
                                                                                                                                                                                                                                                                                                                                                     SPTREMBL_21:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55...
77...
110...
112...
114...
116...
                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
```

Minimum DB Maximum DB

Database

Searched:

ö

Result õ

```
EMBL; U20824; AAC13865.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Equine herpesvirus 2.
                                                             210 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                01-OCT-2001
                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                              CAC3095
                                                                                                                                                                                                                                                                       Q97EL5
Q97EL5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9YJN5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
Q9YJN5
                                                                                                                                                                                                                                                  RESULT 4
                                                                                                                                                                                                                                                                          Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ID DT DT OS OS
 δ
                                                                                                                                                             g
                                                                                                                                                                                     δ
                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 EET -- LWE-MMESHRHRIVRCICPSRLTPYL--RQAKVLCQLDEEEVLHSPRLTNSAMRA 61
                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-21231161; PubMed-11331580;
MEDLINE-21231161; PubMed-11331580;
MENGONG A., Meroin G., Fantozzi A., Merla G., Cairo S., Luzi L.,
Riganelli D., Zanarla E., Messali S., Cainarca S., Guffanti A.,
Minucci S., Pelicci P.G., Ballabio A.;
The tripartite motif family identifies cell compartments.";
EMBO J. 20.2140-2151(2001).
--- SIMILARITY: CONTAINS I RING-TYPE ZINC FINGER.
EMBL, AR520124, AAG53497.1;
--- MGD; MGI:2137355; Triml1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDILINE-95302501; Pubmed=7783207;
Telford E.A., Watson M.S., Aird H.C., Perry J., Davison A.J.;
"The DNA sequence of equine herpesvirus 2.";
J. Mol. Biol. 249:520-528(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Telford E.A.R.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                             467 AA; 52579 MW; 82B7CF68807E9DA8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Equine herpesvirus type 2 (strain 86/87) (EHV-2).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae.
NCBI_TaxID=82831;
                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
13.4%; Score 75; DB 11
Best Local Similarity 32.2%; Pred. No. 3.4;
Matches 29; Conservative 17; Mismatches
467 AA
                                                                                                                                                                                                                                                                              InterPro; IPR001870; Gamma_carbxylse.
InterPro; IPR001870; Gamma_carbxylse.
InterPro; IPR003878; SPRY_domain.
InterPro; IPR003877; SPRY_interPro; IPR001841; Znf_Bbox.
InterPro; IPR001841; Znf_Bbox.
Pfam; PF00642; SPRY; I._
Pfam; PF00643; Zf_Bbox; I.
Pfam; PF00697; Zf_C3HC4; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 | : : | : | : | : | 3 | 218 | 20STQLAALISELESRCQLPALGLLQDIK 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 GH-----LLDLLKTRGKNGAIAFLESLK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
 PRT;
                                                             Tripartite motif protein TRIM11.
                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00518; ZF_RING_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00336; BBOX;
                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                         SM00449;
                                                                                                                                                                                                                                                                                                                                                                                                                                Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORF E10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       066677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
Q66677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
 ò
```

```
5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=21359325, PubMed=11466286;
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubols J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.;
Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium accoboutylicum.";
J. Bacteriol. 1834813-4838 (2001).

EMBL; AE07806; AA481035-1;
InterPro; IPR004399; HMP-P.Kinase.
TIGRPAMS; TIGR00097; HMP-P.Kinase; 1.
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                       ----MESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVL 49
                                                                                                                                                                                                                                                                                                                                                                     16 LTEEDIWDVERLCLEELRVLLVSHLKSHKH------LDHLRAKKILSREDAEEV- 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 RIVRCICP--SRLTPYLRQAKVLCQL---DEEEVLHSPRLTNS-----AMRAGHLLD-L 67
                                                                                                                                                                                                                                                 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.0%; Score 73; DB 16; Length 265; ilarity 23.8%; Pred. No. 3; Conservative 23; Mismatches 29; Indels
                                                                                                                                                                               13.0%; Score 73; DB 12; Length 210; 29.5%; Pred. No. 2.3;
                                                                                                                                                                                                                                                 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kinase; Complete proteome.
SEQUENCE 265 AA; 28539 MW; 327DA3CEAE6D06EB CRC64;
                                                                                                                       22943 MW; 136D639DD8BC2D40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9YJN5,
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
10-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Hypothetical 32.6 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hydroxyethylthiazole kinase ThiM/ThiK (FS!).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 -SSRAT-SRSRAGLLVDMCQDHPR-GFQCLKESCK 95
                                                                                                                                                                                                                                              13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 50 HSPRLTNSAMRAGHLLDLLKTRGKNGAIAFLESLK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 TDLFYKNGYIEWFKLEKIDNPNTH 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 LKTRGKNGAIAFLESLKFHNPDVY 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 18, (TrEMBLrel. 18, (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium acetobutylicum
InterPro; IPR001315; CARD. Pfam; PF00619; CARD; 1. SMART; SM00114; CARD; 1. PROSITE; PS50209; CARD; 1.
                                                                                                                                                                                  Query Match
Best Local Similarity 29.59
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                             5 LDEETLWEM------
```

```
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09V466
                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
  δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S.
                                                                                                                                                                                                                                                                              MEDLINE-99292766; PubMed=10364242; Srinivasula S.M., Ahmad M., Lin J.-H., Poyet J.-L., Fernandes-Alnemri T., Tsichlis P.N., Alnemri E.S.; "CLAP, a novel caspase recruitment domain-containing protein in the tumor necrosis factor receptor pathway, regulates NF-kappaB activation
                                                                                                                                                                                   Thome M., Martinon F., Hofmann K., Rubio V., Steiner V., Schneider P., Mattman C., Tschopp J.:

"Equine herpesvirus-2 E10, but not its cellular homologue, activates NF'8B transcription factor and c-jun N-terminal kinase.";
J. Biol. Chem. 0:0-0(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A., Craxton M., Dear S., Du Z., Durbin R., Favello A., Filton L., Gardher A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 LTEEDIWDVERLCLEELRVLLVSHLKSHKH------LDHLRAKKILSREDAEEV- 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----MESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVL 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
Eukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                           Willis T.G., Jadayel D.M., Du M.Q., Peng H., Perry A.R.,
Abdul-Rauf M., Price H., Karran L., Majekodunmi O., Wlodarska I.,
Trook T., Hamoudi R., Isaacson P., Dyer M.J.;
"Bcll0 is involved in t(1;14)(p22;q32) of MALT B cell lymphoma and
mutated in multiple tumor types.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 311 AA; 32602 MW; 04EC68C7353D723B CRC64;
 Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.0%; Scor.
29.5%; Pred. No. 3.0,
"'ne 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        265 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 HSPRLTNSAMRAGHLLDLLKTRGKNGAIAFLESLK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - SSRAT-SRSRAGLLVDMCQDHPR-GFQCLKESCK 95
                                                                                                                                                                                                                                                                                                                                                     and apoptosis.";
J. Biol. Chem. 274:17946-17954(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed-7906398;
                                                                 MEDLINE=99142601; PubMed=9989495;
                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ006410; CAA07016.1; -.
EMBL; AF100340; AAD16430.1; -.
EMBL; AF134394; AAD39146.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-BCC-2001 (TrEMBLrel. 19, K03H6.2.
                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001315; CARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00114; CARD; 1.
PROSITE; PS50209; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 LDEETLWEM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00619; CARD; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       061218
061218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
061218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

```
Adams M.D., Celliker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., In P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S. Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.K., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
M. Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Botshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R., Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Thomas K., Vaughan K., Waterston J., Weinstock L., Wilkinson-Sproat J., Wohldman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoá; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 WEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLD--EEEVLHSPRLTNSAMR------ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.7%; Score 71; DB 5; Length 265; 23.9%; Pred. No. 5.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ------AGHLL----DLLKTRGKNGAIAFLESLKFHNPDVYTLVTG 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40; Indels
                                                                                                                                                                                                                                                                              cosmid K03H6.";
EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF047658; AAC04418.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPASE_SER; UNKNOWN_1.
30644 MW; E7536832B08BDAFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000734; Lipase.
InterPro; IPR002921; Lipase.
InterPro; IPR003921; Lipase.
InterPro; IPR00343; Zn_carbopept.
PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.
PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         845 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                 "The sequence of C. elegans
Submitted (FEB-1998) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BCDNA:LD18761 protein.
BCDNA:LD18761 OR CG6743.
                                                                                                                                                                Nature 368:32-38(1994).
                                                                                                                                                                                                                                  STRAIN=BRISTOL N2;
Wamsley P., Gibson A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                   Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000
```

٠.

```
Query Match
                                                                                                                                                                                                                                               L1994.04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9BTQ5
                                                                                                                                                                                         095ZC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
                                                                                                                                                                      RESULT 9
0952C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09BTQ5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ΟŻ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                        g
                                                                                                                         δŏ
                                                                                                                                           qq
   DR
DR
SQ
                                                                                      δ
ر.
د
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEDLINE-99287316; PubMed=10360571;
MEDLINE-99287316; PubMed=10360571;
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.C., Ketchum K.A.,
MCDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.,
"Evidence for lateral gene transfer between Archaea and Bacteria from
                                                                                                                                                                                                                                                                                                                                                                                        201 LHAHDRMMAWENTLFQLENLQGAAFGKGHKIV----TRLDPDAPVREKRPLHALDEEDN 255
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                       2 LTALDEETLWE----MMESHR-----HRIVRCICPSRLTP--YLRQAKVLCQLDEEEV 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermotoga maritima.
Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
                                                                                                                                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                                                  12.6%; Score 70.5; DB 5; Length 845; 30.7%; Pred. No. 22; Live 13; Mismatches 36; Indels 2:
                                                                                                                                                                                                                                               Tsang G., Brokstein P., Frise E., Harvey D., Evans-Holm M., Lewis S.E., Suh C., Rubin G.M.;
"Full Length Drosophila melanogaster cDNA sequence.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003629; AAF53002.1; -
EMBL; AF160938; AAAD46878.1; -
                                                                                                                                                                                                                                                                                                        FBG00027868; BCDNA:LD18761.
845 AA; 97381 MW; 0A75B807A6AFD6B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein TM0663.
                                                                                                                                                                                                                                                                                                                                                                                                                             256 LRLSRAIFELIRAGRVDDGLKLCKHFGQTWRAAILEGWRLH 296
                                                                                                                                                                                                                                                                                                                                                                                                           49 LHSPRLTNSAMRAGHL --- LDLLKTRGKNGAIAFLESLKFH 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            522 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                       Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                       31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Thermol
                                                                                                                                                                                                                                                                                                           FlyBase; I
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9WZD1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9WZD1
                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GZM60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q
                                                                                                                                                                                                                                                                                                                                                                                                             ò
       à
                                                                                                                                                                                                                                                                                                                                                                                           g
```

```
9
                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 KVAASTDVLEVPLHAPRLRVPTNLPLEQTTLLDLLATAVVQGGPTTEEEIVKREMGRG-N 245
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                        8 ETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTIN-----SAMRAG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----RGKN 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32;
                                                                                                                Length 522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=FRIEDLIN;
MEDLINE-98146435; PubMed-9477341;
Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ξ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A physical map of the Leishmania major Friedlin genome."; Genome Res. 8:135-145(1998).
EMBL; ALS96274; CAC44741.1; -. SEQUENCE 979 AA; 102709 MW; D43039D7F172DE02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 979;
                                                                                                                                                                                                                                                                                                                                     407 YWDFPHILD-LDERVLNGAV-YIHS----TSEAYT----EEQEIDAKRF 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Rieger
Ivens A.C., Quail M., Rajandream M.A., Barrell B.G.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
EMBL; AE001739; AAD35747.1; -.
TIGR; TM0663; -.
Hypothetical protein; Complete proteome.
SEQUENCE 522 AA; 60668 MW; D7A5E16AA88F79CC CRC64;
                                                                                                                                                                                                                                                                                                      63 ----HLLDLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFSNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Hypothetical 24.5 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TIEMBLrel. 19, Created)
01-DEC-2001 (TIEMBLrel. 19, Last sequence update)
01-JUN-2002 (TIEMBLrel. 21, Last annotation update)
Possible hypothetical 110.9 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                12.4%; Score 69.5; DB 16; 28.4%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38 KVLCQLDEEEV-LHSPRL---TNSAMRAGHLLDLLKT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   221 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       979 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                               16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.3%; Score 69; 34.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246 PAFAFLGE-KFNHPCMLYYRWRLYSLLQG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 GAIAFLESLKFHNP-----DVYTLVTG 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 31; Conserv
                                                                                                                     Query Match
Best Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-FRIEDLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith D.F.;
```

S

```
TISSUE=OVARY;
                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8VDX5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8VDX5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8TDN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
Q8TDN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8VDX5
     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SON DEN TEN TO THE TEN TO THE TEN THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Π
                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                              4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 ALSFQEELAYWGIEEAH---LERC-CLRKLLRKLEELEELAKLHREDVLRQQRETRRPAS 195
                                                                                                                                                                                                                                                                                                                                                                                                         97 DEECTCVYEFQEGAPVRPVSPRCSLRLTHYIEEANVGRGYIKELCFSPDGRMISSPHGYG 156
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ALTALDEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLT----N 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unknown (protein for MGC:4558).

Homo sapiens (Human)

Mammalia: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           096ET5.
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 28.4 kDa protein.
Hypothetical 28.4 kDa protein.
Hypothetical Section (Treman).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidee; Homo.
                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
                                                                                                                                                                                                                                                                                                                                                                       6 DEE--TLWEMMESHRHRIVRCICPSRLTPYLRQAKV-----LCQLDEEEVLHSP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : | : | : | | : | 106 HSSRWGLCMNRLREMVENPQSGLPGKVFACLSILFVATTAVSLCVSTMPDL 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 SAMRAGHLLDLLKTRGKN-----GAIAFLESLKFHNPDVYTLVTGLQPDV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 12.1%; Score 68; DB 4; Length 256; Best Local Similarity 25.2%; Pred. No. 11; Matches 28; Conservative 20; Mismatches 49; Indels
                                                                                                                                                                                                                                                                        Query Match 12.1%; Score 68; DB 4; Length 221; Best Local Similarity 28.7%; Pred. No. 9.2; Matches 29; Conservative 11; Mismatches 45; Indels
                                              Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BE003520; ARH03520.1; -.
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                    SMARY; SM00320; WD40; 1.
Hypothetical protein; Repeat; WD repeat.
SEQUENCE 221 AA; 24472 MW; 39CCF8979C10DB53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14, 1.
29333 MW; 5A48EFC68637F8B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          096H34;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 IRLLGFDKQCSELVDCLPKEA--SPLRVIRSLYSHNDVVLT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 -RLTNSAMRAGHLLDLLKTRGKNGAIAFLESLKFHNPDVYT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (MAY-2001) to the EMBI
EMBL, BCO08969, AAH08969.1; -.
INTERPRO, IPRO03131; K_tetra.
Pfam, PPO2214; K_tetra.
SEQUENCE 256 AA; 29333 MW; !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A. TISSUE=UTERUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q96ETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

```
4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                 6 DEE--TLWEMMESHRHRIVRCICPSRLTPYLRQAKV-----LCQLDEEEVLHSP---- 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 EET--LWE-MMESHRHRIVRCICPSRLTPYL--RQAKVLCQLDEEEVLHSPRLTNSAMRA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 11; Length 483;
23;
                                                                                                                                                                                                                       Length 258;
                                                                                                                                                                                                                                                                    45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC020102; AAH20102.1;
InterPro; IPR001870; Gamma_carbxylse.
InterPro; IPR001877; SPRY_domain.
InterPro; IPR001877; SPRY_receptor.
InterPro; IPR001817; SPRY_receptor.
InterPro; IPR001811; Znf_Bbox.
InterPro; IPR001841; Znf_Ling.
Strausberg R.; Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC011959; AAH11959.1; InterPro: PRR001680; WD40. InterPro: PRF00400; WD40. Hypothetical protein; Repeat; WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50119; ZF_BBOX; 1.
PROSITE; PS5018; ZF_RING_1; UNKNOWN_1.
PROSITE; PS50089; ZF_RING_2; 1.
SEQUENCE 483 AA, 54313 MW; 51BDFFCD514046FC CRC64;
                                                                                                                                                                       F50D287B1FAEE9E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Similar to tripartite motif protein 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 IRLLGFDKQCSELVDCLPKEA--SPLRVIRSLYSHNDVVLT 232
                                                                                                                                                                                                                                                                                                                                                                                                                 53 -RLINSAMRAGHLLDLLKTRGKNGAIAFLESLKFHNPDVYT 92
                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      483 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     519 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16; Mismatches
                                                                                                                                                                                                                12.1%; Score 68; DB 28.7%; Pred. No. 11; ive 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.1%; Score 68; 32.2%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GOOSTOLAALISELESRCOLPALGLLO 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GH-----LLDLLKTRGKNGAIAFLE 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00643; Zf-B_box; 1.
Pfam; PF00097; Zf-C3HC4; 1.
PRINTS; PR01406; BBOXZNFINGER.
SMART; SM00336; BBOX; 1.
SMART; SM00184; RING; 1.
                                                                                                                                                 ll protein; Repeat;
258 AA; 28385 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                           Best Local Similarity 28.7%
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
```

```
RP SEQUENCE FROM N.A.

RX TAIN 1.41

RX TAIN J. Kim S., Heilig E., Ruderman J.V.;

RT Tidentification of XPR-1. Ruderman J.V.;

RT Tidentification of XPR-1. a progesterone receptor required for Xenopus RT Tidentification. Sci. U.S.A. 97:14358-14363(2000).

RY TOC. Natl. Acad. Sci. U.S.A. 97:14358-14363(2000).

C. -: SUMCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

C. -: SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.

DR RESP: P06536, Hormone_rec_lig.

RICEPTO: IPR00128; Progest_receptor.

DR InterPro: IPR00128; Progest_receptor.

DR InterPro: IPR001723; Std/mnn_receptor.

DR PEam; PP00104; hormone_rec_lig.

RICEPTO: IPR001638; Znf_C4steroid.

DR PEAM; PF00105; zf-C4; 1.

PRINTS; PR00199; STRDHORNORE.

DR PRINTS; PR00199; STRDHORNORE.

DR PRINTS; PR00199; Znf_C4steroid; 1.

DR SMART; SM00139; Lof_C4steroid; 1.

DR SMART; SM00139; Nuclear Protein; Receptor; Transcription regulation;

KW Zinc-finger.

AND SEATOR PROSECT.

CONTINUED TAIL TAIL TRANSCRIPTION;

CONTINUED TAIL TAIL TRANSCRIPTION;

CONTINUED TAIL TAIL TRANSCRIPTION;

CONTINUED TAIL TRANSCRIPTION;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 ALSFQEELAYWGIEEAH---LERC-CLRKLLRKLEELEELAKLHREDVLRQQRETRRPAS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ALTALDEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLT----N 56
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Ottschytsch N., van Hoorick D., Raes A.L., Snyders D.J.;
Identification, cloning and functional analysis of 3 new human K+chanel subunits.",
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF348984; AAL83911.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 HSSRWGLCMNRLREMVENPQSGLPGKVFACLSILFVATTAVSLCVSTMPDL 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 SAMRAGHLLDLLKTRGKN-----GAIAFLESLKFHNPDVYTLVTGLQPDV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.1%; Score 68; DB 4; Length 519; 25.2%; Pred. No. 25; tive 20; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 732 AA; 82022 MW; BF0BA3A14F022199 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      519 AA; 58979 MW; E5BBA354931AB0A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                     01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Voltage-gated potassium channel Kv6.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              732 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 25.2
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Progesterone receptor.
XPR-1.
                                                                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopodinae; Xenopus
NCBL_TaxID=8355;
                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 600060
Q8TDN1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
Q9DDU9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
```

```
9
                                                                                                                 69 SHLHSWTHFAAPEVSRVTPH------MCPSDEAKALSIHHTSSLEETSLWAAPTLVERKE 122
                                           Gaps
                                                                                16 SHRHRIVRCICP--SRLTPYLRQAKVLCQLDEEEVL---HSPRLTNSAMRAGHLL---- 65
                                         30;
                                                                                                                                                                                                123 PGDSMPLKGKNS----LEETKEPNSSLTMDSDETVTSILPILPPDLNLNN 168
                                                                                                                                                                     66 -- DLLKTRGKNGAIAFLESLKFHNPD-----VYTLVTGLQPDVDFSN 105
DB 13; Length 732;
37;
                                           Indels
                                           35;
  Ouery Match
12.1%; Score 68; DB
Best Local Similarity 26.4%; Pred. No. 37;
Matches 29; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                          Search completed: January 22, 2003, 08:56:31 Job time: 20.6828 secs
                                                                                                                                                                                                                 Pb
                                                                                                                              g
                                                                                                                                                                            δ
                                                                                           δŻ
```

```
(without alignments) 683.714 Million cell updates/sec
                                                                                                                                                                                                                                                                                   January 22, 2003, 08:49:35; Search time 57.4933 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ECLAGAIGSLQEELNQEKGQ..........1QLRQLQAEPPGVLKQEART 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS2/gcddata/geneseq/geneseqp emb1/AA1992.DRT:*/SIDS2/gcddata/geneseq/geneseqp emb1/AA1993.DRT:*/SIDS2/gcddata/geneseq/geneseqp-emb1/AA1994.DAT:*/SIDS2/gcddata/geneseq/geneseqp-emb1/AA1995.DAT:*/SIDS2/gcddata/geneseq/geneseqp-emb1/AA1995.DAT:*/SIDS2/gcddata/geneseq/geneseqp-emb1/AA1995.DAT:*/SIDS2/gcddata/geneseq/geneseqp-emb1/AA1995.DAT:*/SIDS2/gcddata/geneseq/geneseqp-emb1/AA1997.DAT:*/SIDS2/gcddata/geneseq/geneseqp-emb1/AA1998.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS2/gcgdata/geneseq/genesegp-emb1/AA1980.DAT:*/SIDS2/gcgdata/geneseq/genesegp-emb1/AA1981.DAT:*/SIDS2/gcgdata/geneseqg-emb1/AA1981.DAT:*/SIDS2/gcgdata/geneseqg-emb1/AA1982.DAT:*/SIDS2/gcgdata/geneseqg-emb1/AA1983.DAT:*/SIDS2/gcgdata/geneseqg-emb1/AA1984.DAT:*/SIDS2/gcgdata/geneseqg-emb1/AA1985.DAT:*/SIDS2/gcgdata/geneseqg-emb1/AA1985.DAT:*/SIDS2/gcgdata/geneseqg-emb2/AA1986.DAT:*/SIDS2/gcgdata/geneseqg-emb2/AA1987.DAT:*/SIDS2/gcgdata/geneseqg-emb2/AA1987.DAT:*/SIDS2/gcgdata/geneseqg-emb2/AA1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqg-emb1/AA1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqg-emb1/AA1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqg-emb1/AA1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqg-emb1/AA1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqg-emb1/AA1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqg-emb1/AA1988.DAT:*/SIDS2/gcgdata/geneseq/geneseqg-emb1/AA1988.DAT:*/SIDS2/gcgdata/geneseq/geneseqg-emb1/AA1988.DAT:*/SIDS2/gcgdata/geneseqg-emb1/AA1988.DAT:*/SIDS2/gcgdata/geneseqg-emb1/AA1988.DAT:*/SIDS2/gcgdata/geneseqg-emb1/AA1988.DAT:*/SIDS2/gcgdata/geneseqg-emb1/AA1988.DAT:*/SIDS2/gcgdata/geneseqg-emb1/AA1988.DAT:*/SIDS2/gcgdata/geneseqg-emb1/AA1988.DAT:*/SIDS2/gcgdata/geneseqg-emb1/AA1988.DAT:*/SIDS2/gcgdata/geneseqg-emb1/AA1988.DAT:*/SIDS2/gcgdata/geneseqg-emb1/AA1988.DAT:*/SIDS2/gcgdata/geneseqg-emb1/AA1988.DAT:*/SIDS2/gcgdata/geneseqg-emb1/AA1988.DAT:*/SIDS2/gcgdata/geneseqg/geneseqg-emb1/AA1988.DAT:*/SIDS2/gcgdata/geneseqg/geneseqg-emb1/AA1988.DAT:*/SIDS2/gcgdata/geneseqg/geneseqg-emb1/AA1988.DAT:*/SIDS2/gcgdata/geneseqg/geneseqg-emb1/AA1988.DAT:*/SIDS2/gcgdata/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/geneseqg/gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          908470
version 5.1.3
- 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-767-215-2_COPY_126_420
1462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                                                                                                                              protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
     GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A_Geneseq_101002:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                              OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                        Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMAKIES	
		æ				
Result		Query				
Ño.	Score	Match	Match Length DB ID	DB	ID	Description
	1462	100.0	:	22	AAE07164	Human Caspase recr
7	1443	98.7			AAE07165	Human predicted ca
٣	396.5	27.1	1147	22	AAU01207	Human caspase recr
4	329.5			22	AAU01206	Human caspase recr
5	329.5			23	AAU73247	Human plakoglobin
9	283.5				AAU01204	Rat caspase recrui
7	274.5			22	AAU01205	Human caspase recr
æ	230				AAM93822	Human polypeptide,
6	198			22	AAB95617	Human protein segu
10	197				ABG05850	Novel human diagno

*			į	0		
7	<b>T</b>	7)	7	77	AABY5546	orein se
12	2	m	2	12	_	e of the i
13	ð	m	10	22	AAG65799	Nuclear mitotic ap
14	S)	$\sim$	11	22	AAU32040	Novel human secret
15	σ,	3	19	18	173	LexA/NuMA fusion p
16	ð	3	20	22	AAU32041	Novel human secret
17	σ	$^{\circ}$	27	18	AAW21731	GAL4/HA/NuMA fusio
18	σ <sub>ν</sub>	$^{\circ}$	11	21	AAY49937	Human NuMA protein
19	σ	$^{\circ}$	1456	22	ABB58673	Drosophila melanog
20		3	69	22	ABB61144	Drosophila melanog
21	91.	$\mathbf{c}$	69	22	ABB61173	Drosophila melanog
22	cη.	$^{\circ}$	10	21	AAY49936	Human NuMA protein
23	σħ.	$^{\circ}$	38	23	ABG65631	Human breast speci
24	88.	$^{\prime}$	63	22	ABG06505	Novel human diagno
25	88.	$^{\circ}$	99	22	AAM39097	Human polypeptide
26		$^{\circ}$	68	22	AAM4 0883	
27	87.	$^{\circ}$	71	22	ABG20672	Novel human diagno
28	86.	$^{\circ}$	44	21	AAY77575	
29	œ	7	580	22	AAM42158	Human polypeptide
30	œ	$^{\circ}$	580	22	AAM42159	Human polypeptide
31	æ	$\sim$	069	22	AAB95603	Human protein sequ
32	œ	$\sim$	691	22	AAM40372	Human polypeptide
33	α	2	691	22	AAU12179	Human PRO4996 poly
34	185	12.7	691	23	ABB07265	Human APRG polypep
35	æ	N	71	22	AAM40373	Human polypeptide
36	Ф	7	69	23	ABB06335	Human GDMLP-1 orth
37	æ	2	1286	21	AAB43359	Human ORFX ORF3123
38	Θ	2	05	22	AAU03501	_
39	œ	$^{\circ}$	05	23	AAE24079	MDPK pi
40	œ	2	05	23	AAE24150	kinase
41	œ	2	93	22	ABG23862	l human di
42	œ	2	45	22	921	polypeptid
43	œ	2	46	22		īg
44	œ	2	1988	22	660	Human polypeptide
45	æ	2	98	22	AAM41000	įq
					ALIGNMENTS	
RESULT 1	<del></del>					
		9 10 11				

```
nuclear factor-kappa B; NF-kB; cell growth; cell death; cancer; therapy; autoimmune disorder; systemic lupus erythematosus; neurological disorder; Alzheimmet's disease; Parkinson's disease; inflammatory disorder; anaemia haematological disorder; myelodysplastic syndrome; myocardial infarction; stroke; immune disorder; crohn's disease; allergic rhinitis; infection; cell signalling disorder; cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antibacterial.
                                                                                                                                                                                                                                                                                                                                      /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Casein kinase II phosphorylation site"
25..27
/note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                      "Casein kinase II phosphorylation site"
                                                                                                                              Human; caspase recruitment domain-14; CARD-14; chromosome 17;
                                                                                             Human caspase recruitment domain-14 (CARD-14).
AAE07164 standard; Protein; 1004 AA
                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                         10..116
/label= CARD_domain
                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
18..21
                                                                                                                                                                                                                                                                                                          Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                          Homo sapiens
                                                             06-NOV-2001
                               AAE07164;
                                                                                                                                                                                                                                                                                                                                                                         Domain
```

```
note= "cAMP- and cGMP-dependent protein kinase
hosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .947
ce= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "N-myristoylation site"
1002..1004
/note= "Protein kinase C phosphorylation site"
note= "Protein Ainson".
725..728
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                    .761
e= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                   796..799
/note= "Casein kinase II phosphorylation site"
800..805
                                                                                                                                                                                                                                                                                                                                                                                    ...844
ote= "Protein kinase C phosphorylation site"
                                                                                                                                              .727
e= "Protein kinase C phosphorylation site"
                                            "Casein kinase II phosphorylation site"
                                                                           777.
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   An isolated caspase recruitment domain polypeptide useful for
                                                                 'note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 870.872
/note= "RGD cell attachment sequence"
893.896
/note= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                               incte= "Casein Ainer"
368..870
Anote= "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .929
.e= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              700...979
/note= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                              85. 793 note= "Peroxisomal targetting signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      941..949
/note= "Peroxisomal targetting signal"
                                                                                                                                                                                                                                                                                                                                                                          Tabel= Guanylate_kinase_domain
                                                                                                                                                                             719
:e= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                    "N-myristoylation site"
                                                                                                                                                                                                                            "N-glycosylation site"
                                                                                                             'label= SH3_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JAN-2001; 2001WO-US02087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-FEB-2000; 2000US-0181159
                                          /note= "Le
                                                                                     /note= "C?
<76 745
                                                                                                                                                                                                                                                                                                                                                              1004
                                                                                                                                                                                                                                                          60..763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note=
                                                                                                                                     note=
                                                                                                                                                                                                                                                                                                                                                       note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-497073/54
N-PSDB; AAD13447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200159065-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
           Mod'ified-site
                                  Modified-site
                                                        Modified-site
                                                                             Modified-site
                                                                                                                        Modified-site
                                                                                                                                              Modified-site
                                                                                                                                                                    Modified-site
                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                     4odified-site
                                                                                                                                                                                                                                                             Aodified-site
                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bertin J;
                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                    Domain
                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
  700.00 "Protein Kinase c .... 700.00 "Casein Kinase II phosphorylation site" 700.00 "Casein Kinase II phosphorylation site" 700.00 "Casein Kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     770...472
/note= "Protein kinase C phosphorylation site"
501...504
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                               /note= "Protein Kindss - .
253..256
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                      fnote= "Casein Kinase ...,
297.300
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            307..310

Mote= "Casein kinase II phosphorylation site"
359..365

Mote= "Tyrosine kinase phosphorylation site"
366..368

Mote= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49..452
hote= "Casein kinase II phosphorylation site"
163..466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "Casein kinase II phosphorylation site" [63..465]
                                                                                                                                                                                                                                                                                                                                                                .262
e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                           .. 293
ce= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "Casein κιπανς -- .
184..386
'note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                    . 252
te= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                      .
e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      .309
e= "Protein kinase C phosphorylation site"
   60..62
/note= "Protein kinase C phosphorylation site"
/note= "Protein kinase C phosphorylation site"
                                                                                         .123
:e= "Protein kinase C phosphorylation site"
                                                                                                                                                          . 137
te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                     .
e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                 ...224
te- "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                               ..243
te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                           ...227
ce= "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185..406
note= "Leucine zipper pattern"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              587..592
/note= "N-myristoylation site"
589..592
                                                                 122
ce= "N-myristoylation site"
                                                                                                                                   ...135
ce= "N-myristoylation site"
                                                                                                                                                                              .166
.e= "N-myristoylation site"
                                                                                                                           'label - Coiled_Coil_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
.516
e= "N-myristoylation
                                                         "N-glycosylation
                                                                                                                                                                                                                                                                                   - k-Box_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDZ_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       label=
                                                                                                                                                                       /note=
161..16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note=
                                                                                                                                                'note=
                                                                                                                                                                                                                                          'note=
                                                                                                                                                                                                                                                                                                            'note=
                                                                                                                                                                                                                                                                                                                                                                                                    note-
                                                             'note=
                                                                                  'note=
                                                                                                                                                                                             'note=
                                                                                                                                                                                                                   'note=
                                                                                                                                                                                                                                                                                                                                                                               'note=
                                                                                                                                                                                                                                                                                     'label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Addified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Addified-site
    Modified-site
                         Modified-site
                                               Modified-site
                                                                    Modified-site
                                                                                           Modified-site
                                                                                                                                      Modified-site
                                                                                                                                                            Modified-site
                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                  Domain
                                                                                                                                                                                                                                                                           Domain
```

site"

site" site"

```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nuclear factor-kappa B; NF-kB; cell growth; cell death; cancer; therapy; autoimmune disorder; systemic lupus erythematosus; neurological disorder. Alzheimer's disease; Parthnson's disease; inflammatory disorder; anaemia; haematological disorder; myelodysplastic syndrome; myocardial infarction; stroke; immune disorder; crohn's disease; allergic rhinitis; infection;
                                                           The present sequence is human caspase recruitment domain-14 (CARD-14). The CARD-14 gene is located on chromosome 17. The CARD-14 is used for the detection of modulators that modulates the ability of CARD-14 to bind to Bcl-10 and stimulates phosphorylation of Bcl-10 or activation of nuclear factor-kappa B (NF-kB). The CARD-14 is useful for regulating growth and cell death and useful for the treatment of cancer. It is also useful for the treatment of cancer. It is also useful for the treatment of autoimmune disorders (e.g., systemic lupus erythematosus), neurological disorders e.g., Alzheimer's and Parkinson's disease, inflammatory disorders, haematological disorders (e.g., anomenia, myelodysplastic syndromes), myocardial infarctions, strokes, immune disorders (e.g., crohn's disease, allergic rhinitis), cell signalling disorders and certain viral and bacterial infections.
regulating growth and cell death and useful for the treatment of cancer
                                                                                                                                                                                                                                                                                                                                     AHFHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLOEELYLLKOELORANMVSSCELE 120
                                                                                                                                                                                                                                                                                                                                                                                                    245
                                                                                                                                                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                                                                                                                                       305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            365
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                      ECLAGAIGSLQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell signalling disorder; cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                          AHFHEVLRIKDEMISISIHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELE
                                                                                                                                                                                                                                                                                                                                                                                                                              LQEQSLRTASDQESGDEELNRLKEENEKLRSLTFSLAEKDILEQSLDEARGSRQELVERI
                                                                                                                                                                                                                                                                                                                                                                                                                                            HSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306 HSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                 Length 1004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        caspase recruitment domain-14; CARD-14; chromosome 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLRQLQAEPPGVLKQEART
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human predicted caspase recruitment domain-14 (CARD-14).
                                                                                                                                                                                                                                                                ; Score 1462; DB 22;
; Pred. No. 6.9e-107;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Encoded by TGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                     Claim 1; Fig 1A-1E; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE07165 standard; Protein; 1139
                                                                                                                                                                                                                                                                 100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                           Matches 295; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference 700
                                                                                                                                                                                                                                        1004 AA;
                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200159065-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-AUG-2001
                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE07165;
                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human;
                                                                                                                                                                                                                                                                                                                      ٦
                                                                                                                                                                                                                                                                                                                                               126
                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                  186
                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                       246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE07165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                       õ
```

```
systemic lupus erythematosus), neurological disorders e.g., Alzheimer's and Parkinson's disease, inflammatory disorders, haematological disorders (e.g., amemala, myelodysplastic syndromes), myocardial infarctions, strokes, immune disorders (e.g., Crohn's disease, allergic rhinitis), cell signalling disorders and certain viral and bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CARD-14). The CARD-14 gene is located on chromosome 17. The CARD-14 is used for the detection of modulators that modulates the ability of CARD-14 to bind to Bel-10 and stimulates phosphorylation of Bel-10 or activation of nuclear factor-kappa B (NP-KB). The CARD-14 is useful for regulating growth and cell death and useful for the treatment of cancer. It is also useful for the treatment of autoimmune disorders (e.g.,
                                                                                                                                                                                                                                                                            An isolated caspase recruitment domain polypeptide useful for regulating growth and cell death and useful for the treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      267
                                                                                                                                                                                                                                                                                                                                                                                                                             present sequence is predicted human caspase recruitment domain-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 AHFHEVLRIKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANNVSSCELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ECLAGAIGSLQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AHFHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQEQSLRTASDQESGDEELNRLKEENEKLRSLTFSLAEKDILEQSLDEARGSRQELVERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSLRERAVAAERORE-------OYWEEKEOTLLOFOKSKMACOLYREKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NALQAQVCELQKERDQAYSARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLRQLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; caspase recruitment domain; CARD-11; Bcl-10; NF-kappaB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human caspase recruitment domain, CARD-11 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1443; DB 22;
Pred. No. 2.6e-105;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 2A-2C; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU01207 standard; Protein; 1147 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.7%;
94.2%;
                                                                                                 (MILL-) MILLENNIUM PHARM INC
22-JAN-2001; 2001WO-US02087.
                                               09-FEB-2000; 2000US-0181159.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 94.2
Matches 295; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               460
                                                                                                                                                                                                WPI; 2001-497073/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1139 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEPPGVLKQEART
                                                                                                                                                                                                                          N-PSDB; AAD13448
                                                                                                                                                   Bertin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU01207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           388
                                                                                                                                                                                                                                                                                                                                                                                                                                   The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU01207
```

ä

```
WO200140468-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                              Modified-site
                                                                                                                                       Modified-site
                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
                        Domain
apoptosis; hyperproliferative disorder; autoimmune; neurological; inflammatory disorder; viral infection; stress-related response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "N-myristoylation site" 634..637 /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "cAMP- and cGMP-dependent protein kinase
phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  //note= "cAMP- and cGMP-dependent protein kinase
phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    //note= "Casein kinase II phosphorylation site"
108.510
//note= "Protein kinase C phosphorylation site"
110..513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290..292
Anote= "Protein Kinase C phosphorylation site"
78..381
129..432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         459..461
/note= "protein kinase C phosphorylation site"
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "protein kinase C phosphorylation site"
578..581
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "Amidation site"
86..289
note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "Coiled coil domain"
162..165
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168.171
//note- Casein kinase II phosphorylation site" //note- Casein kinase II phosphorylation site" //note- 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    443..245
/note= "Protein kinase C phosphorylation site"
282..285
                                                                                                                                                                                                                                                                                                                                                    .102
e= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                          . 103
te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                             'note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                      "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ...183
te- "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .. 195
te= "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "cAMP- and cGMP-dependent protein phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     //note= "Tyros....
241..24
/note= "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72..475
'note=_"N-glycosylation site"
                                                                                                                                                                                                      'note≕ "CARD domain"
                                                                                                                                             ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "C
584..587
/note= "N
587..592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130..431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                           'note=
                                                                                                                                                                                                                                                                                                                               note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fodified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Addified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                              Domain
```

```
710.715
710.715
70.00te= "N-myristoylation site"
725.728
725.728
725.728
725.728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "N-myristoylation site"
1088.1091
/note= "Casein kinase II phosphorylation site"
1120.1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    900
e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .929
:e= "Casein kinase II phosphorylation site"
                                                                                                                                              note="Casein kinase II phosphorylation site"
198..703
note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                 note= "N-glycosymuss...
79.782
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                          .789
:e= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "N-myristuy.cc...
147..850
/hote= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .57. 859
'note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           notes "Casein kinase II phosphorylation site"
182..1147
notes "Guanylate kinase (GUK) domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "Casein kinase II phosphorylation site"
                                                                                                    87..689
"note= "Protein kinase C phosphorylation site"
92..695
                                                                                                                                                                                                                                                             'note= "Tyrosine kinase phosphorylation site" (050..1055
                                              638.641
/note= "Glycosaminoglycan attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                        note= "Protein kinase C phosphorylation 003..1006
                                                                                                                                                                                                                                                                                  /note= "Ca>.
766..834
/note= "SH3 domain"
776..779
'--te= "N-glycosylation site"
                                                                                                                                                                                                                                 note= "Caselu ...
/61..766
/~rte= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Case... .._
853..858
/~^te= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .922
.e= "N-myristoylation site"
                                                                                         /note= "N-myristoylation site"
                                  /note= "MAGUK domain"
/note= "PDZ domain"
635..1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-DEC-1999; 99US-0168780.
18-FEB-2000; 2000US-0507533.
25-FEB-2000; 2000US-0513904.
10-OCT-2000; 2000US-0685791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2000; 2000WO-US32716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "C
935..937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               372..875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "note=
```

us-09-767-215-2\_copy\_126\_420.rag

```
apoptosis; hyperproliferative disorder; autoimmune; neurological; inflammatory disorder; viral infection; stress-related response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               570..573
/note= "Casein kinase II phosphorylation site"
595..598
                                                                                                                                                          "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .315
te= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..481
te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .513
ce= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                          note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Casein kinase II phosphorylation site"
 Human; caspase recruitment domain; CARD-10; Bcl-10; NF-kappaB;
                                                                                                                                                                                                                                                                                                                                                       "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                   .207
.e= "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .552
.e= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..560
te- "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ...415
te= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .514
.e= "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                      'note= "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Leucine zipper homology region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Leucine zipper homology region"
                                                                                                            15..20
/note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                      "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "N-glycosylation site"
                                                                                                                                                                                                                                                      'note= "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                      "Coiled coil domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Tropomyosin domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "N-myristoylation
                                                                                                                                                                                                                                                                                                                       'note= "Amidation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "MAGUK domain"
                                                                                                                                                                         23..123
/note= "CARD domain"
58..70
                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .1032
                                                                                                                                                                                                                                                                                                                                                                       .118
                                                                                                                                                                                                                                                                                                                                        .115
                                                                                                                                                                                                                                                                                                                                                                                                       .457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230..251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66..398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note=
                                                                                                                                                                                                                                                                                                                                                          'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note=
                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                          note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note=
                                                                                                                                                                                                                                                                                                                                                                                                                         'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note-
                                                                                              Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                           Modified-site
                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                Homo sapiens
                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
 The present sequence represents novel numan caspase recruitment domain, CARD-11. The polyvuclectide encoding this sequence was isolated from a human T-cell cDNA library, Also described are covel human sequences for CARD-9. CARD-10 (AAU01205). AAU01206)

covel human sequences for CARD-9. CARD-11 interact and appotosis: The sequences of the invention can be used for treating a disorder associated with abnormal levels of apoptosis by creating the expression or activity of CARD-9, CARD-10, or CARD-11.

CC frey can be used for the treatment of hyperproliferative disorders or an be used for the treatment of hyperproliferative disorders (e.g. cancer), autoimmune disorders (e.g. systemic lupus erythematosus), neurological disorders (e.g. Alzheimer's disease), inflammatory disorders (c.g. cancer), autoimmune and viral infection (e.g. HTV). The CARD polypeptide, polynucleotide and an antibody which selectively binds to cappy in screening and detection assays (e.g. chromosomal compaping, tissue typing), predictive medicine (prognostic assays, monitoring clinical trials, and therapy (treatment and prophylaxis). The CARD polypeptide may be used to screen for drugs that bind to and/or concer, modulate it. CARD sequences are potential targets for regulating contining a polynucleotide apoptosis in human disease. A host create transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
9
                                                                                                        Novel caspase recruitment domain (CARD) proteins, CARD-9, CARD-10, CARD-11, useful as targets for therapy, as immunogens, and in screening and detection assays -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HFHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELEL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAGAIGSLOEELNOEKGOKEVLLRRCOOLO-EHLGLAETRAEGLHOLEADHSRMKREVSA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LMNEVIKLOOOMKAKDLORCELLARLROLEDEKKOMTLTRVE-LLTFOERYYKMKEERDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YNDELVKVKDDNYNLAMRYAQLSEEKNMAVMRSRDLQLEIDQLKHRLNK--MEEECKLE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -AEKDILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164 QSLDEARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224 ALQAQVCELQKERDQAYSARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLRQLQA
                                                                                                                                                                                                         present sequence represents novel human caspase recruitment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human caspase recruitment domain, CARD-10 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.1%; Score 396.5; DB 22; 34.0%; Pred. No. 1.1e-22; ive 66; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QEQSLRTASDQES - - GDEELNRLKEENEKLRSLTFSL -
                                                                                                                                                                        Claim 9; Fig 14A-14C; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU01206 standard; Protein; 1032 AA.
(MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                             2001-367809/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 102; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1147 AA;
                                                                            N-PSDB; AAS05389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU01206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ٣
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU01206
```

Dp

ò g ò

ð

qq

g ò g

ò

XEXEX

site"

site

site

site"

N-PSDB; AAS05388

```
/30.1032
/note= "Guanylate kinase (GUK) domain"
830..832
/note= "Protein kinase C phosphorylation site"
                                                                                        .693
:e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                           site"
                                                                                                                                                                                                                                                                                                                                                      .872
.e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Protein kinase C phosphorylation site"
981..986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Protein kinase C phosphorylation site"
1028..1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1028..1031
/note= "Casein kinase II phosphorylation site"
                                                                       .684
.e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                  ..751
te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                      757
e= "Casein kinase II phosphorylation site"
603..605
/note= "Protein kinase C phosphorylation site"
                                    .644
.e= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                      "Protein kinase C phosphorylation site"
                                                                                                                                                          "Casein kinase II phosphorylation site"
                                                                                                                                                                          "Tyrosine kinase phosphorylation site"
       /note= "Protelu All.......638..641
/note= "Glycosaminoglycan attachment site"
                                                                                                                                                                                                                                                                                                                                                                      .885
.e= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                 868...870
/note- "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1021..1026
/note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                        "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note- "N-myristoylation site"
                                                                                                                                                                                                                                                   "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                    "N-myristoylation site"
                                                    ..661
re= "N-myristoylation site"
                                                                                                                            ..715
Le= "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                          ..918
te= "Amidation site"
                                                                                                            704..772
/note= "SH3 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-FEB-2000; 2000US-0507533.
25-FEB-2000; 2000US-0513904.
10-OCT-2000; 2000US-0685791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2000; 2000WO-US32716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0168780
                                                                                                                                                                                                                                                                                                                                                                                        3..898
                                                                                                                                         /note= "N
714..717
                                                                                                                                                                                                                                                     /note= "N
782..784
                                                                                                                                                                  ..739
                                                                                                                                                                                                                                                                               ..814
                                                                                                                                                                                                                                           992..
                                                                                                                                                                                                                                                                                                                                                         /note=
882
                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                            'note=
                                                                                                                                                                                                                                                                                                                                                                                   'note-
                                                                 'note=
                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                          'note=
                                                                                                                                                                                                                                                                                        /note-
                                                                                   "note=
                                                                                                     'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-367809/38
                                                                         681
                                                                                                                                                                                                                                            761
                                                                                                                                                                                                                                                                                 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200140468-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aodified-site
                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                         Modified-site
Modified-site
                                                                         Modified-site
                                                                                          Modified-site
                                                                                                                              Modified-site
                                                                                                                                                Modified-site
                                                                                                                                                                  Modified-site
                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                             Modified-site
                   Modified-site
                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bertin J;
```

```
The present sequence represents novel human caspase recruitment domain, CARD-10. The polynucleotide encoding this sequence was isolated domain, CARD-10. The polynucleotide encoding this sequence was isolated domain, CARD-10. The polynucleotide encoding this sequences of from a human skin CDAD-11 (AAU01205, AAU01207) and rat CARD-9 (AAU01204).

CARD-9, CARD-10 and CARD-11 interact with Bcl-10 which is thought to activate nuclear factor (NF)-kappaB and apoptosis. The sequences of the invention can be used for treating a disorder associated with abnormal levels of apoptosis by modulating the expression or activity of CARD-9, CARD-10, or CARD-11. They can be used for the treatment of hyperproliferative disorders (e.g. cancer), autoimmune disorders (e.g. Alzheimer's disease), inflammatory disorders (e.g. Crohn's disease), and an antibody which selectively binds to CARD can be used in screening and an antibody which selectively binds to CARD can be used in screening cand election assays (e.g. chromosomal mapping, tissue typing), predictive medicine (prognostic assays, monitoring clinical trials, and therapy (treatment and prophylaxis). The CARD polypeptide may be used to screen for drugs that bind to and/or modulate it. CARD sequences are potential targets for requisitantial inflammation, cancer. NF kappaB signalling, stress-related response and apoptosis in human disease. A host cell containing a polynucleotide encoding CARD can be used to create transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
9
                               Novel caspase recruitment domain (CARD) proteins, CARD-9, CARD-10, CARD-11, useful as targets for therapy, as immunogens, and in screening and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; plakoglobin; cytostatic; osteopathic; dermatological; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 LMTEVRRLREARKSQLQREQQLQARGRVLEEERAGLEQRLRDQQQAQERCQRLREDWEAG 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 FHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELELQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQSLRTASDQESGDEELNRLKEENE------KLRS----LTFSLAE----- 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---LRRARGPPPGAEEKEKEKEKEKEPDNVDLVSELRAENQQLTASLRELQEGLQQEASR 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSAQREISQSLVEKDSLRRQVFELT 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 LQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADH-----SRMKREVSAH 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----KDILEQSLDEARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 329.5; DB 22; Length 1032; Pred. No. 1.8e-17; ); Mismatches 115; Indels 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human plakoglobin interacting protein #3.
                                                                                                                        Claim 9; Fig 10A-10C; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU73247 standard; Protein; 1032 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.5%; Scc
31.8%; Pre
tive 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 31.83
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOVCELRTQLRQLQ 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                428 AERDELLTTLTSLE 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1032 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU73247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU73247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

RESULT

```
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated plakoglobin interacting polypeptide (I). (I) is useful as a medicament and in the manufacture of a medicament for treating plakoglobin related diseases, such as skin carcinoma or an acantholytic disease, and to screen compounds that interfere with the interaction of the polypeptide with plakoglobin related diseases, include basal cell carcinoma, squamous cell carcinoma, extramammary Paget's disease, Naxos disease, heart diseases, skin blistering and acantholytic diseases such as subcorneal acantholysis, Grover's disease, Hailey's disease or Darier's disease, and ectodermal dysplasia/skin fragility syndrome. AAU73245-AAU7324 represent novel human plakoglobin interacting protein amino acid sequences and related sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LMTEVRRLREARKSQLQREQQLQARGRVLEEERAGLEQRLRDQQQAQERCQRLREDWEAG 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELELQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        427
                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide, useful for treating skin carcinoma or acantholytic diseases such as Grover's and Darier's disease, comprises a protein interacting with human plakoglobin and involved in transduction of plakoglobin related signal to nucleus -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADH-----SRMKREVSAH 62
plakoglobin related disease; skin carcinoma; acantholytic disease; basal cell carcinoma; Basos disease; extramammany Paget's disease; heart disease; skin blistering; subcorneal acantholysis; Grover's disease; Hailey Hailey's disease; Darler's disease; skin fragility syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGAPGSERILLDILEHDWREAQDSRQELCQKLHAVQGELQWAEELRDQYLQEMEDLRLKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSAQREISQSLVEKDSLRRQVFELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---LRRARGPPPGAEEKEKEKEKEKEKEPDNVDLVSELRAENQRLTASLRELQEGLQQEASR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----KDILEQSLDEARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQSLRTASDQESGDEELNRLKEENE------KLRS----LTFSLAE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50; Mismatches 115;
                                                                                                                                                                                                                                                                               (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.5%; Score 329.5; DB 2
31.8%; Pred. No. 1.8e-17;
                                                                                                                                                                                                                                                                                                                 Vanlandschoot A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Figure 3; 98pp; English.
                                                                                                                                                                                                           02-MAY-2001; 2001WO-EP04872
                                                                                                                                                                                                                                             09-MAY-2000; 2000EP-0201668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : || | | |:
AERDELLTTLTSLE 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DQVCELRTQLRQLQ 282
                                                                                                                                                                                                                                                                                                                 Bonne S,
                                                                                                                                                                                                                                                                                                                                                WPI; 2002-062246/08.
N-PSDB; AAS98203.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1032 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                      WO200185933-A2
                                                                                                        Homo sapiens
                                                                                                                                                                         15-NOV-2001
                                                                                                                                                                                                                                                                                                                 Van Roy F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ω
   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ογ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          οy
```

```
Rat; caspase recruitment domain; CARD-9; Bcl-10; NF-kappaB; apoptosis; hyperproliferative disorder; autoimmune; neurological; inflammatory disorder; viral infection; stress-related response.
                                                                                                                                                                                                                                                                            "cAMP- and cGMP-dependent protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "cAMP- and cGMP-dependent protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .365
te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                               "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         483..486
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                       "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                         "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                               .174
te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Indole-3-glycerol phosphate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                364
ce= "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ...453
te= "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ...428
te= "Casein Kinase II phosphorylation
                                                                                                                                                                                                                                   "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                       "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                           "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                               "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                  "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                              "Tyrosine kinase phosphorylation
                                                                    Rat caspase recruitment domain, CARD-9 polypeptide.
                                                                                                                                                                                                                                                                                      phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                         140...416
/note= "Coiled coil domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Indoxe - -- , note= homology region"
                                                                                                                                                                                           "CARD domain"
                                                                                                                                                Location/Qualifiers
2..5
        AAU01204 standard; Protein; 536 AA.
                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .338
                                                                                                                                                                                                                                                                                                                                      .140
                                                                                                                                                                                                                                                                                                                                                         .141
                                                                                                                                                                                                                                                                                                                                                                                                                   176..183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..231
                                                                                                                                                                                                                                                                                                                                                                                                                                       213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231..233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note=
                                                                                                                                                                                                      12..15
/note=
                                                                                                                                                                                                                         16..18
/note=
                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                            /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note=
                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                'note=
                                                                                                                                                                                                                                                                                                                                                                                                           'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note=
                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                        'note=
                                                                                                                                                                                                                                                                                                                                                                     'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                            Modified-site
                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                             Modified-site
                                                12-SEP-2001
                                                                                                                                Rattus sp.
                             AAU01204;
                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
AAU01204
```

```
/note= "Pr
233.336
                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "T
197..213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "P
267..270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138..140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            363..366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228..231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92..95
/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95..97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95..98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231.
                                                                                                                                                   | | | | | | | E--GRLKQQ 416
                                                                                                                                    284 EPPGVLKQE 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                   Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                         12-SEP-2001
                                                                                                                                                                                                                                                AAU01205;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                           410
                                                                                                                                                                                                            AAU01205
                                                                                                                                                                                                                                                  qq
                                                                                                                                    ōλ
                                                                                                                                                           Op
                                                         a
                                                                                  δ
                                Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents novel rat caspase recruitment domain, CARD-9. The polynucleotide encoding this sequence was domain, CARD-9. The polynucleotide encoding this sequence was consolated from a rat neuronal CDNA library. Also described are novel human sequences for CARD-9, CARD-10 and CARD-11 (AAU01207-).

CARD-9, CARD-10 and CARD-11 interact with Bcl-10 which is thought card rector (WT)-kappaB and apoptosis. The sequences of the invention can be used for treating a disorder associated with abnormal levels of apoptosis by modulating the expression or activity of CARD-9, CARD-11. They can be used for the treatment of hyperproliferative disorders (e.g. cancer), neurological autoimmune disorders (e.g. systemic lupus erythematosus), neurological disorders (e.g. Alzheimer's disease), inflammatory disorders (e.g. Alzheimer's disease), inflammatory disorders (e.g. cancer), neurological disorders disease), and viral infection (e.g. HIV). The CARD polypeptide, crohic and an antibody which selectively binds to CARD can be used in screening and detection assays (e.g. chromosomal mapping, tissue criping), predictive medicine (prognostic assays, monitoring clinical cripins, and therapy (treatment and prophylaxis). The CARD polypeptide may be used to screen for drugs that bind to and/or modulate it. CARD sequences are potential targets for regulating inflammation, cancer, concerved the containing a polynucleotide encoding CARD can be disease. A host cell containing a polynucleotide encoding CARD can be used to create transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                Novel caspase recruitment domain (CARD) proteins, CARD-9, CARD-10, CARD-11, useful as targets for therapy, as immunogens, and in screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAELKRCKDENYDLAMRLAHLSEEKGAALMRNRDLQLEVDQLRHSLMKAE--DDCKVERK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQ-SLRTASDQESGDEELNRLKEENE----KLRSLTFSLAEK------DILEQSLDE 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELELQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --RMKREVSAH 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37;
                                                                      526..529
/note= "Casein kinase II phosphorylation site"
531..534
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 536;
           "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.4%; Score 283.5; DB 22; 29.4%; Pred. No. 3.5e-14; Live 58; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKGQKEVLLRRCQQLQEHL - - - GLAETRAEGLHQLEADHS - -
                                    "N-myristoylation site"
                                                            "N-glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Fig 1A-1B; 145pp; English.
                                                                                                                                                                                                              99US-0168780.
2000US-0507533.
2000US-0513904.
2000US-0685791.
                                                                                                                                                                                                                                                                             (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                       01-DEC-2000; 2000WO-US32716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
           /note= "P:
523..528
                                               .527
                                                             /note=
526..52
                                     'note=
                                                                                                                                                                                                                                                                                                                                                                                          and detection assays
                                                                                                                                                                                                                                                                                                                           WPI; 2001-367809/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 91; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 536 AA;
                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAS05386
                                                                                                                                     WO200140468-A2.
                                                                                                                                                                                                              03-DEC-1999;
18-FEB-2000;
25-FEB-2000;
10-OCT-2000;
Modified-site
                                                                                                  Modified-site
                       Modified-site
                                                                          Modified-site
                                                                                                                                                               07-JUN-2001
                                                                                                                                                                                                                                                                                                      Bertin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
  ò
```

```
230 HTLKLRHAMEQRPSQELLWDLQQERDLLQARVQELEVSVQEGKLHRNSPYIQVLEEDWRQ 289
                                                                                                                                          ALQEHQEQASTIFSLRKDLRQAEALRTRCMEEKEMFELQCLALRKDAKMYKDRIEAILQO 349
                                                                                                                                                                                                                      229 VCELQKERDQAYSARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQL-----RQLQA 283
                                                                                                                                                                                                                                                       350 MEEVSIERDQAMISREELHAQCAQSFQDKDKLRKQVRELDEKADELQLQLFQTESRLLAA 409
                                                                                         169 ARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQ 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; caspase recruitment domain; CARD-9; Bcl-10; NF-kappaB; apoptosis; hyperproliferative disorder; autoimmune; neurological; inflammatory disorder; viral infection; stress-related response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "cAMP- and cGMP-dependent protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "cAMP- and cGMP-dependent protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .305
e= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Casein Kinase II phosphorylation site"
7..98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cysteine rich repeat homology region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Indole-3-glycerol phosphate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human caspase recruitment domain, CARD-9 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphorylation site". 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Coiled coil domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homology region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "CARD domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU01205 standard; Protein; 536
```

Pred. No.

28.48;

Similarity

σ

```
The present sequence represents novel human caspase recruitment
domain, CARD-9. The polynucleotide encoding this sequence was isolated
from a human magakaryocyte cDNA library. Also described are novel human
sequences for CARD-10 and CARD-11 interact with Bcl-10 which is
cancer and the invention can be used for treating a disorder
cassociated with abnormal levels of apoptosis by modulating the
sequences of the invention can be used for treating a disorder
cassociated with abnormal levels of apoptosis by modulating the
expression or activity of CARD-9, CARD-10, or CARD-11. They can
be used for the treatment of hyperproliferative disorders (e.g.
cancer), autoimmune disorders (e.g. systemic lupus erythematosus),
neurological disorders (e.g. Alzheimer's disease), inflammatory disorders
(e.g. Cronn's disease), and viral infection (e.g. CARD
coplypeptide, polynucleotide and an antibody which selectively binds to
CARD can be used in screening and detection assays (e.g. chromosomal
capping, tissue typing), predictive medicine (prognostic assays).
CARD polypeptide may be used to screen for drugs that bind to and/or
computation; clinical trials, and therapy (treatment and prophylaxis). The
condition cancer, NF kappab signalling, stress related response and
apoptosis in human disease. A host cell containing a polynucleotide
encoding CARD can be used to create transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   caspase recruitment domain (CARD) proteins, CARD-9, CARD-10, 11, useful as targets for therapy, as immunogens, and in screening
 .428
e= "Casein kinase II phosphorylation site"
                           ..433
Le- "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                 .529
.e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                 /note= "Casein kinase II phosphorylation site"
                                                                           "Protein kinase C phosphorylation site"
                                                                                                                       .462
.e= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                     "Casein kinase II phosphorylation site"
                                                                                                           "N-myristoylation site"
                                                                                                                                                    .486
e= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                 "N-myristoylation site"
                                                                                                                                                                                                                                    "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Fig 5A-5B; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-FEB-2000; 2000US-0507533.
25-FEB-2000; 2000US-0513904.
10-OCT-2000; 2000US-0685791.
                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2000; 2000WO-US32716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0168780
                                                                                                                                                                        /note= "N
483..486
                                                                                           .458
                                                                                                                                                                                                                    .527
                                                                                                                                                                                                                                                                                                                 ..534
                                                 /note=
                 'note=
                                                                              'note∍
                                                                                                             /note=
                                                                                                                                            /note-
                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                  'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-367809/38.
N-PSDB; AAS05387.
                                                                                                                                                         481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             536 AA;
                                                                                                                                                                                                                                                                                                                                                                WO200140468-A2
Modified-site
                               Modified-site
                                                            Modified-site
                                                                                         Modified-site
                                                                                                                        Modified-site
                                                                                                                                                      Modified-site
                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bertin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel
```

Length 536;

DB 22;

18.8%; Score 274.5;

Query Match

```
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily
                                                                                                                                                                                                                                      ALRDHQEQANTIFSLRKDLRQGEARRLRCMEEKEMFELQCLALRKDSKMYKDRIEAILLQ 349
                                                                                                  FHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELELQ 122
                                                                                                                             172 SRELKRCKEENYDLAMRLAHQSEEKGAALMRNRDLQLEIDQLKHSLMKAE--DDCKVERK 229
                                                                                                                                                         EQ-SLRTASDQESGDEELNRLKEE----NEKLRSLTFSLAEK------DILEQSLDE 168
                                                                                                                                                                                   230 HTLKLRHAMEQRPSQELLWELQQEKALLQARVQELEASVQEGKLDRSSPYIQVLEEDWRQ 289
                                                                                                                                                                                                                                                                          VCELOKERDOAYSARDSAOREISOSLVEKDSLRROVFELTDOVCELRTOLROLOAEPPGV 288
                                                                                                                                                                                                                                                                                           830 Primers useful for synthesizing full length cDNA clones and their
                                                                     ESGLTQLLMTEVMKLQKKVQDLTALLSSKDDFIKELRVKDSLLRKHQERVQRLKEECEAG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ή;
                                                                                                                                                                                                                 ARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kawai Y;
T, Koga
               33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; SEQ ID NO 3879; 1380pp + sequence listing; English.
               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ishii S,
S, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; full length cDNA; cDNA synthesis; oligo-capping.
1.8e-13;
ches 125;
                                          EKGQKEVLLRRCQQLQEHL----GLAETRAEGLHQLEADHS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashi K,
K, Kojima S
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM93822 standard; Protein; 746 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO: 3879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isogai T,
a T, Nagai
            61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in genetic manipulation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JUL-1999; 99JP-0194486.
11-JAN-2000; 2000JP-0118774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUL-2000; 2000EP-0114089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000JP-0183765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sugiyama T,
               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-524255/58.
N-PSDB; AAK94778.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human polypeptide,
                                                                                                                                                                                                                                                                                                                                    LKQEAR 294
                                                                                                                                                                                                                                                                                                                                                               LAVEGR 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP1130094-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-NOV-2001
             87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM93822;
Best Local
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ė
                                                                                                                                                                                                                                                                                                                                                               407
                                          17
                                                                     112
                                                                                                  63
                                                                                                                                                                                                                 169
                                                                                                                                                                                                                                              290
                                                                                                                                                                                                                                                                          229
                                                                                                                                                                                                                                                                                                       350
                                                                                                                                                                                                                                                                                                                                    289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ota
                                                                                                                                                                                                                                                                                                                                                                                                                        AAM93822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                 Op
                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                         δŏ
                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                               q
                                                               q
                                                                                                δ
                                                                                                                                                        ŏ
```

```
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-OCT-2001
                                                                                                                                                                                                                                                                                                              Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG05850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG05850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δy
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an Oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a
without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                                                                                                                                                                                                            :: : ||: |::|||||| :|| | : ||||| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|
                                                                                                                                                                                                                                             160 DILEQSLDEARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYR 219
                                                                                                                                                                                                                                                                                                                                   220 EKVNALQAQVCELQKERDQAYSARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLR 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; primer; detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                  DILEHDWREAQDSRQELCOKLHAVQGELQWAEELRDQYLQEMEDLRLKHRTLQKDCDLYK 92
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamamoto
                                                                                                                                                                                                      ö
                                                                                                                                                      Length 746;
                                                                                                                                                                                                      47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saito K,
, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; SEQ ID 18328; 2537pp + CD ROM; English.
                                                                                                                                                          15.7%; Score 230; DB 22;
41.5%; Pred. No. 8.8e-10;
iive 25; Mismatches 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human protein sequence SEQ ID NO:18328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nishikawa T, Haya
T, Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB95617 standard; Protein; 366 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99JP-0248036.
99JP-0300253.
2000JP-0118776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000JP-0183767
2000JP-0241899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                               1 Similarity 41.5 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-318749/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isogai T,
                                                                                                                   746 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                           280 QLQ 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 SLE 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ś
                                                                                                                     Sequence
                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB95617
                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ishii
                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                            33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
AAB95617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8×3000×8
                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
9
polynucleotide which comprises a 3'-end sequence, where the coligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs are the full-length and AAH13628 and AAH13638 to AAH13628 to AAH13628 consequences; AAB95486 to AAH13632 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 EQ-SLRTASDQESGDEELNRLKEE----NEKLRSLTFSLAEK------DILEQSLDE 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 ARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQ 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 FHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELELQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 EKGQKEVLLRRCQQLQEHL----GLAETRAEGLHQLEADHS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.5%; Score 198; DB 22 26.7%; Pred. No. 1.2e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human diagnostic protein #5841.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG05850 standard; Protein; 2246 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                       of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 VCELQKERDQA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        350 MEEVAIERDOS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                               366 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAS70037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200175067-A2.
```

```
polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerase chain reaction (PCR) primers, oligomers, and for chromosome production of (II). The polymerased genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010 ABG30377 represent novel human amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:||:|| ||:|
954 DLQSSISNLSQAKEELEQASQAHGARLTAQVASLTSELTTLNATIQQQ-DQELAGLKQQA 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----NEKLRSLTFSLAEKDILEQSLDEARGSRQELVERIHSLR 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AHFHEVLRLKDEMLSLS------103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          851 EGLCGNLKCLEE-----KNEILQGKLSQLEEHLS-----QLQDNPPQEKGEVL 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ECLAGAIGSLQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :: || | :|: |
894 GDVLQLETLKQEAATLAANNTQLQARVEMLETERGQQEAKLLAERGHFEEEKQQLSSLIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARD
diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47; Mismatches 108; Indels 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAQREISQSLVEKDSLRRQVFEL------TDQVCELRTQLRQLQ 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2246;
                                                                                                                                    The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.5%; Score 197; DB 22; 26.4%; Pred. No. 1.4e-06;
                                                                                   Claim 20; SEQ ID No 36209; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human protein sequence SEQ ID NO:18167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB95546 standard; Protein; 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2246 AA;
                                            biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB95546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

```
The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a 3'-end sequence. Or complementary to the complementary strand of a polynucleotide which comprises a 1'-end sequence. The primer sets can be used in antisense therapy and the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the cetection and/or diagnosis of the abnormality of the full-length cDNAs. The primers are also useful for the cetection and/or diagnosis of the abnormality of the full-length cDNAs. The primers are also useful for AMH13628 and AMH136131 to AAHH3612 represent human amino acid sequences; and AMH13629 to AAHH3632 represent human amino acid sequences; and AMH13632 to AAHH3632 represent human amino acid sequences; and AMH13632 to AAHH3632 represent human amino acid sequences; and the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LQEENEKLQGRSEELERRVAQLQRQ------IEDLKGDEAKAKETLKKYEGEIRQL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 KDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELELQ-EQSLRT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :: :: : : : : | | : | | : | | : | | : | : | : | : | : | EBALVHV -----RKEEKAVSAR-RALENEL-----EAAQGNLSQTTQEQKQLSEKLKE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 ASDQESGDEELNRLKEENEKLRSLTFSLAEK-----DILEQSLDEARGSRQELVERIHS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESEOK---EQLRRLKNEMENERWHLGKTIEKLQKEMADIVEAS----RTSTLELQNQLDE 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 LRE--RAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 LQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAHFHEVLRL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saito K, Ya
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SARDSAQREISQSLVE-----KDSLRRQVFELTDQVCELRTQLRQ 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.4%; Score 196; DB 22; 25.8%; Pred. No. 3.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; SEQ ID 18167; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sugiyama T, Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62;
                                                                                                                                                                                                                                                             99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                          99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   612 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                              09-JUN-2000;
                                                                                                                                                                                                                                                                                                11-JAN-2000;
02-MAY-2000;
   EP1074617-A2
                                                                                                                                                                                                                          29-JUL-1999;
                                                                                                                                                                                                                                                                27-AUG-1999;
                                                                         07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187
NAMES OF COLOR COL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

g

```
531 KQAQLAQTLQQQEQASQGLRHQVEQLSSSLKQK---EQQLKEV-AEKQEATRQDHA-QQL 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-610603/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2101 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Number Z11584).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    US6287790-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-NOV-1998;
                                                                                                                                                                                                                                                                                              30-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lelievre S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                             AAG65799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                       247
                                                                                                                                                                                           RESULT 13
                                                                                                                                                                                                            AAG65799
                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                   οy
                                                                     g
                                                                                                         δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIT and MT2 proteins were islated from malignant cells essentially following the method of Penman and Fey, described in US Pat. Nos. 4, g812,286 and 4,885,236. DNA sequences encoding these proteins were cloned by probing expression libraries using monoclonal antibodies raised against the isolated INM proteins. The genetic sequence encoding MT2 has been disclosed by Yang et al. 1992, J. Cell Biol. 16:1395-1408, and is referred to by them as 'NuMA'. The nucleotide sequence encoding MT1 has not beed described previously. Both the MT1 and MT2 proteins are distributed throughout the nucleus (with the exception of the nucleolus) in non-mitotic cells, and localise to the spindle during mitosis. A binding protein having a binding affinity of greater than about 10(9) M(-1) for AAR47173 is claimed for use in the manufacture of a medicament.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -NEKLRSLIFSLAEKDILEQSLDEARGSRQELVERIHSLRER 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 LQEELN---QEK----GQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAH 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    412 VLOLETLKQEAATLAANNTQLQARVEMLETERGQQEAKLLAERGHFEEEKQQLSSLITDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        472 QSSISNLSQAKEELEQASQAHGARLTAQVASLTSELTTLNATIQQQ-DQELAGLKQQAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 -----AKQELQRANMVSSCELELQEQSLRT-----ASDQESGDEELNRLKEE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel malignant cell type markers of the interior nuclear matrix - used for detecting abnormal cell types e.g. malignant breast, prostate, lung, etc., for determining deg. of cell death in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 FHEVLRLKDEMLSLS------LHYSNALQEKELAASRCRSLQEELYL----
                                                                                                                                                                                                                              Malignant cell type marker; interior nuclear matrix; MT2; NuMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
       343 TKRQLLEQTLKDLEYELEAKSHLKDDRSRLVKQMEDKVSQLEMELEE 389
                                                                                                                                                                                              the inner nuclear matrix (INM) protein MT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.3%; Score 194; DB 15; 26.6%; Pred, No. 2.2e-06; ive 49; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 39; Page 56-66; 93pp; English.
                                                                                          AAR47173 standard; Protein; 2101
                                                                                                                                                                                                                                                                                                                                                                    93WO-US06160.
                                                                                                                                                                                                                                                                                                                                                                                                      92US-0901701
                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 13.3'
Best Local Similarity 26.6'
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Toukatly G;
                                                                                                                                                                                                                                                                                                                                                                                                                                        (MATR-) MATRITECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1994-026210/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2101 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAQ54841
                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                    21-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                    22-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lidgard GP,
                                                                                                                                                              15-JUL-1994
                                                                                                                                                                                                Sequence of
                                                                                                                                                                                                                                                                                                  WO9400573-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue, etc.
                                                                                                                                                                                                                                                                                                                                    06-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence
                                                                                                                          AAR47173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146
                                                              RESULT 12
```

g ò g õ

ò

```
15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to methods of distinguishing malignant or growth arrested malignant cells from proliferating non-malignant cells by staining specifically Nuclear Mitotic Apparatus (NUMA) protein in a sample of intact mammalian cells and imaging the cells to determine the three-dimensional pattern of labeled NUMA protein within nucleic of the cells. The method is useful for distinguishing malignant or growth arrested malignant cells from proliferating non-malignant cells. Lumors cells and different stages in the tumor progression and different stages in the tumor progression and differentiation processes. NUMA proteins may be used to identify functional proteins or drugs to specific locations inside the cells. The present sequence represents the human NUMA protein (GenBank Accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NuMA; Nuclear Mitotic Apparatus protein; malignant; cell growth; human; tumor progression; structural protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Distinguishing growth arrested malignant cells from proliferating non-malignant cells, comprises staining the nuclear mitotic apparatus protein in intact mammalian cells and determining the 3-dimensional pattern of the labeled protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --LHYSNALQEKELAASRCRSLQEELYL----- 103
                                            10 LQEELN----QEK-----GQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAH 62
187 AVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2101;
                                                                                                                              ----TDQVCELRTQLRQLQ 282
                                                                                                                                                                   Score 194; DB 22;
Pred. No. 2.2e-06;
9; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nuclear mitotic apparatus protein (NuMA) sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _
_
_
_
                                                                                                                                                                                                                                                                                                                                                                  Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 15; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                              AAG65799 standard; protein; 2101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.3%;
26.6%;
                                                                                                                              QREISQSLVEKDSLRRQVFEL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0452294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-110420P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 FHEVLRLKDEMLSLS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bissell M;
```

2117 AA;

```
AAW21732;
  Sequence
                           Query Match
                                      Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                 Matches
                                                                                                                                                                           104
                                                                                                                                                                                                                             146
                                                                                                                                                                                                                                                                              187
                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                           AAW21732
 S
                                                                          δλ
                                                                                                 Dp
                                                                                                                          δλ
                                                                                                                                                 QQ
                                                                                                                                                                          ò
                                                                                                                                                                                                  QQ
                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                    Op
                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                Οy
                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically chip proteins are useful in genetic vaccination, testing and the proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bond, cartillage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
                                                                                       -----LKQELQRANMVSSCELELQEQSLRT-----ASDOESGDEELNRLKEE--- 145
                                         AVAAERQREQYWEEKEGTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSA 246
412 VLQLETLKQEAATLAANNTQLQARVEMLETERGQQEAKLLAERGHFEEEKQQLSSLITDL 471
                                                                         --NEKLRSLTFSLAEKDILEQSLDEARGSRQELVERIHSLRER 186
                                                                                                                                                586 ATAAE-EREASLRERDAALKOLE-----ALEKEKAAKLEI----LOOOLOVANEARDSA 634
                                                                                                                                                                                                                                                                                                                                                                 Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                          ------ 282
                                                                                                                                                                                      AAU32040 standard; Protein; 2117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; Page 547; 765pp; English.
                                                                                                                                                                                                                                                                                                                                          Novel human secreted protein #2531.
                                                                                                                                                                          OREISQSLVEKDSLRRQVFEL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-APR-2001; 2001WO-US08656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-APR-2000; 2000US-0552929
26-JAN-2001; 2001US-0770160
                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drmanac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-611725/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200179449-A2
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                 18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rang YT,
                                                                                                                                                                                                                                                                                        AAU32040;
                                                                        146
                        104
                                                                                                                        187
                                                                                                                                                                         247
                                                                                                                                                                                                                                      RESULT 14
                                                                                                                                                                                                                                                     AAU32040
                        ò
                                               g
                                                                     οy
                                                                                              qq
                                                                                                                        οχ
                                                                                                                                             g
                                                                                                                                                                         ò
                                                                                                                                                                                               g
```

```
15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIP-1; NIP-2; NUMA; nuclear mitotic apparatus; NuMA interacting protein; cell division; proliferation; antibody; Ab; detection; malignant cell growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   246
                                                                                                                                                                                                                                                                    -----LKQELQRANMVSSCELELQEQSLRT-----ASDQESGDEELNRLKEE--- 145
                                                                                                                                                                                                                                                                                             586 ATAAE-EREASLRERDAALKQLE-----ALEKEKAAKLEI----LOOOLOVANEARDSA 634
                                                                                                                                 362 LEKELSAALQDKKCLEEKNEILQGKLSQLEEHLS------QLQDNPPQEKGEVLGD 411
                                                                                                                                                                            63 FHEVLRLKDEMLSLS------ LHYSNALQEKELAASRCRSLQEELYL----- 103
                                                                                                                                                                                                          Gaps
                                                                                         10 LQEELN----QEK-----GQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAH 62
                                                                                                                                                                                                                                                                                                                                                                                                     531 KOAQLAOTLOQQEQASQGLRHQVEQLSSSLKQK---EQQLKEV-AEKQEATRQDHA-QQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSA
                                              Indels 104;
  Length 2117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding nuclear mitotic appts. interacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ::|: || || || || || 635 QTSVTQAQRELELQLRSEQ 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QREISQSLVEKDSLRRQVFEL------TDQVCELRTQLRQLQ
Score 194; DB 22;
Pred. No. 2.2e-06;
); Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Residues_18-2116_of_NuMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           label = LexA_DNA_binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285..1784
/label= Coiled_coil_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW21732 standard; Protein; 2192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Polylinker
                                         49;
  13.3%;
26.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96WO-US09504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95US-0478408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McPherson SMG, Snyder MP;
                       Similarity 26.6
93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LexA/NuMA fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .2192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-077270/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYYA ) UNIV YALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAT77783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9640917-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-DEC-1996
                                           93;
```

```
The sequences given in AAW21731-32 represent fusion proteins which contain NuMA (nuclear mitotic apparatus). The fusion proteins were used in the identification of NuMA interacting proteins (NIP's) (see also AAW21729-30). Compounds which interfere with the interaction of NuMA proliferation. Ab. raised conventionally using NIP-1 or -2 as immunogen, are used to detect NIP (or their complexes) and to block their activity for diagnostic or therapeutic use, e.g. to detect defective NuMA or NIP (which may be markers for aberrant (including malignant) cell growth (which can also be detected by nucleic acid sequencing). Also where malignancy is related to defects in NUMA or NIP, it can be treated by andistration of the appropriate functional protein.
proteins - useful for modulating cell division and proliferation and
                                                                          Claim 15; Page 42-50; 78pp; English.
                             in diagnosis
```

2192 AA; Sequence

15; 489 VLOLETLKOEAATLAANNTOLQARVEMLETERGOOEAKLLAERGHFEEEKOOLSSLITDL 548 608 KQAQLAQTLQQQEQASQGLRHQVEQLSSSLKQK---EQQLKEV-AEKQEATRQDHA-QQL 662 AVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSA 246 63 FHEVLRLKDEMLSLS------ 103 -----LKQELQRANMVSSCELELQEQSLRT-----ASDQESGDEELNRLKEE--- 145 ------NEKLRSLTFSLAEKDILEQSLDEARGSRQELVERIHSLRER 186 439 LEKELSAALQDKKCLEEKNEILQGKLSQLEEHLS------QLQDNPPQEKGEVLGD 488 Gaps 10 LQEELN---QEK----GQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAH 62 Query Match 13.3%; Score 194; DB 18; Length 2192; Best Local Similarity 26.6%; Pred. No. 2.3e-06; Matches 93; Conservative 49; Mismatches 104; Indels 104; 247 QREISQSLVEKDSLRRQVFEL------TDQVCELRTQLRQLQ 282 146 187 104 qq QQ q g δ ò qq δ ò δ ò

QTSVTQAQREKAELSRKVEELQACVETARQEQHEAQAQVAELELQLRSEQ 761 712

Search completed: January 22, 2003, 08:52:16 Job time : 63.4933 secs

```
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Appli
                                                                       (without alignments)
429.229 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                            January 22, 2003, 08:52:30 ; Search time 20.2218 Seconds
                                                                                                            1462
1 ECLAGAIGSLQEELNQEKGG......TQLRQLQAEPPGVLKQEART 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence Sequence Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                 /ogn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                            Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S-08-533-306A-6
S-08-742-923A-6
S-08-533-306A-4
S-08-742-923A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -08-477-831C-11
-08-468-576B-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·08-468-577B-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -08-468-579B-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US95-16216-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -08-533-306A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS-08-477-831C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -08-056-200-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-800-644-94
US-09-572-191-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US93-06160-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -09-104-324B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-328-254-6
US-08-353-700-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-452-294-1
                                                                                                                                                                         262574 segs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                    US-09-767-215-2_COPY_126_420
                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                        OM protein - protein search, using sw model
                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                           Issued_Patents_AA:*
                                                                                                                                                                                                                  length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21001
221001
221001
221001
221001
33248
33248
33248
13848
13888
576
8116
8116
8816
606
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                   Title:
Perfect score:
                                                                                                                                            Scoring table:
                                                                                                                                                                          Searched:
                                                                                                                        Seguence
                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ģ
```

```
Sequence 2, Appragate 10 Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                     Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 FHEVLRLKDEMLSLS------ 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 LQEELN---QEK----GQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAH 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1, A
85,
                                                                                                                                                                                                                                                                                                                Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: TOUKATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.3%; Score 194; DB 1; Length 2101; 26.6%; Pred. No. 9.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,390
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY APPLICATION: 435
US-09-723-262-2
US-09-723-219-2
S210183-3
US-08-402-217A-3
US-08-95-654-3
US-08-95-654-3
US-08-282-845-2
US-09-310-187A-1
US-09-154-750A-85
US-09-085-199B-11
US-09-085-199B-11
US-09-085-199B-11
US-09-085-199B-11
US-09-08-199B-11
US-09-08-199B-11
US-09-08-199B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 125 HIGH STREET
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: PITCHER ESO, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08466390 Patent No. 5686562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2101 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93; Conservative
             1388
1388
6833
4777
4777
1939
9555
11068
11068
11034
11034
11034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1
US-08-466-390-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-466-390-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
             162
162
160
160
160
150
159
159
159
159
154
156.5
1154.5
1154.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
             2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
```

 $\alpha$ 

```
-----LKQELQRANMVSSCELELQEQSLRT-----ASDQESGDEELNRLKEE--- 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MIP-013
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08467781
Patent No. 5780596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAILED
                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: TOUKATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (617) 248-7000
(617) 248-7100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2101 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 FHEVLRLKDEMLSLS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 93; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                         RESULT 3
US-08-467-781-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-467-781-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
                                                                      146
                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                               qq
                                                                    δλ
                                                                                                        g
                                                                                                                                           δy
                                                                                                                                                                                                                  δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
                                                                          531 KQAQLAQTLQQQEQASQGLRHQVEQLSSSLKQK---EQQLKEV-AEKQEATRQDHA-QQL 585
                                                                                                                                                                                                 AVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 FHEVLRLKDEMLSLS------1HYSNALQEKELAASRCRSLQEELYL----- 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              412 VLQLETLKQEAATLAANNTQLQARVEMLETERGQQEAKLLAERGHFEEEKQQLSSLITDL 471
------NEKLRSLTFSLAEKDILEQSLDEARGSRQELVERIHSLRER 186
                                                                                                                                                                                                                      ------LKQELQRANMVSSCELELQEQSLRT-----ASDQESGDEELNRLKEE--- 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 LQEELN---QEK----GQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAH 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 104;
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: TOURATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: TESTA, HURWITZ & THIBEAULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2101;
                                                                                                                                                                                                                                                                      -----TDQVCELRTQLRQLQ 282
                                                                                                                                                                                                                                                                                                  OTSVIQAQREKAELSRKVEELQACVETARQEQHEAQAQVAELELQLRSEQ 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 13.3%; Score 194; DB 1; Best Local Similarity 26.6%; Pred. No. 9.6e-08; Matches 93; Conservative 49; Mismatches 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/470,950
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION UNMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08470950 Patent No. 5698439
                                                                                                                                                                                                                                                                      OREISQSLVEKDSLRRQVFEL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2101 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 HIGH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-470-950-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: BOSTON
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02110
                                                                                                                                                                                                                                                                                                                                                                                US-08-470-950-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                       472
                                                                                                                                                                                               187
                                                                                                                                                                                                                                   286
                                                                                                                                                                                                                                                                      247
                                                                                                                                                                                                                                                                                                         635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                      qq
                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                      qq
                                                     ò
                                                                                     g
                                                                                                                          ò
                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                      ò
```

```
15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 -----LKQELQRANMVSSCELELQEQSLRT-----ASDQESGDEELNRLKEE--- 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           472 QSSISNLSQAKEELEQASQAHGARLTAQVASLTSELTTLNATIQQO-DQELAGLKQQAKE 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            472 QSSISNLSQAKEELEQASQAHGARLTAQVASLTSELTTLNATIQQQ-DQELAGLKQQAKE 530
                                                                            ---NEKLRSLTFSLAEKDILEQSLDEARGSRQELVERIHSLRER 186
                                                                                                                     531 KQAQLAQTLQQQEQASQCLRHQVEQLSSSLKQK---EQQLKEV-AEKQEATRQDHA-QQL 585
                                                                                                                                                                                                     187 AVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSA 246
                                                                                                                                                                                                                                           412 VLOLETLKOEAATLAANNTOLOARVEMLETERGOGEAKLLAERGHFEEEKOOLSSLITDL 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 LQEELN---QEK----GQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAH 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --LHYSNALQEKELAASRCRSLQEELYL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2101;
                                                                                                                                                                                                                                                                                                                           247 QREISQSLVEKDSLRRQVFEL------TDQVCELRTQLRQLQ 282
                                                                                                                                                                                                                                                                                                                                                                       635 QTSVTQAQREKAELSRKVEELQACVETARQEQHEAQAQVAELELQLRSEQ 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCHWARE: Patentin Release #1.0, Version #1.25
SCHWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,781
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
9.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.3%; Score 194; DB 26.6%; Pred. No. 9.6e tive 49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURMITZ & THIBEAULT
STREET: 125 HIGH STREET
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

a

qq

ò

q

õ

```
-NEKLRSLTFSLAEKDILEQSLDEARGSRQELVERIHSLRER 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 FHEVLRLKDEMLSLS------ 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      412 VLOLETLKOEAATLAANNTOLOARVEMLETERGOOEAKLLAERGHFEEEKOOLSSLITDL 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 ------LKQELQRANMVSSCELELQEQSLRT-----ASDQESGDEELNRLKEE--- 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------NEKLRSLTFSLAEKDILEQSLDEARGSRQELVERIHSLRER 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 LQEELN---QEK----GQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAH 62
                           AVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104; Indels 104;
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: TOUKATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2101;
                                                                                                                                                           247 QREISQSLVEKDSLRRQVFEL------TDQVCELRTQLRQLQ 282
                                                                                                                                                                                      Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.3%; Score 194; DB 2; 26.6%; Pred. No. 9.6e-08; Live 49; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: TESTA, HURWITZ & THIBEAULT STREET: 125 HIGH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/483,924 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MTP-013
                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08483924 Patent No. 5882876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEPRONE: (617) 248-7100
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2101 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS LENGTH: 2101 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-483-924-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ψ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                 RESULT 5
US-08-483-924-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                     635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146
    146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQ
                                      g
                                                                              ò
                                                                                                              QQ
                                                                                                                                                             δy
                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                              246
                                                                                                                586 ATAAE-EREASLRERDAALKQLE-----ALEKEKAAKLEI----LOOOLOVANEARDSA 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                412 VLOLETLKOEAATLAANNTOLOARVEMLETERGOGEAKLLAERGHFEEEKOOLSSLITDL 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----LKQELQRANMVSSCELELQEQSLRT-----ASDQESGDEELNRLKEE--- 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              472 QSSISNLSQAKEELEQASQAHGARLTAQVASLTSELTTLNATIQQQ-DQELAGLKQQAKE 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 LQEELN---QEK----GQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAH 62
-----NEKLRSLTFSLAEKDILEQSLDEARGSRQELVERIHSLRER
                                      531 KOAQLAQTLQQQEQASQGLRHQVEQLSSSLKQK---EQOLKEV-AEKQEATRQDHA-QQL
                                                                              AVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 104;
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: TOUKATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALICNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA HURMITZ & THIBEAULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---LHYSNALQEKELAASRCRSLQEELYL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2101;
                                                                                                                                                           247 QREISQSLVEKDSLRRQVFEL------TDQVCELRTQLRQLQ 282
                                                                                                                                                                                    | ::|: || | |:| || | OTSVTQAQREKAELSRKVEELQACVETARQEQHEAQAQVAELELQLRSEQ 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.3%; Score 194; DB 1; 26.6%; Pred. No. 9.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 53 STATE STREET
CITY: BOSTON
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/901,701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MTP-013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: 27,829
REFERENCE/TOWN NUMBER: 37,829
REFERENCE/TOWN INFORMATION:
TELEPHONE: 617/248-7000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08195487 Patent No. 5783403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 FHEVLRLKDEMLSLS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 13.3
Best Local Similarity 26.6
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-195-487-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ropology:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                  US-08-195-487-4
  146
                                                                            187
                                                                                                                                                                                                   635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
```

15;

g

õ

õ

```
RESULT 8
US-09-104-324B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dβ
                                                                                                                                                                                                                  Sequence 1, Application US/09452294

Patent No. 6287790

GENERAL INFORMATION:
APPLICANT: Lelievre, Sophie
APPLICANT: Bissell, Mina
TITLE OF INVENTION: UTILIZATION OF NUCLEAR STRUCTURAL PROTEINS FOR TARGETED
TITLE OF INVENTION: DIFFERENTIATION DISORDERS
TITLE OF INVENTION: DIFFERENTIATION DISORDERS
FILE REPERENCE: IB-1454 - Sequence Submittal
Patent No. 6287790
CURRENT APPLICATION NUMBER: US/09/452, 294
CURRENT FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: 60/110,420
PRIOR PILING DATE: 1998-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      412 VLOLETLKOEAATLAANNTOLOARVEMLETERGOGEAKLLAERGHFEEEKOOLSSLITDL 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 ...--LKQELQRANMVSSCELELQEQSLRT-----ASDQESGDEELNRLKEE--- 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  472 OSSISNLSQAKEELEQASQAHGARLTAQVASLTSELTILNATIQQQ-DQELAGLKQQAKE 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          531 KQAQLAQTLQQQEQASQGLRHQVEQLSSSLKQK---EQQLKEV-AEKQEATRQDHA-QQL 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 LQEELN---QEK----GQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAH 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187 AVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSA
                                    187 AVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 FHEVLRLKDEMLSLS------LHYSNALQEKELAASRCRSLQEELYL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; DB 4; Length 2101; 9.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 QREISQSLVEKDSLRRQVFEL-------TDQVCELRTQLRQLQ 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 635 OTSVTOAOREKAELSRKVEELOACVETAROEOHEAOAOVAELELOLRSEO 684
                                                                                                       247 QREISQSLVEKDSLRRQVFEL------TDQVCELRTQLRQLQ 282
                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.3%; Score 194; 26.6%; Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application PC/TUS9306160 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 1 SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 13.3
Best Local Similarity 26.6
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US93-06160-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 1
LENGTH: 2101
                                                                                                                                                                                                             US-09-452-294-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-452-294-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146
                                                                                                                                           635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                    ò
                                                                     g
                                                                                                           ò
                                                                                                                                          g
```

```
T reci, Ozlem; Sahin, Ugur; Pfreundschuh, Michael VENTION: Methods For Diagnosis And Treating Cancers, NVENTION: And Methods For Identifying Pathogenic Markers In A Sample VENTION: No. 6232460mal Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 FHEVLRLKDEMLSLS-------LHYSNALQEKELAASRCRSLQEELYL----- 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :: || | :|: || 412 VLQLETLKQEAATLAANNTQLQARVEMLETERGQQEAKLLAERGHFEEEKQQLSSLITDL 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 ------LKQELQRANMVSSCELELQEQSLRT-----ASDQESGDEELNRLKEE--- 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----NEKLRSLTFSLAEKDILEQSLDEARGSRQELVERIHSLRER 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 AVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             362 LEKELSAALQDKKCLEEKNEILQGKLSQLEEHLS------QLQDNPPQEKGEVLGD 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 LQEELN---QEK----GQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAH 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49; Mismatches 104; Indels 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----TDQVCELRTQLRQLQ 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 194; DB 5;
Pred. No. 9.6e-08;
ADDRESSEE: TESTA HURWITZ & THIBEAULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: Fulbright & Jaworski LLP
666 Fifth Avenue
                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06160
FILING DATE: 19930621
                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: MTP-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7100
TELEFAX: 617/248-7100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 QREISQSLVEKDSLRRQVFEL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09104324B Patent No. 6232460 GENERAL INFORMATION: APPLICANT: T reci, Ozlem; Sahin,
                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
MAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
13.3%;
Best Local Similarity 26.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2101 amino acids
                                                                                                                                                              Floppy disk
                   53 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Met'l
TITLE OF INVENTION: And
TITLE OF INVENTION: NO.
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein PCT-US93-06160-4
                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                            USA
                                              BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                         Ψ
```

Wed Jan 22 10:56:38 2003

```
10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||| : |:|| || :| :| || 434 EELKKVLGEKETLLYENKQFEKIAEELKGTEQELIGLLQAREKEVHDLEIQLTAITTSEQ 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AHFHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               494 YYSKEVKDLKTEL-----ENEKLKNTEL-TSHCNKLSLENKELTQE-----TSDMTLE 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQEQSLRTASDQESGDEELNRLKEENEKLRSLTFSLAE-------KDILEQSLDE 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 ARGSROELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMA----CQLYREKVNA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      590 VKCKLDKSEENCNNLRKQV----ENKNKYIEELQQENKALKKKGTAESKQLNVYEIKVNK 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 EELNQEKGQKEVLLRRCQQL------QEHLGLAETRAEGLHQLEADHSRMKREVS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-328-254-6
Sequence 6, Application US/08328254
Sequence 6, Application US/08328254
GENERAL INCEMATION:
APPLICANT: Zhu, Xueliang
APPLICANT: Lee, Wen-Hwa
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |---LELESAKQKFGEITDTYQKEIEDKKISEENLLEEVEKAKVIADEAVKLQKEI 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQAQVCELQKERDQAYSARDSAQREISQSLVEKDSLRRQVFE---LTDQVCELRTQL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.1%; Score 176.5; DB 4; Length 976; 23.9%; Pred. No. 1.1e-06; tive 53; Mismatches 112; Indels 61
                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ...unesSE: ...unesS: ...unesSE: .
                                                                                                                                                               COMPUTER: IBM
COMPUTER: IBM
CORRENT SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,324B
FILING DATE: 25-June-1998
CLASSIFICATION NUMBER: 08/892,702
FILING DATE: 15-July-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, NO. 6222460man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5491
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 976 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 23.99
Matches 71; Conservative
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-104-324B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    οy
```

```
1787 ENILOEKEQEKVOMKEKSSTAMEMLOTOLKELNERVAALHNDOEACKAKEQNLSSOVECL 1846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNALQEK-----NWVSSCE-L 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LAGAIGSLQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGL-HQLE-----ADHSRMK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 ELQEQSLRTASDQ--------ESGDEELNRLKEENEKLRSLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 FSLAEKD----ILEQSLDEARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSAQREIS-------QSLVEK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08353700
Patent No. 559919
GENERAL INFORMATION:
APPLICANT: YEN, TIMOTHY J.
APPLICANT: RATINER, JEROME B.
TITLE OF INVENTION: NUCLEIC ACID ENCODING A
TITLE OF INVENTION: TRANSIENTLY EXPRESSED KINETOCHORE PROTEIN,
TITLE OF INVENTION: AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2482;
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: DANN, DORFMAN, HERRELL AND SKILLMAN 1601 MARKET STREET, SUITE 720
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 11.9%; Score 173.5; DB 1; Best Local Similarity 22.4%; Pred. No. 5.9e-06; Matches 89; Conservative 66; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2026 KSSKDQLKELTLENSELKKSLDCMHKDQVEKEGKVREE 2063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 DSLRRQVFELTDQVCELRTQL---RQLQAEPPGVLKQE 292
                                                                                   PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/141,239
FILING DATE: 22-0CT-1993
ATTOTNEY AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERNCE/DOCKET NUMBER: P-CJ 1191
TELECOMMUNICATION:
TELEPHONE: (619) 535-9001
   24-OCT-1994
NN: 435
                                                                                                                                                                                                        P-CJ 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 REVSAHFHEVLRLKDEMLSLSLH----
                                                                                                                                                                                                                                         TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 2482 amino acids
TYPE: amino acid
               CURRENT APPLICATION DATA
APPLICATION NUMBER: US
FILING DATE: 24-OCT-19
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-328-254-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHILADELPHIA
                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-08-353-700-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

1601 Market Street

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  С
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application PC/TUS9516216
GENERAL INFORMATION:
APPLICANT: Yen, Timothy J.
APPLICANT: Ratiner, Jerome B.
TITLE OF INVENTION: Expressed Kinetochore Protein, and Methods of Use NUMBER OF SEQUENCES:
AUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----ELAASRCRSLQEELYLL--KQELQRA---NMVSSCE-L 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 ELQEQSLRTASDQ--------ESGDEELNRLKEENEKLRSLT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 QKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSAQREIS------QSLVEK- 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 LAGAIGSLQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGL-HQLE-----ADHSRMK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2515 ENILGEKEQEKVOMKEKSSTAMEMLQTQLKELNERVAALHNDQEACKAKEQNLSSQVECL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 FSLAEKD----ILEQSLDEARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTILLQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2635 SKLSQVEGEHQLWKEQNL-ELRNLTVELEQXIQVLQSKNASLQDTLEVLQSSYKNLENEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 3248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparatible
OPERATUNG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/353,700
FILING DATE: 09-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 11.9%; Score 173.5; DB 1; Best Local Similarity 22.4%; Pred. No. 8.3e-06; Matches 89; Conservative 66; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2754 KSSKDQLKELTLENSELKKSLDCMHKDQVEKEGKVREE 2791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 REVSAHFHEVLRLKDEMLSLSLH---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258 DSLRRQVFELTDQVCELRTQL---RQLQAEPPGVLKQE 292
                                                                                                        FILING DATE: 09-DEC-1994
CLASSIFTCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REED, JANET E.
REGISTRATION NUMBER: 36,252
TELECOMMUICATION: TELEPHONE: (215) 563-4100
TELEPHONE: (215) 563-4100
TELEPHONE: (215) 563-404
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3248 amino acids
                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 SNALQEK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                               0N
                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US95-16216-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-353-700-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
2694 ELTKMDKMSFVEKVNKMTAKETELQREMHEMAQKTAELQEELSGEKNRLAGELQLLLEEI 2753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2575 ELEKAQILLOGLDEAKNNYIVLQSSVKGLIQEVEDGKQKLEKKDEEISRLKNQIQDQEQLV 2634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNALQEK-----NMVSSCE-L 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----ESGDEELNRLKEENEKLRSLT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 FSLAEKD----ILEQSLDEARGSROELVERIHSLRERAVAAERQREQYWEEKEQTLLQF 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             209 QKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSAQREIS------QSLVEK- 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 LAGAIGSLQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGL-HQLE-----ADHSRMK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2635 SKLSQVEGEHQLWKEQNL-ELRNLTVELEQKIQVLQSKNASLQDTLEVLQSSYKNLENEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3248;
                                                                                                                                                      SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.9%; Score 173.5; DB 5; 22.4%; Pred. No. 8.3e-06; tive 66; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               258 DSLRRQVFELTDQVCELRTQL---RQLQAEPPGVLKQE 292
                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16216
                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,700
FILING DATE: 09-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 REVSAHFHEVLRLKDEMLSLSLH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08685576
Patent No. 5906819
GENERAL INFORMATION:
APPLICANT: Kalbuchi, Kozo
                                                              ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                NAME: Reed, Janet E. REGISTRATION NUMBER: 36,252
                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SS: not relevant not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELQEQSLRTASDQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 3248 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO
Philadelphia
                                                                                                                                    COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino a STRANDEDNESS:
                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT-US95-16216-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
US-08-685-576-1
```

```
:::||| :::||| 322 SLEADLMQLQEDLAAABRARKQADLEKEELAEELASSLSGRNALQDEKRRLEARIAQ--- 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----NEKLRSLTFSLAEKDI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEQSLDEARGSRQELVERIHSLRERA-----VAAERQREQYWEEKEQTLLQFQKSKMAC 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---YREKVNALQAQVCELQKERDQAYSARDSAQREISQS-----LVEKD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 RDEQNEEK-----RR--QLQRQLHEYET------ELEDERNERALAAAAKK--KLE 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      438 KLHEMEGAVKSKFKSTIAALEAKIAQLEEQVEQEAREKQAATKSLKQKDKKLKEILLQVE 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 QEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAHFHEVLRLK 70
                                                                                                                                                                                                                                                                                                                  Markers for Detection of Chromosome 16 Rearrangements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 11.6%; Score 170; DB 2; Length 57 Best Local Similarity 21.0%; Pred. No. 1.9e-06; Matches 70; Conservative 73; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 DEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PELLOATION NUMBER: US/08/533,306A
FILING DATE: September 25, 1995
                                                                                                                                                                                                                                                                                                                                                                                            SSEE: Harness, Dickey & Pierce, P.L.C.
T: P.O. Box 828
Bloomfield Hills
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLRRQVFELTDQ-----VCELRTQLRQLQAE 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 2115-00869COB
TELECOMMINICATION INFORMATION:
TELEPHONE: (810) 641-1600
TELEFAX: (810) 641-0270
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                               921 KADSEQLARSIAE -- EQYSDLEKEKIMKELE 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 MVSSCELELQEQSLRTASDQESGDEELNRLKEE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : Floppy disk
IBM PC compatible
YYTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                           APPLICANT: Liu, Pu
APPLICANT: Collins, Francis S.
APPLICANT: Siciliano, Michael J.
APPLICANT: Claxton, David
                                                                                                                                                                   Sequence 2, Application US/08533306A Patent No. 5837457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Deann F.
REGISTRATION NUMBER: 36683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                576 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-533-306A-2
                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48303
                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ξ
                                                                                                                                               US-08-533-306A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216
                                                                                                                           RESULT 13
                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RMKREVSAHFHEVLRLKDE---MLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQR 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----TASDQESGDEELN- 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    760 RCSILDCDLKQSQQKINELLKQKDVLNEDVRNLTLKIEQETQKRCLTQNDLKMQTQQVNT 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 -----RLKEENEKLRSLTFSLAEKDI-LEQSLDEARGSRQELVERIHSLRERAVAAERQ 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 REQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSAQREISQS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 644 LOGRISGLEEDVKNGK----ILLAKVELEKROLOERFTDLEKEKNNMEIDMTYOLKVIQQ 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----- 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 LAGAIGSLQEELNQEKGQKEVLLRRCQ----QLQEHLGLAETRAEGL-----HQLEADHS 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.7%; Score 171; DB 2; Length 138 22.1%; Pred. No. 4.7e-06; Live 67; Mismatches 115; Indels
APPLICANT: Iwamatsu, Akihiro
APPLICANT: Nakano, Takeshi
APPLICANT: ILO, Masaaki
APPLICANT: Takabashi, No. 5906819uaki
TITLE OF INVENTION: RHO TARGET PROTEIN RHO-KINASE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEV F T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       820 LKMSEKQLKQENNHLLEMKMSLEKQNAELRKERQDADGQMKELQDQL-
                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 24-JUL-1996
CLASSIFICATION: 435
                                                                                                                                                                                                     SSEE: Foley & Lardner
F: 3000 K Street, N.W., Suite 500
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254 LVEKDSLRRQVFELTDQVCELRTQ--LRQLQ 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16887/843
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPHANE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PULCASSIFICATION: 435
PULCASSIFICATION DATA:
APPLICATION NUMBER: JP 7-325129
FILING DATE: 20-NOV-1995
PRIOR APPLICATION NUMBER: JP 8-17150
FILING DATE: 05-JAN 1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: JP 8-131206
FILING DATE: 26-APR-1996
ATORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A:
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 ANMVSSCELELQEQSLR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1388 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 22.15
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-685-576-1
                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                            20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              οχ
```

12;

82;

498 DERKMAEQYKEQAEKGNARVKQLKRQLEEAEEE 530

----------

```
12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         322 SLEADLMOLQEDLAAAERARKQADLEKEELAEELASSLSGRNALQDEKRRLEARIAQ--- 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEQSLDEARGSRQELVERIHSLRERA-----VAAERQREQYWEEKEQTLLQFQKSKMAC 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----NEKLRSLTFSLAEKDI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QL-----YREKVNALQAQVCELQKERDQAYSARDSAQREISQS-----LVEKD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLHEMEGAVKSKFKSTIAALEAKIAQLEEQVEQEAREKQAATKSLKOKDKKLKEILLQVE 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 RDEQNEEK-----RR--QLQRQLHEYET------ELEDERNERALAAAAKK--KLE 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 QEBLNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAHFHEVLRLK 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82;
                                                                                  APPLICANT: Liu, Pu
APPLICANT: Collins, Francis S.
APPLICANT: Collins, Francis S.
APPLICANT: Claxton, David
APPLICANT: Claxton, David
TITLE OF INVENTION: Markers for Detection of Chromosome 16
TITLE OF INVENTION: Rearrangements
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
STREET: P.O. Box 828
CITY: Bloomfield Hills
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.6%; Score 170; DB 2; Length 57 21.0%; Pred. No. 1.9e-06; Live 73; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 DEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Smith, DeAnn F.
REGISTRATION NUMBER: 3683
REFERENCE/DOCKET NUMBER: 2115-00869DVC
TELEPHONE: (810) 641-050
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 576 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MVSSCELELQEQSLRTASDQESGDEELNRLKEE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |: : | | : : | DERKMAEQYKEQAEKGNARVKQLKRQLEEAEEE 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLRRQVFELTDQ-----VCELRTQLRQLQAE 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/742,923A FILING DATE: No. 5869611ember 1, 1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                               E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                Sequence 2, Application US/08742923A Patent No. 5869611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 21.0 Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                     ZIP: 48303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC of OPERATING SYSTEM:
                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                             CITY: Bloc
STATE: MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-742-923A-2
                 US-08-742-923A-2
                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                498
RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
```

```
-----RAN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 MVSSCELELQEQSLRTASDQESGDEELNRLKEE-----NEKLRSLTFSLAEKDI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       562 SLEADLMOLOEDLAAAERARKOADLEKEELAEELASSLSGRNALODEKRRLEARIAO--- 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEQSIDEARGSRQELVERIHSLRERA-----VAAERQREQYWEEKEQTILQFQKSKMAC 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   619 LEEELEEEGGNMEAMSDRVRKATQQAEQLSNELATERSTAQKNESARQQ-LERONKELRS 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216 QL-----YREKVNALQAQVCELQKERDQAYSARDSAQREISQS-----LVEKD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :| : : | |:: : ||:|: : | |:: : | |:: : | |: : | |: : | |: : | |: : | |: : | |:: : | |:: : | |:: : | |:: : | |: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : | |:: : : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |:: : | |::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 502 GDLKDLELQADSAIKGREEAIKQLRKLQAQMKDFQRELEDARASRDEIFATAKENEKKAK 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               461 RDEQNEEK-----RR--QLQRQLHEYET-----ELEDERNERALAAAAKK--KLE 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 QEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAHFHEVLRLK 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82;
                                                                                                                                                                                                                       APPLICANT: Siciliano, Michael J.
APPLICANT: Claxton, David
TITLE OF INVENTION: Markers for Detection of Chromosome 16
TITLE OF INVENTION: Rearrangements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 DEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 11.6%; Score 170; DB 2; L
Best Local Similarity 21.0%; Pred. No. 2.9e-06;
Matches 70; Conservative 73; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: Harness, Dickey & Pierce, P.L.C.
STREET: P.O. Box 828
CITY: Bloomfield Hills
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |: :| |:|: |
738 DERKMAEQYKEQAEKGNARVKQLKRQLEEAEEE 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259 SLRRQVFELTDQ-----VCELRTQLRQLQAE 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Smith, DeAnn F.
REGISTRATION NUMBER: 36683
REFERENCE/DOCKET NUMBER: 2115-00869COB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/533,306A
FILING DATE: September 25, 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PC-DOS/MS-DOS
Sequence 6, Application US/08533306A Patent No. 5837457
                                                                                           GENERAL INFORMATION:
APPLICANT: Liu, Pu
APPLICANT: Collins, Francis S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (810) 641-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (810) 641-0270 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   816 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-533-306A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
```

Search completed: January 22, 2003, 08:57:35 Job time: 28.2218 secs

THIS PAGE BLANK (USPTO)

```
SEQ ID NO 2
LENGTH: 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-767-215-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-767-215-2
                                                                                                                                                                                                                                       151.5
1521.5
1531.5
1531.5
1531.5
1531.5
1531.5
1531.5
1531.5
1531.5
1531.5
1531.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 12, Appl. Sequence 12, Appl. Sequence 2, Appl. Sequence 16, Appl. Sequence 6, Appl. Sequence 7, Appl. Sequence 19, Appl. Sequence 7, Appl. Sequence 2, Appli. Sequence 2, Appli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 120, App
Sequence 120, App
Sequence 6, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Appli
Sequence 5, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 625, App
                                                                                                                                                     (without alignments)
500.428 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                            January 22, 2003, 08:49:35 ; Search time 11.8952 Seconds
                                                                                                                                                                                                              US-09-767-215-2_COPY_126_420
1462
1 ECLAGAIGSLQEELNQEKGO.....TQLRQLQAEPPGVLKQEART 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-991-496-120

US-09-874-923-120

US-09-727-384-6

US-09-764-868-625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-767-215-5

US-09-767-215-5

US-10-032-159A-18

US-10-032-159A-12

US-10-032-159A-20

US-10-032-159A-20

US-10-032-159A-20

US-10-017-216-6

US-10-017-216-6

US-10-017-216-5

US-10-017-216-7

US-09-884-001-19
                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-028-946-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-028-946-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-017-216-2
                                                                                                                                                                                                                                                                                                                                                                   122226 segs, 20178551 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                       length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10004
1247
1247
1247
3166
366
691
1597
1059
1058
2055
2055
2055
2310
2310
2310
2455
6455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1000.0
245.2
245.2
245.3
133.5
133.5
132.7
122.7
122.7
122.7
122.7
122.7
122.7
122.7
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
122.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                              sed
                                                                                                                                                                                                                                    Perfect score:
                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1462
1443
369
369
369
198
198
185
185
183
183
183
177
174 . 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB
Maximum DB
                                                                                   OM protein
                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database
                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
```

```
20 167.5 11.5 576 10 US-09-925-297-787 Sequence 787, App 21 11.6 660 10 US-09-925-295-305 Sequence 787, App 22 160.5 11.0 660 10 US-09-864-761-47959 Sequence 17, App 22 160.5 11.0 1884 10 US-09-785-770A-16 Sequence 17, App 24 160.5 11.0 1884 10 US-09-785-770A-16 Sequence 17, App 26 157.5 10.8 2125 10 US-09-919-172-29 988 Sequence 29, App 18 151.5 10.4 704 9 US-09-919-172-29 Sequence 29, App 18 152 10.4 704 9 US-09-919-173-191 Sequence 191, App 29 152 10.4 704 9 US-09-925-297-740 Sequence 191, App 19 152 10.4 774 10 US-09-925-297-740 Sequence 191, App 19 152 10.4 774 10 US-09-925-302-711 Sequence 191, App 19 152 10.4 774 10 US-09-925-302-711 Sequence 191, App 19 152 10.4 774 10 US-09-925-302-711 Sequence 711, App 19 151.5 10.4 530 12 US-10-023-529-8 Sequence 8, Appli 19 151.5 10.4 530 12 US-10-023-529-8 Sequence 64, App 19 151.5 10.4 540 10 US-09-956-05-8 Sequence 71, App 19 151.5 10.4 540 10 US-09-952-05-8 Sequence 74, App 19 19 151.5 10.4 540 12 US-10-023-523-8 Sequence 5, Appli 19 151.5 10.4 557 12 US-10-023-523-8 Sequence 5, Appli 19 151.5 10.4 557 12 US-10-023-523-5 Sequence 5, Appli 19 151.5 10.4 557 12 US-10-023-523-5 Sequence 5, Appli 19 151.5 10.4 557 12 US-10-023-523-5 Sequence 5, Appli 19 151.5 10.4 557 12 US-10-023-523-5 Sequence 5, Appli 19 151.5 10.4 557 12 US-10-023-523-5 Sequence 5, Appli 19 151.5 10.4 557 12 US-10-023-523-5 Sequence 5, Appli 19 151.5 10.4 557 12 US-10-023-523-5 Sequence 5, Appli 19 151.5 10.4 557 12 US-10-023-523-5 Sequence 5, Appli 19 151.5 10.4 557 12 US-10-023-523-5 Sequence 5, Appli 19 151.5 10.4 557 12 US-10-023-523-5 Sequence 5, Appli 19 151.5 10.4 557 12 US-10-023-523-5 Sequence 5, Appli 19 151.5 10.4 557 12 US-10-023-523-5 Sequence 5, Appli 19 151.5 10.4 557 12 US-10-023-523-5 Sequence 5, Appli 19 151.5 10.4 557 12 US-10-023-523-5 Sequence 5, Appli 19 151.5 10.4 557 12 US-10-023-523-5 Sequence 5, Appli 19 151.5 10.4 557 12 US-10-023-523-5 Sequence 5, Appli 19 151.5 10.4 557 12 US-10-023-523-5 Sequence 5, Appli 19 151.5 10.4 151.1 10 US-03-523-5 Sequence 5, Appli 19 151.5
```

## ALIGNMENTS

```
61 AHFHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ECLAGAIGSLQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 LQEQSLRTASDQESGDEELNRLKEENEKLRSLTFSLAEKDILEQSLDEARGSRQELVERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LQEQSLRTASDQESGDEELNRLKEENEKLRSLTFSLAEKDILEQSLDEARGSRQELVERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLRQLQAEPPGVLKQEART 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                      GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-142001
CURRENT APPLICATION NUMBER: US/09/767,215
CURRENT FILING DATE: 2001-01-22
PRIOR FILING DATE: 2000-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1462; DB 10;
Pred. No. 2.6e-92;
Mismatches 0;
                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version
Sequence 2, Application US/09767215 Patent No. US20020081636A1
                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Sc
100.0%; Pr
tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 295; Conservative
                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
```

ö

```
Matches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                    Query Match
Best Local 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69
                                                                                                                                                                     62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                      g
                                                                                                                                                                   δy
                                                                                                                                                                                              g
                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                  δy
                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                         Ω
                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                               δà
                                                                                                                                                                                                                                                                                                                                                                                    ή
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NALQAQVCELQKERDQAYSARDSAQREISOSLVEKDSLRRQVFELTDQVCELRTGLRQLQ 282
                                                                                                                                                                                                                                                                                                                                                                                                                               AHFHEVLRIKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 LQEQSLRTASDQESGDEELNRLKEENEKLRSLTFSLAEKDILEQSLDEARGSRQELVERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               1 ECLAGAIGSLQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/10032159A
Factor No. US20020164703A1
GENERAL INFORMATION:
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Reed, John C.
APPLICANT: Reed, John C.
APPLICANT: Godzik, Adam
TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,
TITLE OF INVENTION: CARD-DOMAIN COLEIC ACIDS, AND METHODS OF USE
FILE REFERENCE: P-LJ 5100
CURRENT APPLICATION NUMBER: US/10/032,159A
CURRENT FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 37
SEQ ID NOS: 37
SEQ ID NOS: 37
SEQ ID NOS: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                                                                                                        Length 1138;
                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                            GENERAL INFORMATION:
APPLICANT: BETLIN, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-142001
CURRENT APPLICATION NUMBER: US/09/767,215
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 60/181,159
PRIOR FILING DATE: 2000-02-09
                                                                                                                                                                                                                                                                                                                                                      Score 1443; DB 10;
Pred. No. 5.9e-91;
0; Mismatches 0;
                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1138
TYPE: PRT
                                                                                 Sequence 5, Application US/09767215
Patent No. US20020081636A1
                                                                                                                                                                                                                                                                                                                                                         98.78;
94.28;
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEPPGVLKQEART 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens US-09-767-215-5
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 295; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
US-10-032-159A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1247
                                                                    US-09-767-215-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
             366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223
                                                                                                                                                                                                                                                                                                                                                                                                                                           QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Вp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
             QQ
```

```
7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELELQEQSLRT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASDQES--GDEELNRLKEENEKLRSLTFSL-------AEKDILEQSLDEAR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171 GSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVC 230
                                                                                                                                                                                             -----AEKDILE 163
                                                                                                                                                                                                                                                                                                                                                                 164 OSLDEARGSROELVERIHSLRERAVAAEROREOYWEEKEOTLLOFOKSKMACOLYREKVN 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                   : |: || || || 360 TVMLQLEEVERERDQGQAVAFQGHCIKALNTEPATSKGRTIGSVIALMKKAFHSKDEAQT 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                  HFHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELEL 121
                                                                                                                                                                   3 LAGAIGSLQEELNQEKGQKEVLLRRCQQLQ-EHLGLAETRAEGLHQLEADHSRMKREVSA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-032-159A-12

US-10-032-159A-12

US-10-032-159A-12

Sequence 12, Application US/10032159A

Patent No. US20020164703A1

GENERAL INFORMATION:

APPLICANT: Pawlowski, Krzysztof

APPLICANT: Reed, John C.

TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,

TITLE OF INVENTION: ENCOING NUCLEIC ACIDS, AND METHODS OF USE

FILE REFERENCE: P-LJ 5100

CURRENT APPLICATION NUMBER: US/10/032,159A

CURRENT FILING DATE: 2000-12-19

PRIOR APPLICATION NUMBER: US 60/257,457

PRIOR FILING DATE: 2000-12-21

NUMBER OF SEQ ID NOS: 37

SEQ ID NOS: 37

SEQ ID NOS: 37

FENGEN 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 LQEELNQEKGQKEVLLRRCQQLQ-EHLGLAETRAEGLHQLEADHSRMKREVSAHFHEVLR
                                                                                                                                                                                                                                                                             58;
                                                                                                                         58;
                                                                               Length 1247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                           Indels
                                                                           ; Score 369; DB 9; L; Pred. No. 8.2e-18; 66; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.9%; Score 364; DB 9; ilarity 31.1%; Pred. No. 3.8e-18; Conservative 62; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                           122 QEQSLRTASDQES -- GDEELNRLKEENEKLRSLTFSL --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 EISQSLVEKDSLRRQVFELTDQVCELRTQLRQLQA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.2%;
                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 ALQAQVCELQKERDQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-159A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 100; Conserv
                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: HOMU
US-10-032-159A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
```

9

```
US-10-028-072-16
                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT
                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                       δλ
                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290 ALRDHQEQANTIFSLRKDLRQGEARRIRCMEEKEMFELQCLALRRDSKMYKDRIEAILLQ 349
                                                                         63 FHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELELQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 SRELKRCKEENYDLAMRLAHQSEEKGAALMRNRDLQLEIDQLKHSLMKAE--DDCKVERK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 EQ-SLRTASDQESGDEELNRLKEE----NEKLRSLTFSLAEK------DILEQSLDE 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 HTLKLRHAMEORPSQELLWELQQEKALLQARVQELEASVQEGKLDRSSPYIQVLEEDWRQ 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 ARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQ 228
ELQKERDQ-----AYSARDSAQREISQSLV 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 EKGOKEVLLRRCQOLQEHL---GLAETRAEGLHQLEADHS------RMKREVSAH 62
                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

APPLICANT: Pawlowski, Krzysztof

APPLICANT: Pawlowski, Krzysztof

APPLICANT: Redzik, Adam

TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,

TITLE OF INVENTION: ENCOING NUCLEIC ACIDS, AND METHODS OF USE

FILE REFERENCE: P-LJ 5100

CURRENT APPLICATION NUMBER: US/10/032,159A

CURRENT FILING DATE: 2001-12-19

PRIOR RPPLICATION NUMBER: US 60/257,457

PRIOR PELLING DATE: 2000-12-21

NUMBER OF SEQ ID NOS: 37

SEQ ID NOS: 37

SEQ ID NOS: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20, Application US/10032159A

Sequence 20, Application US/10032159A

Patent No. US200201647031A

GENERAL INFORMATION:
APPLICANT: Pawlowski, Krzysztof

APPLICANT: Reed, John C.

APPLICANT: Great, John C.

APPLICANT: Great, Adam

TITLE OF INVENTION: ENCODING NUCLEIC ACIDS, AND METHODS OF USE

FILE REFERENCE: P-LJ 5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.5%; Score 198; DB 9; 26.7%; Pred. No. 8.8e-07; tive 48; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/032,159A CURRENT FILING DATE: 2001-12-19
                                                                                                                                                                                                                                                    Sequence 2, Application US/10032159A Patent No. US20020164703A1
                                                                                                                                              ||| |:|: || :: EKDKYRKQIRELEEKNDEMRIE 319
                                                                                                                          EKDSLRRQVFELTDQVCELRTQ 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 VCELQKERDQA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350 MEEVAIERDOS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                 US-10-032-159A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-032-159A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                        256
                                                                                    238
                                                                                                                                                           298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
                                                    à
                                                                                    g
                                                                                                                        ò
                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

```
63 FHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELELQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 EQ-SLRTASDQESGDEELNRLKEE----NEKLRSLTFSLAEK------DILEQSLDE 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 ARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQ 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 ALRDHQEQANTIFSLRKDLRQGEARRLRCMEEXEMFELQCLALRKDSKMYKDRIEAILLQ 349
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                            112 ESGLTQLLMTEVMKLQKKVQDLTALLSSKDDFIKELRVKDSLLRKHQERVQRLKEECEAG 171
                                                                                                                                                                                                                                                                                                                                                     -----RMKREVSAH 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 HTLKLRHAMEORPSOELLWELQOEKALLQARVOELEASVQEGKLDRSSPYIQVLEEDWRQ
                                                                                                                                                                                                                                                                                                    30;
                                                                                                                                                                                                                                                 Length 366;
                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                              ; Score 198; DB 9; L, Pred. No. 8.8e-07; 48; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                17 EKGQKEVLLRRCQQLQEHL----GLAETRAEGLHQLEADHS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR PLILNG DATE: 1997-06-18
PRIOR FILING DATE: 1997-08-26
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/059115
PRIOR PILING DATE: 1997-09-17
PRIOR PLILNG DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: US 60/257,457
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 37
SSOFTWARE: FastSEQ for Windows Version 4.0
SSO ID NO 20
LENGTH: 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16, Application US/10028072 Publication No. US20030004311A1
                                                                                                                                                                                                                                                 13.5%; 26.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith, Victoria
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Watanabe, Colin K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Godowski, Paul J. Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Desnoyers, Luc
Filvaroff, Ellen
Gao, Wel-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sherwood, Steven
                                                                                                                                                                                                                                                                                                    67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wood, William
                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-159A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : |: ||||:
350 MEEVAIERDQS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 VCELQKERDQA 239
                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhanq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE
```

```
PRIOR APPLICATION NUMBER: 60/059184

PRIOR FILING DATE: 1997 (0911)

PRIOR FILING DATE: 1997 (0911)

PRIOR FILING DATE: 1997 (0912)

PRIOR FILING DATE: 1997 (0912)

PRIOR PLING ADME: 1997 (0912)

PRIOR PLING ADME: 1997 (0912)

PRIOR PLING DATE: 1997 (0913)

PRIOR PRIOR DATE: 1997 (0913)

PRIOR PLING DATE: 199
```

PRICE APPLICATION NUMBER: 60/074092
PRICE PLILIC DATE: 1998-02-09
PRICE FILING DATE: 1998-03-12
PRICE FILING DATE: 1998-03-12
PRICE FILING DATE: 1998-03-27
PRICE PLING DATE: 1998-03-27
PRICE PLING DATE: 1998-03-27
PRICE PLING DATE: 1998-03-27
PRICE PLING DATE: 1998-03-37
PRICE PLING DATE: 1998-03-37
PRICE PLING DATE: 1998-03-37
PRICE PLING DATE: 1998-03-37
PRICE PLING DATE: 1998-04-14
PRICE PLING DATE: 1998-04-15
PRICE PLING DATE: 1998-05-07
PRICE PLING DATE: 1998-05-15
PRICE PLING DATE: 1998-06-10

```
GENERAL INFORMATION:
APPLICANT: KAPELLER-LIBERMANN, Rosana
APPLICANT: KAPELLER-LIBERMANN, Rosana
TITLE OF INVENTION: 13245, A No. US20020160483Alel Human Myotonic Dystrophy Type
TITLE OF INVENTION: Kinase and Uses Therefor
FILE REFERENCE: 10147-57U1
CURRENT APPLICATION NUMBER: US/10/017,216
CURRENT FILING DATE: 2001-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                             16;
                                                                                                                                                                                                                                                                                                                   499 AEAEEEIQALTAHRDEIQRKFDALRNSCTVITDLEEQLNQLTEDNAELNNQNFYLSKQ-- 556
                                                                                                                                                                                                                                                                                                                                                                                                   ---LDEASGANDEIVQLRSEVDHLRREIT----EREMQLTSQKQTM---EALKTTCTML 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | | : |:| | : || | 543 AEAEEIQALTAHRDEIQRKFDALRNSCTVITDLEEQLNQLTEDNAELNNQNFYLSKQ-- 600
                                                                                                                                    HFHEVLRLKDEMLSLSLHYSNALQEKE----LAASRCRSLQEELYLLKQELQRANMVSS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HFHEVLRLKDEMLSLSLHYSNALQEKE----LAASRCRSLQEELYLLKQELQRANMVSS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 CELELQEQSLRTASDQ------ESGDEELNRLKEENEKLRSLTFSLAEKDI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 601 ----LDEASGANDEIVQLRSEVDHLRREIT----EREMQLTSQKQTM---EALKTTCTML 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      650 EEQVIDLEALNDELLEKERQWEAWRSVLGDEKSQFECRVRELQRMLDTEKQSRARADQRI 709
                                                                                                                                                                                                                                                                                     117 CELELQEQSLRTASDQ------ESGDEELNRLKEENEKLRSLTFSLAEKDI 161
                                                                  Gaps
                                                                                                       11 QEELNQE-KGQKEVLLRRCQQLQEHLGLAETRAEGL-HQLEADHSRM-----KREVS-A 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 QEELNQE-KGOKEVLLRRCQQLQEHLGLAETRAEGL-HQLEADHSRM-----KREVS-A 61
                                                                                                                                                                                                                                                                                                                                                                       162 LEQSLDEARGSRQELVE---RIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----QVCELQKERDQAYSARDSAQREI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 LEQSLDEARGSRQELVE---RIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------QVCELQKERDQAYSARDSAQREI
                                                                                                                                                                                                                                         448 HEEQKLELKRQLTELQL----SLQERESQLTALQAARA-ALESQLRQAKTELEE----TT
                                                                92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1641;
                  Length 1597;
                    12.7%; Score 185; DB 9; 26.5%; Pred. No. 3.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.7%; Score 185; DB 9;
illarity 26.5%; Pred. No. 3.8e-05;
Conservative 54; Mismatches 98
                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 SQSLVEKDSLRRQVFELTDQVCELRTQLRQLQ 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   666 TES-----RQVVELA--VKEHKAEILALQ 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/242,429
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/10017216 Patent No. US20020160483A1
                                                             54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. 2.1
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              REKVNALQA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REKVNALQA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                  Best Local Similarity
Matches 88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
US-10-017-216-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-017-216-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                   557
                                                                                                                                                                                                                                                                                                                                                                                                                                                              219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
                                                                                                                                                                                              62
                                                                                                           ò
                                                                                                                                                g
                                                                                                                                                                                              δλ
                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                       δy
                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \overset{\circ}{\Delta}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δý
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: 13245, A No. US20020160483Alel Human Myotonic Dystrophy Type Prot TITLE OF INVENTION: 13245, A No. US20020160483Alel Human Myotonic Dystrophy Type Prot TITLE OF INVENTION: Kinase and Uses Therefor FILE REFERENCE: 10147-5701 CURRENT APPLICATION NUMBER: US/10/017,216 CURRENT FILING DATE: 2000-10-23 PRIOR APPLICATION NUMBER: US 60/242,429 PRIOR FILING DATE: 2000-10-23 SEQ ID NOS: 7

SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 SLRERAVAAE------RQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---SRLEVAEVNGRLAELGLHLKEEKCOWSKERAGLLQ-----SVEAEKDKILKLSAEI 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------ELNRLKEENEKLRSLTFSLAEK-DILEQSLDEARGSRQELVERIH 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----TRAEGLH-----QLEADHSRMKREVSAHFHEVLRLKDEMLSLSLHYSNA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGEITEERDILSRQQGDHVARILELEDDIQTISEKVLTKEVELDRLRDTVKALTREQEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CELQK ---- ERDQAYSARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLRQLQAEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L-QEKELAASRCRSLQEELYLLKQELQRANMVSSCELELQE----QSLRTASDQESGDE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 LAGAIGSLQEELN-----QEKGQKEVLLRRCQQL------QEHLGLAE----
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     12.7%; Score 185; DB 9; 24.9%; Pred. No. 1.4e-05; Live 55; Mismatches 129
         PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR PAPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR APPLICATION NUMBER: 60/090445
PRIOR APPLICATION NUMBER: 60/090445
PRIOR APPLICATION NUMBER: 60/090445
PRIOR PELING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/10017216
Patent No. US20020160483A1
GENERAL INFORMATION:
APPLICATION NUMBER: 60/(
                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 24.9°
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGVL----KQEAR 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         494 QELLEYMRKLEAR 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Mus musculus US-10-017-216-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGIH: 1597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-017-216-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84
```

g

ò qq

à g ö q ò Q ò g ò q ò

g à

```
APPLICANT: KAPELLER-LIBERMANN, Rosana
TITLE OF INVENTION: 13245, A No. US20020160483Alel Human Myotonic Dystrophy Type ITTLE OF INVENTION: Almase and Uses Therefor
FITLE OF INVENTION: Almase and Uses Therefor
FITLE REFERENCE: 10147-5701
CURRENT APPLICATION NUMBER: US/10/017,216
PRIOR PILING DATE: 2001-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                   14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 HFHEVLRLKDEMLSLSLHYSNALQEKE-----LAASRCRSLQEELYLLKQELQRANMVSS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 QEEMISELRQQKFYLETQAGKLEAQNRKLEEQLEKISHQDHSDKNRLLELETRLREVSLE 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 CELELQEQSLRTASDQ------ESGDEELNRLKEENEKLRSLTFSLAEKDI 161
                                                                                                                                                                                                                                                                                                                                                              103 SSAKELLESSLFEAQQQNSVIEVTKGQLEVQIQTVTQAKEVIQGEVRCLKLELDTERSQA 162
                                                                                                                                                                                                                                                                                                                                                                                                      QRANMVSSCELELQEQSLRTASDQESG--DEELNRLKEENEKLRSLTFSLAEKDILEQSL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEARGSRQELVERIHSLRERAVAAERQRE------QYWEEKE----QTLLQF 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209 QK--SKMACQLYR-----SAQRE 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                        ----HYSNALQEKELAASRCRSLQEELYLLKQEL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278 QKELADASQQLERLRQDMKVQKLKEQETTGILQTQLQEAQRELKEAARQHRDDLAALQEE 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 QEELNQE-KGQKEVLLRRCQQLQEHLGLAETRAEGL-HQLEADHSRM-----KREVS-A 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 EELNQE-KGQKEVLLRRCQQ----LQEHLGLAETRAEGLHQLEADHSRMKREVSAHFHEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98; Indels
                                                                                                                                                              Length 868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250 ISQSLVEKDSLRRQVFELTDQVC------ELRTQLRQLQ 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.6%; Score 184; DB 9; L6
25.9%; Pred. No. 2.1e-05;
iive 52; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 12.5%; Score 183; DB 9;
Best Local Similarity 26.2%; Pred. No. 3.9e-05;
Matches 87; Conservative 55; Mismatches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/10017216 Patent No. US20020160483A1 GENERAL INFORMATION:
                 SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                             TYPE: PRT
CORGANISM: Homo sapiens
US-09-884-001-19
                                                                                                                                                                                                                                                                                                                                68 RLKDEMLSLSL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ver
                                                                                                                                                                                      Similarity
                                                                                                                                                                 Query Match
Best Local Simi
Matches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1286
NUMBER OF SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
US-10-017-216-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-017-216-7
                                                            868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 7
                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167
                                                                                                                                                                                                                                                                                                                                                                                                               109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQ
                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          οy
                                                                                                                                                                                                                                                  δy
                                                                                                                                                        Sequence 4, Application US/10017216
Patent No. US20020160483A1
GENERAL INFORMATION:
APPLICATION:
APPLICATION:
TITLE OF INVENTION: 13345, A No. US20020160483A1e1 Human Myotonic Dystrophy Type Prot
TITLE OF INVENTION: Kinase and Uses Therefor
TITLE REFERENCE: 10147-5701
CURRENT PAPLICATION NUMBER: US/10/017,216
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: US 60/242,429
RROR FILING DATE: 2000-10-23
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1064 EEQVLDLEALNDELLEKERQWEAWRSVLGDEKSQFECRVRELQRMLDTEKQSRARADQRI 1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   846 QEEMISELRQQKFYLETQAGKLEAQNRKLEEQLEKISHQDHSDKSRLLELETRLREVSLE 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 HFHEVLRLKDEMLSLSLHYSNALQEKE-----LAASRCRSLQEELYLLKQELQRANMVSS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 CELELQEQSLRTASDQ------ESGDEELNRLKEENEKLRSLTFSLAEKDI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 QEELNQE-KGQKEVLLRRCQQLQEHLGLAETRAEGL-HQLEADHSRM-----KREVS-A 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bird, Timothy A. APPLICANT: Bird, Timothy A. APPLICANT: Bird, Timothy A. APPLICANT: Bird, John E. APPLICANT: Sims, John E. APPLICANT: Virca, G. Duke APPLICANT: Willis, Cynthia R. TITLE OF INVENTION: Methods for Regulating Vascularization Using GEF TITLE OF INVENTION: Containing NEK-Like Kinase (GNK) FILE REPERBNE: Immunex GNK/SGNK PCT CURRENT APPLICATION NUMBER: US/09/884,001 CURRENT FILING DATE: 2001-06-18 PRIOR PLICATION NUMBER: 60/113,003 PRIOR FILING DATE: 1998-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 LEQSLDEARGSRQELVE---RIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 12.7%; Score 185; DB 9; Length 205
Best Local Similarity 26.5%; Pred. No. 4.8e-05;
Matches 88; Conservative 54; Mismatches 98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQSLVEKDSLRRQVFELTDQVCELRTQLRQLQ 282
                                               110 TES------RQVVELA--VKEHKAEILALQ 731
                       251 SQSLVEKDSLRRQVFELTDQVCELRTQLRQLQ 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19, Application US/09884001
Publication No. US20020182656A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CRCANISM: Mus musculus
US-10-017-216-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-09-884-001-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2055
                                                                                                                                                    US-10-017-216-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
```

```
APPLICANT: Yu, Xuanchuan
APPLICANT: Yu, Xuanchuan
APPLICANT: Yu, Xuanchuan
APPLICANT: Miranda, Maricar
APPLICANT: Friadla Johan
TITLE OF INVENTION: No. US20020123622Alel Human Kinases and Polynucleotides Encodi
FILE REFERENCE: LEX-0289-USA
CURRENT APPLICATION NUMBER: US.10/028,946
CURRENT FILING DATE: 2001-12-20
PRIOR FILING DATE: 2000-12-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1049 EEQVMDLEALNDELLEKERQWEAWRSVLGDEKSQFECRVRELQRMLDTEKQSRARADQRI 1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 HFHEVLRLKDEMLSLSLHYSNALQEKE----LAASRCRSLQEELYLLKQELQRANMVSS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 CELELQEQSLRTASDQ------ESGDEELNRLKEENEKLRSLTFSLAEKDI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         847 QEEMISELRQQKFYLETQAGKLEAQNRKLEEQLEKISHQDHSDKNRLLELETRLREVSLE 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 HFHEVLRLKDEMLSLSLHYSNALQEKE-----LAASRCRSLQEELYLLKQELQRANMVSS 116
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                11 QEELNQE-KGQKEVLLRRCQQLQEHLGLAETRAEGL-HQLEADHSRM-----KREVS-A 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 QEELNQE-KGQKEVLLRRCQQLQEHLGLAETRAEGL-HQLEADHSRM-----KREVS-A 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 LEQSLDEARGSRQELVE---RIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1000 ----LDEASGANDEIVQLRSEVDHLRREIT----EREMQLTSQKQTM---EALKTTCTML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            219 REKVNALQA------------------QVCELQKERDQAYSARDSAQREI
                                                                                                                                                                                                                                                                                                                                         92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2054;
                                                                                                                                                                                                                                                                                         Length 2053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.5%; Score 183; DB 12; 26.2%; Pred. No. 6.6e-05; iive 55; Mismatches 98;
                                                                                                                                                                                                                                                                                         12.5%; Score 183; DB 9; 26.2%; Pred. No. 6.6e-05; iive 55; Mismatches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1109 TES-----RQVVELA--VKEHKAEILALQ 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQSLVEKDSLRRQVFELTDQVCELRTQLRQLQ 282
FILE REFERENCE: 10147-5701
CURRENT APPLICATION NUMBER: US/10/017,216
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: US 60/242,429
PRIOR FILING DATE: 2000-10-23
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/10028946 Patent No. US20020123622A1
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 26.2%
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 26.2%
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: homo sapiens
                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                               2053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2054
                                                                                                                                                                                                                                               US-10-017-216-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-028-946-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-028-946-2
                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                        SEQ ID NO 2
                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251
                                                                                                                                                                                                                                                                                                                                                                                  δy
                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: KAPELLER-LIBERNANN, ROSana
TITLE OF INVENTION: 13245, A No. US20020160483Alel Human Myotonic Dystrophy Type Prot
TITLE OF INVENTION: Kinase and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Yu, Xuanchuan
APPLICANT: Yu, Xuanchuan
APPLICANT: Yu, Xuanchuan
APPLICANT: Wiranda, Maricar
APPLICANT: Fridale, Carl Johan
APPLICANT: Fridale, Carl Johan
APPLICANT: Fridale, Carl Johan
APPLICANT: Fridale, Carl Johan
APPLICANTO: No. 0202020123622Alel Human Kinases and Polynucleotides Encoding
FILE REFERENCE: LEX-0289-USA
CURRENT APPLICATION NUMBER: US/10/028,946
CURRENT FILING DATE: 2001-12-20
PRIOR PILING DATE: 2000-12-27
NUMBER OF SEQ ID NOS: 4
SEQ ID NOS 4
SEQ ID NO 4
LENGTH: 1958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               847 QEEMISELRQQKFYLETQAGKLEAQNRKLEEQLEKISHQDHSDKNRLLELETRLREVSLE 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HFHEVLRLKDEMLSLSLHYSNALQEKE----LAASRCRSLQEELYLLKQELQRANNVSS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----QVCELQKERDQAYSARDSAQREI 250
                                                                                                            219 REKVNALQA-------20RENDSAQREI 250
                                                                                                                                                     297 EEQVMDLEALNDELLEKERQWEAWRSVLGDEKSQFECRVRELQRMLDTEKQSRARADQRI 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 CELELQEQSLRTASDQ------ESGDEELNRLKEENEKLRSLTFSLAEKDI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 QEELNQE-KGQKEVLLRRCQQLQEHLGLAETRAEGL-HQLEADHSRM-----KREVS-A 61
                         162 LEQSLDEARGSRQELVE----RIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         907 HEEQKLELKROLTELOL----SLOERESOLTALQAARA-ALESQLRQAKTELEE----TT
                                                  248 ----LDEASGANDEIVQLRSEVDHLRREIT----EREMQLTSQKQTM---EALKTTCTML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 LEQSLDEARGSRQELVE---RIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.5%; Score 183; DB 12; 26.2%; Pred. No. 6.3e-05; iive 55; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357 TES------RQVVELA--VKEHKAEILALO 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 SQSLVEKDSLRRQVFELTDQVCELRTQLRQLQ 282
                                                                                                                                                                                                   SQSLVEKDSLRRQVFELTDQVCELRTQLRQLQ
                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/10028946 Patent No. US20020123622A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/10017216
Patent No. US20020160483A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 26.2 Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219 REKVNALQA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-10-017-216-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-028-946-4
                                                                                                                                                                                                                                                                                                                                    US-10-028-946-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
                                                                g
                                                                                                            δ
                                                                                                                                              Ω
                                                                                                                                                                                               ò
                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

Search completed: January 22, 2003, 08:52:51 Job time: 17.8952 secs

```
GenCore version 5.1.3

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 22, 2003, 08:49:35; Search time 22.6008 Seconds (without alignments)

1254.807 Million cell updates/sec

Title: US-09-767-215-2_COPY_126_420

Perfect score: 1462
Sequence: 1 ECLAGAIGSLQEELNQEKGO......TQLRQLQAEPPGVLKQEART 295

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
```

Total number of hits satisfying chosen parameters: 2
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

283224 segs, 96134422 residues

Searched:

283224

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Max.num Macch 100
Listing first 45
Database : PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

probable myosin he myosin heavy chain interaptin - slime trichohyalin - rab nuclear mitotic ap microtubule bindin centromere protein hypothetical prote centrosome associa myosin II heavy ch hypothetical prote giantin - human myosin heavy chain kinesin-related pr golgin-245 - mouse myosin heavy chain myosin heavy chain nonmuscle myosin I hypothetical prote plectin [imported] 364K Golgi complex myosin heavy chain embryonic muscle m myosin heavy chain plectin - human - human ninein - mouse - mouse plectin - rat Description giantin citron SUMMARIES A42184 T30171 T13030 S28261 T22976 T26101 T08621 G02520 A59404 S68420 JC5837 S21801 S04090 C84788 DB Query Match Length 1407  $\frac{13.9}{13.3}$ Score 191.5 188.5 188.5 187.5 186.5 185.5 185.5 185.1 185.5 180.5 180.5 179.5 178.5 177 177 175.5 175.5 202.5 181 181 Result . 9

myosin heavy chain outer dense fiber	nypotneticai prote trichohyalin - she myosin heavy chain	myosin heavy chain myosin heavy chain	yene recii procein protein kinase (EC transport protein	hypothetical prote myosin heavy chain	Synaptonemal compl SCP1 protein - rat	synapionemai compi cell-cycle-depende
B43402 T03791	133318 A40691 A24922	T18296 S06117 T38153	T14039 S67593	T21174 A61231	1481/6 S28061 S49461	PC4035
100	7	777	100	77	7 77 7	2 0
2007	1549 1940	2139 924 899	1732 1790	2020	940 946	1017
12.0	11.9	11.9	11.8	11.8	11.7	11.7
175	173.5	173.5 173 172 5	172.5	172.5	171.5	171.5
30	3 8 8 4 8 8	35 36 37	386	440	4 4 4 4 8 4	45

## ALIGNMENTS

```
Cispecies: Oryctolagus cuniculus (domestic rabbit)
Cispecies: Oryctolagus cuniculus (domestic rabbit)
Cispecies: Oryctolagus cuniculus (domestic rabbit)
Cispecies: 12-Mar-1993 #sequence_revision 01-Mar-1996 #text_change 22-Jun-1999
Cispecies: Submitted to the EMBL Data Library, December 1992
R.Fietz, M.J.; Rogers, G.E.
Submitted to the EMBL Data Library, December 1992
A:Description: Examination of the gene encoding rabbit trichohyalin.
A:Reference number: 528589
A:Reference number: 528589
A:Rocession: S28589
A:Rocession: S28589
A:Residues: 1-1407 <FIE>
A:Cross-references: EMBL:Z19092; NID:g1746; PIDN:CAA79519.1; PID:g1747
C:Comment: Trichohyalin is a protein of the medulla of the hair and of the inner root Covalent modifications to this protein include conversion of arginine to citrulline a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 VSAHFHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LELQEQSLRTASDQESGDEELNRLKEENEKLRSLTFSLAEKDILEQSLDEARGSRQE--- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----LVERIHSLR-------ERAVAAERQR-----EQYWEEK 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           797 KLREEEQILQEREEERLRRQERERKLREEEQLLQEREEERLRRQERERKLREEEQLLRQE 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQTLLQFQKSKMACQLYREKVNALQAQVCELQKERD-------QAYSARDSA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FQELRQERARKL-----REEEQLLRQEEQELRQERDRKLREEEQLLRQEEQELRQERDRK 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----EADHSRMKRE 58
                                                                                                                                                                                                                                                                                                                                   A;Introns: 46/3
C;Superfamily: trichohyalin; calmodulin repeat homology
C;Keywords: calcium binding; citrulline; EF hand; hair; tandem repeat
F;49-81/Domain: calmodulin repeat homology <EF2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247 QREISQSL--VEKDSLRRQVFE--LTDQVCELRTQLRQLQAEPPGVLKQE 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 202.5; DB 1;
Pred. No. 0.0011;
8; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 QEELNQEKGQK----EVLLRRCQQLQEHLGLAETRAEGLHQL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.9%; Sco
27.7%; Pre-
tive 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarion ...
hes 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 trichohyalin - rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

RESULT

Ricantz, V.A.; Miller, K.G. J. Cell Biol. 140, 897-910, 1998 A;Title: A class VI unconventional myosin is associated with a homologue of a microtu A;Reference number: 217588; MUID:98139549; PMID:9472041 A; Accession: T13030
A; Status: preliminary: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-1690 < LAN>
A; Cross-references: EMBL: AF041382; NID: 92773362; PID: 92773363; PIDN: AAB96783.1 microtubule binding protein D-CLIP-190 - fruit fly (Drosophila melanogaster) C; Species: Drosophila melanogaster C; Species: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 17-Nov-2000 C; Accession: T13030 A;Cross-references: FlyBase:FBgn0020503 C;Keywords: cytoskeleton A) Experimental source: strain Oregon R C; Genetics: 13.1%; 21.4%; A; Molecule type: mRNA A; Residues: 1-2168 <BOU> Best Local Similarity Similarity Query Match Best Local Simi Matches 84; - mouse Query Match 146 9 259 RESULT 4 ninein g QQ Op qq ΩD qq QΥ δ ò Qγ QY δ g C. Species: Home sapleans (man)
J. Cell Biol. 116, 1395-1408, 1992
J. Cell Biol. 116, 1395-1408, 1992
J. Cell Biol. 116, 1395-1408, 1992
J. Species: Home sapleans (man)
A. Reference number: AA2184, MUID:92176238; PMID:1541635
A. Reference number: Saliki, I. L. Wu, C. W.
A. Molecule Type: MRN
A. Molecule Type: MRN
A. Molecule Type: MRN
A. Molecule 11-210, CGOPA
A. Molecule Type: MRN
A. Molecule Sapleans extracted from NCBI Dackbone (NCBIN:8575, NCBIP:83760)
A. Title: Molecule Type: MNN
A. Molecule Type: MN
A. Molecule Type: MNN
A. Molecule Typ 15; |:||::|: | | ||:||:472 QSSISNLSQAKEELEQASQAHGARLTAQVASLTSELTTLNATIQQQ-DQELAGLKQQAKE 530 --NEKLRSLIFSLAEKDILEQSLDEARGSRQELVERIHSLRER 186 531 KQAQLAQTLQQQEQASQGLRHQVEQLSSSLKQK---EQQLKEV-AEKQEATRQDHA-QQL 585 AVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSA 246 ATAAE-EREASLRERDAALKOLE----ALEKEKAAKLEI----LQQQLQVANEARDSA 634 362 LEKELSAALQDKKCLEEKNEILQGKLSQLEEHLS------QLQDNPPQEKGEVLGD 411 412 VLOLETLKQEAATLAANNTOLQARVEMLETERGQQEAKLLAERGHFEEEKQQLSSLITDL 471 LQEELN---QEK----GOKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAH 62 --LHYSNALQEKELAASRCRSLQEELYL--Length 2101; ---TDQVCELRTQLRQLQ 282 104; 13.3%; Score 194; DB 2; 26.6%; Pred. No. 0.0049; tive 49; Mismatches 104 mitotic apparatus protein NuMA - human 247 QREISQSLVEKDSLRRQVFEL--FHEVLRLKDEMLSLS----Best Local Similarity 26.6 Matches 93; Conservative Query Match 10 63 187 586 146 g g ò d δ g ô g δ

Length 1690;

.; 7

Score 191.5; DB Pred. No. 0.0053;

```
R; Bouckson-Castaing, V.; Moudjou, M.; Ferguson, D.J.P.; Mucklow, M.; Belkaid, Y.; Mil J. Cell Sci. 109, 179-190, 1996
A; Title: Molecular characterisation of ninein, a new coiled-coil protein of the central R; Reference number: 220751; MUID: 96431720; PMID: 8834802
A; Reference number: T30171
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A)Cross-references: EMBL:U40342; NID:g1113864; PID:g1113865; PIDN:AAA83234.1
A)Experimental source: strain C57B1/6
A;Note: localised specifically in the pericentriolar matrix of the centrosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1780 KSQLAVSQAKVQDLEDVLQNVNLQMAEIESDLQVTRQEKEAVKQEVMSLHRQLQNAIDKD 1839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206 -LQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSAQREIS-----QSLVEKD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 RMKREVSAHFHEVLRLKDEMLSLSLHYSNAL-QEKELAASRCRSLQEELYLLKQEL---- 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AIGSLQ-EELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGL------HQLEADHS 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEKLRSLTFSLAEKDILEQSLDEARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2168;
                                                                                                                                                                                                                                     22-Oct-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.1%; Score 192; DB 2; Length 21 24.4%; Pred. No. 0.0065; Live 68; Mismatches 112; Indels
SLRRQVFELTDQVCELRTQLRQ -----LQAEPPGVLKQEAR 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 -QRANMVSSCELELQEQSLRT-ASDQES--GDEELNRLKE-
                                                                                                                                                                                                         C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision
C;Accession: T30171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
```

Qy         120 ELQEQSLRTASDQESGDEELNRLK	RESULT 6 T22976 hypothetical protein F59A2.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Accession: T22976; T23157 R;Lightning, J. Submitted to the EMBL Data Library, June 1994 A;Reference number: 219645 A;Recession: T22976 A;Status: preliminary: translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-1133 <will> A;Residues: 1-1133 <will> A;Cross.references: EMBL:234801; PIDN:CAA84332.1; GSPDB:GN00021; CESP:F59A2.6 A;Experimental source: clone F59A2 B;Burton, J. S;Ubmitted to the EMBL Data Library, October 1995</will></will>	A; Reference number: 219700 A; Accession: T23157 A; Statute continuary; translated from GB/EMBL/DDBJ A; Statute: preliminary; translated from GB/EMBL/DDBJ A; Statute: preliminary; translated from GB/EMBL/DDBJ A; Residues: 1-1133 - 412> A; Residues: 1-1133 - 412> A; Residues: 1-1131 - 412> A; Residues: L-1131 - 412> A; Residues: Residue Resid
GSLQBELNOEKGQKEVLLRRCQQLQEH	DD	RESULT 5  Sepacian Contromere Dictor Company Contromere 312K protein; kinesin-related protein CENP-E C; Species: Ocartromere 312K protein; kinesin-related protein CENP-E C; Species: Hown sapiens (man) C; Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 19-Jan-2001 N; Yelle: CENP-E is a putative kinetochore motor that accumulates just before mitosis. A; Reference number: 528261; MUID:93024922; PMID:140697 A; References: EMBL:215005; NID:929864; PIDN:CAA7877.1; PID:929865 C; Genetics A; Genetics A; Cross-references: CBB:5164; OMIM:117143 A; Map postition: 4424-4425 C; Superfamily: centromere protein E; kinesin motor domain homology C; Superfamily: centromere protein E; kinesin motor domain homology ckMov-1 C; Superfamily: centromere protein E; kinesin motor domain homology ckMov-1 C; Superfamily: centromere protein E; kinesin motor domain homology ckMov-1 C; Superfamily: centromere protein E; kinesin motor domain homology ckMov-1 C; Superfamily: centromere protein E; kinesin motor domain homology ckMov-1 C; Reywords: APP: colled coll: #status predicted col-1 C; P33/Romain: colled coll: #status predicted col-2 C) Signerian incleotide-binding motif A cl-100p) F; 92/Binding site: APP (Lys) #status predicted col-2 C) Restrict Conservative SO: Mismatches 110; Indels #1; Fill

```
Query Match
Best Local Similarity
Matches 88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :1
QT 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plectin - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125
                     55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ōλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                       Q
                                                                                                                                                                                                                                                                                                             QQ
                                                                                                                                                                                                                                                                                                                                                                    Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        οğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δy
                  δy
                                                                         дq
                                                                                                                                      δ
                                                                                                                                                                                                                                                       δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             read
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Species: Homo sapiens (man)
C; Date: 11-Jun-1999 fsequence_revision 11-Jun-1999 ftext_change 21-Jul-2000
C; Accession: T08621
S: Mack, G.J.; Rees, J.; Sandblom, O.; Balczon, R.; Fritzler, M.J.; Rattner, J.B.
Arthritis Rheum. 41, 551-558, 1998
Arthritie: Autoantibodies to a group of centrosomal proteins in human autoimmune sera A; Reference number: 216462; MUID:98165428; PMID:9506584
A; Reference number: 216462; MUID:98165428; PMID:9506584
A; Recession: T0862
A; Accession: T0862
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Rolecule type: mRNA
A; Residues: 1-2442 cMAC>
A; Residues: 1-2442 cMAC>
A; Rossers references: EMBL:AF022655; NID:q2832236; PIDN:AAC06349:1; PID:g2832237
A; Experimental source: cell line HeLa
                                          Typothetical protein W02B8.2 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Toact-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C.Accession: T26101
R.Sims, M.
Submitted to the EMBL Data Library, October 1996
A.Accession: T26101
A.Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 FLQFSAKIIBETMSELKLKNARLERELSEKEELVKVTKEELQELQKTVTQAMGDSEQATK 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LQRANMVSSCELELQEQSLRTASDQESGDEELNRLKEENEKLRSLT----FSLAEKD- 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ILEQSLDEAR-----GSRQELV----ERIHSLRERAVAAERQREQ--Y 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WEEKEQTLLQFQKSKMACQLY -- REKVNALQAQVCELQKERDQAYSARDSAQR--EISQS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSRMKREVSAHFHEVLRLKDEM - - LSLSLHYSNALQEKELA - - ASRCRSLQEELYLLKQE 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 LQEELNQEKGQKEVLLRRCQQL------QEHLGLAETRAEG----LHQLEAD 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2442,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 12.8%; Score 187.5; DB 2; Length Best Local Similarity 23.9%; Pred. No. 0.0064; Matches 78; Conservative 70; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.8%; Score 186.5; DB 2; 24.6%; Pred. No. 0.015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               centrosome associated protein CEP250 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L-VEKDSLRRQVFELTDQVCELRTQL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ::| ||: | :|:|:|:::
VEIELRSLKLLAEEREEQIDELKSRV 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 24.6%
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
T08621
RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΩQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
A;Gene: PLEC1
C;Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protei
F;68-283/Domain: alpha-actinin actin-binding domain homology <ACT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-4574 <MCL>
A;Cross-references: EMBL:U53204; NID:g1477645; PIDN:AAB05427.1; PID:g1477646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 21-Dec.1996 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999
C;Date: 21-Dec.1996 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999
C;Accession: G02520
R;McLean, W.H.I.; Smith, F.J.D.
submitted to the EMBL Data Library, March 1996
A;Reference number: H01385
A;Accession: G02520
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2406 SAEAERLKLRVAEMSRAQARAEEDAQRFRKQAEEIGEKLHRTELATQEKVTLVQTLEIQR 2465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2466 QQSDHDAER---LREAIAELEREKEKL--QQEAKLLQLKSEEMQTVQQEQLLQETQALQQ 2520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2293 LQEEAEKMKQVAEEAARLSVAAQEAARLRQLAEEDLAQQRALAEKMLKEKMQAVQEATRL 2352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----SLRTAS---DQESGDEELNRLKEE----NEKLRSLTFSLAEKDILEQSLDEAR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 GSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMAC----QLYREKVNALQ 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQVCE----LQKER----- Z60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQEL - - QRANMVSSCELELQEQ - - - 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----LQRANMVSSCELELQEQSLRTASDQESGDEELNRLKEENEKLRSLTFSLA-EKDI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAHFHEVLRL 69
                                                                                                                                                                                                                                                                       -----EVADLRAAAVKLSALNEALALDKVG
                                                                                                                                                                                                                                                                                                                                    162 LEQSL-----DEARGSRQELVERI-HSLRERAVAAERQREQYWEEKEQTLLQFQKSKMA
                                                                                                                                                                                                                                                                                                                                                                          505 GOKEEQQEELHLAVRERERLQEMLMGLEAKOSESLSELITLREALESIHLEGELLRQEQT
                                                                                     -MKREVSAHFH----EVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.7%; Score 185.5; DB 2;
ilarity 27.0%; Pred. No. 0.032;
Conservative 41; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 CQLYREKVNALQAQVCELQKERDQAYSARDSAQREISQ-
                                                                                                                                                                                                                                                           565 EVTAALARAEQ-SIAELSSSENTLKT
```

261 -- RRQVFELTDQVCELRTQLRQLQAE 284

δ

1 ECLAGAIGSLQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLH------QLEADHSR 54

δ

g

```
A Molecule type: mRNA
A; Residues: 1-3187 <TOK>
A; Residues: 1-3187 <TOK>
A; Residues: 1-3187 <TOK>
A; Cross-references: DBBJ:D25543; NID:9516825; PIDN:BAA05026.1; PID:9516826
C; Comment: This protein plays a role in the formation and maintenance of the characte C; Superfamily: glantin
E; 49-549, 624-1176, 1238-1707, 1763-3114/Domain: coiled-coil leucine zipper #status pred F; 3165-3187/Domain: membrane anchor #status predicted <MAD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C) Accession: JC5837
R:Toki, C.; Fujiwara, T.; Sohda, M.; Hong, H.S.; Misumi, Y.; Ikehara, Y.
R:Toki, C.; Fujiwara, T.; Sohda, M.; Hong, H.S.; Misumi, Y.; Ikehara, Y.
Cell Struct. Funct. 22, 565-577, 1997
A; Tille: Identification and characterization of rat 364-kDa Golgi-associated protein A; Reference number: JC5837; MuID:98093490; PMID:9431462
A; Accession: JC5837
A; Accession: JC5837
A; Accession: JC5837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           364K Golgi complex-associated protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        455
    117 CELELQEQSLRTASDQ-------ESGDEELNRLKEENEKLRSLTFSLAEKDI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----KEVLLRRCQ---QLQEHLGLAETRAEGLHQ 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               499 AEAEEEIQALTAHRDEIQRKFDALRNSCTVITDLEEQLNQLTEDNAELNNQNFYLSKQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |||| |: |:||: :|| :|| :|| :|| :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :|: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :|: :||: :|: :||: :|: :||: :||: :||: :||: :||: :||: :|: :||: :|: :||: :||: :||: :||: :|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----LEADHSRMKREVSAHFHEVLRLKDEMLSLSLHYSNALQEK---ELAASRCRSLQEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260 QLQLLEAEHSTLRNTMEAERQE-------SKILMEKVELEMAERK-----EE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYLLKQELQRANMVSSCELELQEQSLRTASDQE-----SGDEEL----NRLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENEKLRSLTFSLAEK - - DILEQSLDEARGSRQELVERIH - - SLRERAVAAERQREQYWEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 KEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSAQREISQSLVEKDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----ALLLSSLELEEL
                                                                                                                         HFHEVLRLKDEMLSLSLHYSNALQEKE-----LAASRCRSLQEELYLLKQELQRANMVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                    162 LEQSLDEARGSRQELVE---RIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---- QVCELQKERDQAYSARDSAQREI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Length 3187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 12.7%; Score 185; DB 2; I
Local Similarity 25.3%; Pred. No. 0.023;
les 82; Conservative 54; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQSLVEKDSLRRQVFELTDQVCELRTQLRQLQ 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | : :| ::| | ::| | :1:| RAENEKLCSRITLLEAQNRAGEAD 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 RRQVFELTDQVCELRTQLRQLQAE 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 IGSLQEELNQEKGQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REKVNALQA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48
                                                                                                                                                                                                  448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          456
                                                                                                                     62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                        g
                                                                                                                 Qγ
                                                                                                                                                                                          QQ
                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                               οq
                                                                                                                                                                                                                                                                                                                                                                                                                                οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         citron - mouse
citron - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C;Accession: S66420
R;Madaule, P.; Furuyashiki, T.; Reid, T.; Ishizaki, T.; Watanabe, G.; Morii, N.; Narumiy FEBS Lett.: 377, 243-248, 1995
A;Accession: S68420
A;Accession: S68420
A;Reference number: S68420; MUID:96128238; PMID:8543060
A;Accession: S68420
A;Accession: S68420
A;Accession: S68420
A;Accession: S68420
A;Accession: S68420
A;Cession: S68420
A;Cession: S68420
A;Cession: S68420
A;Cessiones: L1597 AAAD
A;Cessiones: L1597 AAAD
A;Cross-references: EMBL: U39904; NID:91079733; PIDN:AAC52341.1; PID:91079734
C;Superfamily: protein kinase C zinc-binding repeat homology; pleckstrin repeat homology
C;Keywords: alternative splicing
F;931-979/Domain: protein kinase C zinc-binding repeat homology <KZ2>
                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome loca
                                                                                                                                                                                  plectin {imported} - human cispecies: Homo saplens (man) C;Species: Homo restance rounds (man) Psilu, C.G.; Maeroker, C.; Castanon, M.J.; Hauptmann, R.; Wiche, G. Proc. Natl. Acad. Sci. U.S.A. 93, 4278-4283, 1996 A;Title: Human plectin: organization of the gene, sequence analysis, and chromosome lock A;Title: Human plectin: organization of the gene, sequence analysis, and chromosome lock A;Teference number: C59404 MUID:96210632; PMID:8633055 A;Cession: C59404 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-4684 <STO> A;Cross references: GB:CAA91196; NID:g1296662; PIDN:CAA91196.1 C;Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2403 LQEEAEKMKQVAEEAARLSVAAQEAARLRQLAEEDLAQQRALAEKMLKEKMQAVQEATRL 2462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SFLSEKDSLLQRERFIEGEKAKLEQLEQDEVAKAQQLREEQQRQQQQQQQQRQERQRLVASME 2690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 KDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQEL--QRANMVSSCELELQEQ--- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 QEELNQE-KGQKEVLLRRCQQLQEHLGLAETRAEGL-HQLEADHSRM-----KREVS-A 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 LQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAHFHEVLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2463 KAEAELLO------QOKELAQEQARRLQEDKEQMAQQLAEETQGFQRTLEAERQRQLEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----SLRTAS---DQESGDEELNRLKEE----NEKLRSLTFSLAEKDILEQSLDEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMAC----QLYREKVNALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQVCE----LQKER-------DQAYSARDSAQREISQSLVEKDSL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 4684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 12.7%; Score 185.5; DB 2; Best Local Similarity 27.0%; Pred. No. 0.032; Matches 88; Conservative 41; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 12.7%; Score 185; DB 2; L. Best Local Similarity 26.5%; Pred. No. 0.011; Matches 88; Conservative 54; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2691 EARRQHEAEEGVRRKQEELQQLEQQ 2716
2581 EARRROHEAEEGVRRKQEELQQLEQQ 2606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --RRQVFELTDQVCELRTQLRQLQAE 284
```

125

Qγ

g

ò

엄

2516 171 2576 227 2631 261

셤 ò g

g

à

Q

ð

RESULT 11 S68420

ò

7;

```
A;Cross-references: EMBL:U41994; NID:g1123047; PID:g1123050; PIDN:AAA83454.1; CESP:F5
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein F59A6.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
          C; Species: Naegleria fowler:
C;Date: 20.Apr-2000 #sequence_revision 20.Apr-2000 #text_change 20.Apr-2000
C;Accession: T47237
R;Shaw, D.R.; Sullivan, P.K.; Marciano-Cabral, F.; Ennis, H.L.
A;Description: Codon usage in Naegleria fowler:
A;Reference number: 224413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 KREVSAHFHEVLRL------KDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQEL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 EQSLIDEARGSRQELVERIHSL ---RERAVAAERQREQYWEEKEQTILIQFQKSKMACQLY 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268 TQKKNDADNRVKQLESELQGVKSERDRLNKDLNNTSGDMNGLKRQLDESNNLVAKLKAEI 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 VNLLEDDLKHHOSOIRILONKCSTLEMEKQTLQETIORAQDDKKETETELESSRSRLHVL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 MLSLSLHYSNALQEKELAASRCRSLQEELYLLKQEL----QRANMVSSCELELQEQSL-- 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----RLKEENEKLR----SLTFSLAEKDIL 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 STSLDSKVKSLEDKIRELTALLETERSSKTDLDKKRSKMDKEVKRLAQQLQETEQALKGE 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 IGSLQEELNQEKGQKEVLLRRC------QQLQEHLGLA-ETRAEGLHQLEADHSR---M 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 ELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAHFHEVLRLKDE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 REKVNALQAQVCELQKERDQAYSARDSAQREISQSIVEKDSLRRQVFELTDQVCELRTQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1286;
                                                                                                                                                                                                                                                                                                                                                                                Length 746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
myosin II heavy chain [imported] - Naegleria fowleri (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: T16507
R;Nhan, M.
submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid F59A6.
A;Reference number: Z18526
A;Accession: T16507
                                                                                                                                                                                                       A,Accession: T47237
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1.878A>
A,Cross-references: EMBL:U43192; PIDN:AAB01786.1
A,Experimental source: strain LEE mp; cell type amoeba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 182.5; DB 2;
Pred. No. 0.012;
9; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 12.6%; Score 184; DB 2; Best Local Similarity 21.2%; Pred. No. 0.0058; Matches 65; Conservative 73; Mismatches 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: CESP:F59A6.5
A;Introns: 35/3; 335/3; 685/3; 973/3; 1097/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --RTASDQESGDEELN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-1286 <NHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
es 76; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ::|| :
328 QKLQKD 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RQLQAE 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: CESP: F59A6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                        A; resultues: 1-1999, Sub. 175, 244-249, 1991
R; Sun, W.; Chantler, P.D.
Biochem. Biophys. Res. Commun. 175, 244-249, 1991
R; Sun, W.; Chantler, P.D.
Biochem. Biophys. Res. Commun. 175, 244-249, 1991
A; Title: A unique cellular myosin II exhibiting differential expression in the cerebral A; Reference number: PN0013
A; Recession: PN0013
A; Molecule type: mRNA
A; Residues: 1914-1998, I' < SU2>
A; Residues: actin binding: ATP; coiled coil; hydrolase; methylated amino acid; nucleotid C; Superfamily: myosin motor domain homology < AMOT>
F; 84-763/Domain: myosin motor domain homology < AMOT>
F; 74-181/Region: nucleotide-binding motif A (P-loop)
F; 74-181/Region: actin binding *status predicted
F; 836-1999/Domain: coiled coil *status predicted < CO1>
F; 836-1999/Domain: coiled coil *status predicted
F; 836-1999/Domain: coiled coil *status predicted
F; 135/Addified site: ATP (Lys) *status predicted
F; 135/Addified site: ATP (Lys) *status predicted
F; 1916/Binding site: ATP (Ser) (covalent) *status predicted
F; 1943/Binding site: phosphate (Ser) (covalent) *status predicted
                                                       N'Alternate names: myosin II
N'Contains: myosin ATPase (EC 3.6.4.1)
N'Contains: myosin ATPase (EC 3.6.4.1)
C'Species: Rattus norvegicus (Norway rat)
C'Species: Rattus norvegicus (Norway rat)
C'Accession: S21801; PN0013; S18134
C'Accession: S21801; PN0013; S18134
TR:Sun W.; Chartler, P.D.
J. Mol. Biol. 224, 1185-1193, 1992
A;Title: Cloning of the cDNA encoding a neuronal myosin heavy chain from mammalian brain A;Reference number: S21801; MUID:92235856; PMID:1569576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ٠.
و
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |: |: ::::|: : | |:| ||:| ||:| LEHEKSKLGREGQVWEEKTLEVORGAMKAQFERDLQGRQDDS 1580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1758 QIDQINADLNLERGHAQKNENARQQLERQNKELKVKLQEMEGTVKSK-----YKASITAL 1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1813 EAKIAQLEEQLDNETKERQAACKQVRRTEKKLKDVLLQVDDERRNAEQYKDQADKASTRL 1872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EELNRLKEE------NEKLRSLTFSLAEKDILEQSLDEARGSRQELVERIHSL-- 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -- RERAVAAERQREQYWEEKEQTLLQFQ-----KSKMACQLYREKVNAL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QAQVCELQKERDQAYSARDSA-----QREISQSLVEKDSLRRQVFELTDQVCELRTQL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----EELYLLKQELQRANMVSSCE-LELQEQSLRTASDQESGD 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----AEGLHQLEADHSRMKREVSAHFHEVLRLKDEMLSLSLHYSNALQEKELAASRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.6%; Score 184.5; DB 1;
19.4%; Pred. No. 0.015;
Live 77; Mismatches 119;
                                  myosin heavy chain, neuronal [similarity] - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 LQEELNQEKGQKEVLLRRCQQLQEHLGLAETR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                      A; Accession: S21801
A; Molecule type: mRNA
A; Residues: 1-1999 <SUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 71; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :11: :
KQLKRQ 1878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSLQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RQLOAE 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

Search completed: January 22, 2003, 08:54:36 Job time: 31.6008 secs

THIS PAGE BLANK (USPTO)

٦

```
GenCore version 5.1.3

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 22, 2003, 08:49:35 ; Search time 11.4987 Seconds
```

(without alignments)
1064.082 Million cell updates/sec
Title: US-09-767-215-2\_COPY\_126\_420
Perfect score: 1462

Perfect score: 1462 Sequence: 1 ECLAGAIGSLQEELNQEKGQ......TQLRQLQAEPPGVLKQEART 295 Scoring table: BLOSUM62

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Q9bx16 homo sapien	mus m	homo	7 homo	mus m	Q9epy0 rattus norv		P37709 oryctolagus		rattr		рошоц	mus m		bos t	rattu	homo sa	gallı	homo	рошо	rattı	homo	homo	рошо	рошо	homo	ovis	P12847 rattus norv		36 sacch	in	- 60	Q03410 rattus norv
SUMMARIES	ID	AR	CARE_MOUSE	CARB_HUMAN	CARA_HUMAN	CARA_MOUSE	CAR9_RAT	CAR9_HUMAN	TRHY_RABIT	CENE_HUMAN	MYHA_RAT	PLE1_CRIGR	PLE1_HUMAN	CTRO_MOUSE	CTRO_HUMAN	MYHA_BOVIN	PLE1_RAT	MYHA_HUMAN	MYH9_CHICK	MY HD_HUMAN	MYH3_HUMAN	MYH9_RAT	SCP1_HUMAN	GOG4_HUMAN	MYH8_HUMAN	MYH4_HUMAN	MYH9_HUMAN	TRHY_SHEEP	MYH3_RAT	CENF_HUMAN	USO1_YEAST	SCP1_MESAU	Ξ.	SCP1_RAT
	Length DB	1004	σ.	_	~	_		'n	_	<u>~</u>	ıo	m		7			7	'n	σ.	m	0	_	ເດ	0	7	σ.	0	æ	0	0	0	845 1	<u>س</u>	7
di	Query Match L	0							13.9																							11.7		
	Score	1462	1166	396.5	329.5	322.5	283.5	274.5	202.5	188.5	186.5	186	185.5	185	183	182	181.5	181	180.5	179.5	178.5	177	176.5	176	175.5	174	174	173.5	173.5	173.5	172.5	171.5	171.5	171.5
	Result No.	-	2	3	4	S	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

P10587 gallus gall P35749 homo sapien P55937 mus musculu Q00547 mus musculu Q28628 oryctolagus P0559 acanthamoeb P35458 gallus gall P11516 mus musculu P48678 mus musculu P48679 rattus norv Q11102 caenorhabdi P54697 dictyosteli
MYHB_CHICK MYHB_HUMAN G160_MOUSE G160_MOUSE G180_MOUSE AKA9_RABIT MYSN_ACACA MYSN_ACACA LAMC_MOUSE LAMC_MOUSE LAMA_MOUSE LAMA_MOUSE LAMA_RAT YLI7_CAEEL MYSJ_DICDI
лапапапапап
1978 1972 1325 1987 1087 1224 574 665 665
11.7 11.7 11.6 11.6 11.6 11.6 11.5 11.5
171.5 171 170.5 170 170 170 168.5 168.5 168.5 168.5 168.5
88888888444444488888888888888888888888

## ALIGNMENTS

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 14 (CARD-containing MAGUK protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Cervix, and Colon;
Strausberg R.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Activates NF-kappaB via Bcl10 and IKK. Stimulates the phosphorylation of Bcl10.
-!- SUBUNIT: CARD14 and Bcl10 bind to each other by CARD-CARD
                                                                                                                                                                                                                               [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. MUDINE-21192234; PubMed-11278692; Bertin J., Wang L., Guo Y., Jacobson M.D., Poyet J.-L., Srinivasula S.M., Merriam S., Distefano P.S., Alnemari E.S.; Arinivasula and CARD14 are novel caspase recruitment domain (CARD)/membrane-associated quanylate kinase (MAGUR) family members that interact with Bc110 and activate NF-kappaB."; J. Biol. Chem. 276:11877-11882(2001).
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=21255663; PubMed=11356195;
Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.;
"Carmal, a CARD-containing binding partner of Bell0, induces Bell0
phosphorylation and NF-kappaB activation.";
FEBS Lett. 496:121-127(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.; FEBS Lett. 505:198-198(2001).
                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                              1004 AA
                                PRT;
                                            Q9BXL6; Q9BVB5;
115-UNN-2002 (Rel. 41, Created)
115-UNN-2002 (Rel. 41, Last sand
15-JUN-2002 (Rel. 41, Last and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-740 FROM N.A.
                                STANDARD;
                                                                                                                                             CARD14 OR CARMA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interaction.
                                                                                                                                 (Carma 2)
                                CARE_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERRATUM.
                 CARE_HUMAN
RESULT 1
```

```
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARB_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DI AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 αd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                   ;
0
modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 14 (Bcl10-interacting MAGUK protein
                                                                                                                                                                                                                                         DYEASEPLEKAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTD
GYRKLLQDLEAK -> SRARPLLSPGLLMGTVAAGGYTQAD
FYSPRRCSTLGWASALSWADVKRSAHL (IN REF. 2;
AAH01326).
                                                                                                                                                                                                                                                                                                                                                                                                                 186 AHFHEVLRIKDEMISISIHYSNALQEKELAASRCRSLQEELYLLKQELQRANWYSSCELE 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 HSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    365
                                                                                                                                                                                                                                                                                                                                                                               ECLAGAIGSLQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVS 185
                                                                                                                                                                                                                                                                                                                                                                                                     AHFHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANWVSSCELE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQEQSLRTASDQESGDEELNRLKEENEKLRSLTFSLAEKDILEQSLDEARGSRQELVERI 180
                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Bimp1, a MAGUK family member linking protein kinase C activation to
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                         1 ECLAGAIGSLQEELNQEKGQKEVLERRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLRQLQAEPPGVLKQEART 295
                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                             Length 1004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-21391892; PubMed-11387339;
MCAllister-Lucas L.M., Inohara N., Lucas P.C., Ruland J., Ber
Lii Q., Chen S., Chen F.F., Yamaoka S., Verma I.M., Mak T.W.,
Nunez G.;
                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                       7469B8B56BE06073 CRC64;
                                                                                                                                                                                                           COILED COIL (POTENTIAL).
                                                                                                                                 PROSITE; PS50209; CARD: 1.
PROSITE; PS50209; CARD: 1.
PROSITE; PS500106; GUANYLATE_KINASE_1; FALSE_NEG.
PROSITE; PS50106; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
Coiled coil.
DOMAIN 128 409 COILED COIL (POTENTIAL DOMAIN 568 658 PDZ.
DOMAIN 858 990 GUANYLATE KINASE.
CONFLICT 619 671 DYEASEPLFRAVLEDTILEEAN
                                                                                                                                                                                                                                                                                                           ; Score 1462; DB 1;
; Pred. No. 3.8e-71;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          999 AA.
                                         EMBL, AF322642, AAG53403.1; -.
EMBL, AV032927, AAK54453.1; -.
EMBL, BC018142.3; -.
EMBL, BC001326, AAH18142.1;
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
SMART; SM00072; GuKC; 1.
                                                                                                                                                                                                                                                                                                             100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 295; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                        1004 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2) (Bimp2).
CARD14 OR BIMP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARE_MOUSE
                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARE_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241
                                                                                                                                                                                                                                                                                                                                                                                 126
                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                       365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246 SRERSLKMASNLEPQGEELNRLKEENEKLRSMTFSLVEKDILEQSLDEARESKOELVDRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ECLAGAIGSLQEELNQEKGOKEVLLRRCQOLQEHLGLAETRAEGLHQLEADHSRMKREVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 LQEQSLRTASDQESGDEELNRLKEENEKLRSLTFSLAEKDILEQSLDEARGSRQELVERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 SARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLRQLQAEPPGVLKQEA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             736 743 QAQQQLLA -> HLLEDHRS (IN R
999 AA; 113496 MW; D18350DA12430255 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.8%; Score 1166; DB 1;
79.9%; Pred. No. 2.1e-55;
iive 29; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfan; PF00595; PD2; 1.
PROSITE; PS50209; CARD; 1.
PROSITE; PS00856; GUANYLATE_KINASE_1; FALSE_NEG.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PDZ; 1.
Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GUANYLATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 41, Created)
(Rel. 41, Last sequence update)
Bc110-mediated NF-kappa B induction."; J. Biol. Chem. 276:30589-30597(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF363457; AAK60137.1; -. EMBL; BC004692; AAH04692.1; -. InterPro; IPR000619; Guanylate_kin. InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDZ.
                                                         SEQUENCE OF 82-743 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     411
655
986
743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                            TISSUE=Breast;
                                                                                                   Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARB_HUMAN
Q9BXL7;
15-JUN-2002 (
15-JUN-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Sim
Matches 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
```

m

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: Detected in adult peripheral blood leukocytes, thymus, spleen and liver. Also found in promyelocytic leukemia HL-60 cells, chronic myelogenous leukemia K562 cells, Burkitt's lymphoma Raji cells and colorectal adenocarcinoma SW480 cells. Not detected in HeLa S3, Molt-4, A549 and G431 cells. Burkitt's CHISANIN: CAND DOWAIN. SIMILARITY: CONTAINS 1 CARD DOWAIN.
SIMILARITY: CONTAINS 1 CARD DOMAIN.
SIMILARITY: CONTAINS 1 G1AND LATE KINASE-LIKE DOMAIN.
PROSITE, Pfam or SMART.
                  (CARD-containing MAGUK protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.; FEBS Lett. 505:198-198(2001).
-!- FUNCTION: Activates NF-kappaB via Bcl10 and TKK. Stimulates the phosphorylation of Bcl10.
-!- SUBUNIT: CARD11 and Bcl10 bind to each other by CARD-CARD
                                                                                                                                                                                          Bertin J., Wang L., Guo Y., Jacobson M.D., Poyet J.-L., Srinivasula S.M., Merriam S., DiStefano P.S., Alnemri E.S.; "CARD11 and CARD14 are novel caspase recruitment domain. (CARD)/membrane-associated quanylate kinase (MAGUK) family members that interact with Bcll0 and activate NF-kappaB."; J. Biol. Chem. 276:11877-11882(2001).
                                                                                                                                                                                                                                                                                                                                                     Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J., "Carmal, a CARD-containing binding partner of Bcll0, induces Bcll0 phosphorylation and NF-KappaB activation."; FEBS Lett. 496:121-127(2001).
                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      > L (IN REF. 2).
913A4B015D2B36CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.1%; Score 396.5; DB 1;
34.0%; Pred. No. 2.2e-14;
... 1ve 66; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GUANYLATE KINASE.
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 11 (CARD-co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50209; CARD; 1.
PROSITE; PS00856; GUANYLATE_KINASE_1;
PROSITE; PS50052; GUANYLATE_KINASE_2;
PROSITE; PS50106; PDZ; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew; HGNC:16393; CARD11.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=21255663; Pubmed=11356195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ٨
                                                                                                                                                                             MEDLINE=21192234; PubMed=11278692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132641 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF322641; AAG53402.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103
442
748
1133
808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00228; PDZ; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                           SEQUENCE FROM N.A.
                                   3) (Carma 1).
CARD11 OR CARMA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11
123
673
966
808
1147
                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coiled coil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                              ERRATUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
```

9

Gaps

23;

Matches 102; Conservative

Query Match Best Local Similarity

Length 1147; Indels

```
ACOLOGNO TO THE TAIL TO THE TOWN TO THE STOCK TO THE TOWN THE TOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21292987; PubMed-11259443; Wang L., Guo Y., Huang W.-J., Ke X., Poyet J.-L., Manji G.A., Merriam S., Glucksmann M.A., Distefano P.S., Alnemri E.S., Bertin J.; "CARDIO is a novel caspase recruitment domain/membrane-associated guanylate kinase family member that interacts with Bcl10 and activates
                                                                                                                                                                                                                                                                              240 RNQSLKLKNDIENRPKKEQVLELERENEMLKTKNQELQSIIQAGKRSLPDSDKAILDILE 299
                                                                                                                                                           360 TVMLQLEEVERERDQAFHSRDEAQTQYSQCLIEKDKYRKQIRELEEKNDEMRIEMVRREA 419
                                                            LMNEVIKLQQQMKAKDLQRCELLARLRQLEDEKKQMTLTRVE-LLTFQERYYKMKEERDS 182
                                                                                                                        HFHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELEL 121
                                                                                                                                                                                                                                              ---AEKDILE 163
                                                                                                                                                                                                                                                                                                                                                                    QSLDEARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVN 223
                                                                                                                                                                                                                                                                                                                                                                                                                             300 HDRKEALEDROELVNRIYNLQEEARQAEELRDKYLEEKEDLELKCSTLGKDCEMYKHRMN 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 10 (CARD-containing MAGUK protein
3 LAGAIGSLQEELNQEKGQKEVLLRRCQQLQ-EHLGLAETRAEGLHQLEADHSRMKREVSA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.; Carmal, a CARD-containing binding partner of Bcil0, induces Bcil0 phosphorylation and NF-kappaB activation."; FEBS Lett. 496:121-127(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.;
FEBS Lett. 505:198-198(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         224 ALQAQVCELQKERDQAYSARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLRQLQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                              QEQSLRTASDQES -- GDEELNRLKEENEKLRSLTFSL -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1032 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol. Chem. 276:21405-21409(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21255663; PubMed=11356195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4AN STANDARD; PI
Q9UGR5; Q9UGR6; Q9Y3H0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3) (Carma 3).
CARD10 OR CARMA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARA_HUMAN
09BWT7; 09U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NF-kappa B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERRATUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARA_HUMAN
                                                                                                                        62
                                                                                                                                                                                                                                           122
                                                                                                                                                                                                                                                                                                                                                                    164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                          Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                              qq
                                                                                                                                                                                                                                           Ω
                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                    Q
```

us-09-767-215-2\_copy\_126\_420.rsp

```
RA COGELL C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T., RA Polilips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T., RA SCOLT C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L. Socatt C.E., Schra H.K., Skuce C.D., Smalley S., Smith M.L. Socatund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M., Walliam S.A., Walliam S.M., Willey D.L., Milley D.L., Milley D.L., Milliams S.A., Williamson H., Wilmer T.E., Wilming L., Milliams S.A., Williamson H., Walmer T.E., Wilming L., Milliams S.A., Williamson H., Walmer T.E., Wilming L., RA B. S., Rawasaki K., Sasaki T., Asakwas S., Kudoh J., Shimizu N., RA B. S., Rawasaki K., Sasaki T., Asakwas S., Kudoh J., Shimizu N., RA B. Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T., RA B. Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H., Ra B., S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H., Ra B., Chens S., Lin S.-P., Loh P., Walaj E., Nguyen T., Pan H., Ra Ann G., Shaull S., Sloan D., Song L., RA Ann M., Zhang G., Wang Z., White J., Willer N., Winx P., Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J., Ra Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J., Hinds K., Latreille P., Layman D., Ozersky P., Rohlfing T., Robermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L., Kaitta S., Budarf M.L., Kirnson M.I., Dumanski J.P., Peyrard M., Kedra D., Kam H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D., Waitkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L., Mar Hartman R., Hub D., Saccussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P., Per H., The P., Mar H., Mar H., Shan B., Shalbhur Y., Wright H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lisb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "FUNCTION: Activates NF. kappaB via Bcll0 and IKK.
-!- FUNCTION: Activates NF. kappaB via Bcll0 and IKK.
-!- SUBUNT: CARD10 and Bcll0 bind to each other by CARD-CARD
INTERACTION: They both participate in a complex with MALT1, where
MALT1 binds to Bcll0 (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- TISSUB SPECTIFICITY: Detected in adult heart, kidney and liver;
-!- Inver levels in intestine, placenta, muscle and lung. Also found
in fetal lung, liver and kidney.
-!- SIMILARITY: CONTAINS 1 CARD DOWAIN.
-!- CAUTION: Supposed to contain a SH3, a PDZ and a guanylate kinase-
-!- Like domain. But none of these 3 domains are detected by PROSITE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         {\tt CAUTION:\ Ref.4} sequence differs from that shown due to various gene identification problems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C -> R (IN REF. 4).

K -> KQ (IN REF. 4; CAB63075).

R -> L (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   > L (IN REF. 4).
8377319AB82A0949 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COILED COIL (POTENTIAL). POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.5%; Score 329.5; DB 1 31.8%; Pred. No. 7.3e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The DNA sequence of human chromosome 22."; Nature 402:489-495(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AY032928; AAK54454.1; -.. EMBL; AL049851; CAB63075.1; ALT_SEQ. EMBL; AL049851; CAB63076.1; ALT_SEQ. EMBL; AL022315; CAB42832.1; ALT_SEQ. PROSITE; PS50209; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AY028896; AAK26165.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289
917
932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 28
917 91
932 93
1032 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam or SMART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 10 (Bcl10-interacting MAGUK protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- TISSUE SPECIFICITY: Highly expressed in kidney, heart followed by brain, lung, liver, skeletal muscle and testis.
-:- SIMILARITY: CONTAINS I CARD DOMAIN.
-:- CAUTION: Supposed to contain a SH3, a PDZ and a guanylate kinase-
                                                                                                                                                                                                                                                                        63 FHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELELQ 122
                                                                                                                     123 EQSLRTASDQESGDEELNRLKEENE------KLRS----LTFSLAE------ 158
                                                                                                                                                                                                                                                                                                                                                              QKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSAQREISQSLVEKDSLRRQVFELT 268
                                                                                                                                                                                                                                                                                                                                                                                                 ---LRRARGPPPGAEEKEKEKEKEKEPDNVDLVSELRAENQQLTASLRELQEGLQQEASR 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                like domain. But none of these 3 domains are detected by PROSITE. Pfam or SWART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21391892; PubMed=11387339; McAllister-Lucas L.M., Inohara N., Lucas P.C., Ruland J., Benito A., Li Q., Chen S., Chen F.F., Yamaoka S., Verma I.M., Mak T.W., Nunez G.;
                                      -----KDILEQSLDEARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4811A09BDB8F792C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COILED COIL (POTENTIAL).
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1021 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114413 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF363456; AAK60136.1; -. PROSITE; PS50209; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269 DOVCELRTQLRQLQ 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115
450
565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    428 AERDELLTTLTSLE 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 11
138 45
558 56
1021 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARD10 OR BIMP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coiled coil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARA_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Bimpl)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P58660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
CARA_MOUSE
                                                                                                                                                                                  251
                                                                                                                                                                                                                                                                                                                                                                 509
                                                                                                                                                                                                                                                                                                                                                                                                                              368
                                                                                                                                                                                                                                               159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HID DESCRIPTION OF STREET AND STR
                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QΥ
                                                                                                                                                                            g
                                                                                                                                                                                                                                           δy
                                                                                                                                                                                                                                                                                                                                                                 ò
                                                      9
                                                                                                                         δ
```

Length 1021;

DB 1;

Score 322.5;

22.1%;

Query Match

g ŏ

10 LQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADH-----SRMKREVSAH 62

9

Gaps

49;

Indels

50; Mismatches 115;

Matches 100; Conservative

Best Local Similarity

ä

```
qq
                                                                                                                                                                                                                   δy
                                                                                                                                                                                                                                                            Q
                                                                                                                                                                                                                                                                                                         δλ
                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11D DJT JDD DJ
                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                        9
                                                                                                                                                                                                 62 HFHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELEL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bertin J., Guo Y., Wang L., Silnivasula S.M., Jacobson M.D., Poyet J.-L., Merriam S., Du M.-Q., Dyer M.J.S., Robison R.E., Distefano P.S., Almeni E.S.; Du M.-Q., Dyer M.J.S., Robison R.E., Distefano P.S., Almeni E.S.; Du M.-Q., Dyer M.J.S., Robison R.E., Disterance a novel caspase recruitment domain-containing protein that interacts with Bc110/CLAP and activates NF-kappa B."; J. Blol. Chem. 275-141082-41086(2000).

-I. FUNCTION: Activates W.F.kappaB via Bc110 (By similarity).

-I. SUBUNT: Self-associates. CARD9 and Bc110 bind to each other by CARD-CARD interaction (By similarity).

-I. SUBCELULAR LOCATION: Cytoplasmic (By similarity).

-I. SIMILARITY: CONTAINS 1 CARD DOMAIN.
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                 10 LQEELNQEKGQKEVLLRRCQQLQ-----EHLGLAETRAEGLHQLEADHSRMKREVSA 61
                                                                                                                                                                                                                                                                                                                                                                       ----KDILEQSLDEARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKM
                                                                                                                                                                                                                                                                                                                                                                                                                                      ACQLYREKVNALQAQVCELQKERDQAYSARDSAQREISQSLVEKDSLRRQVFELTDQVCE
                                                                                                                                                                                                                                                            122 QEQSLRTASDQESGDEE-----LNRLKEENEKLRSLTFSLAE------
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COILED COIL (POTENTIAL).
6F33089CB7E6BAC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COILED COIL (POTENTIAL).
           Pred. No. 1.7e-10;
|: Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
Caspase recruitment domain protein 9 (rCARD9)
CARD9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                536 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Sprague-Dawley;
MEDLINE-20576268; PubMed-11053425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARD.
31.1%; Pic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLTTVTSLEGTKAMLEAQLORT 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 LRTQLRQLQAEPPGVLKQEART 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF311288; AAG28791.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62631 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001315; CARD.
PROSITE; PS50209; CARD; 1.
                                      100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98
277
420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303 4
536 AA;
                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coiled coil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAR9_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                          136
                                        Matches
                                                                                                                                                                                                                                                                                                     251
                                                                                                                                                                                                                                                                                                                                                                                                                                    214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                     ò
                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

```
63 FHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELELQ 122
                                                                                                                                                                                                                                                                         229 VCELQKERDQAYSARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQL-----RQLQA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Retinoblastoma;
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamasu A., Nakamura Y., Nagahari K., Masuho Y.,
"NEDO human cDNA sequencing project.";
                                                             Gaps
                                                                                                                                                                           112 ESGLTQLLMTEVMKLQKKVQDLTALLSSKDDFIKELRVKDSLLRKHQERVQRLKEECELS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDILNE-20576268; PubMed-11053425;
Bertin J., Guo Y., Wang L., Srinivasula S.M., Jacobson M.D.,
Bertin J., Guo Y., Wang L., Srinivasula S.M., Jacobson M.D.,
Boyet J.-L., Merriam S., Du M.-Q., Dyer M.J.S., Robison K.E.,
DiStefano P.S., Alnemri E.S.; Carcuitment domain-containing protein that
interacts with Bc110/CLAP and activates NF-kappa B.";
J. Biol. Chem. 275:41082-41086(2000).
                                                                                                                    17 EKGQKEVLLRRCQQLQEHL----GLAETRAEGLHQLEADHS------RMKREVSAH 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
FUNCTION: Activates NF-kappaB via Bcl10.
SUBUNIT: Self-associates. CARD9 and Bcl10 bind to each other by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 EQ-SLRTASDQESGDEELNRLKEENE----KLRSLTFSLAEK-----DILEQSLDE
                                                                                                                                                                                                                                                                                                                                                                                                             230 HTLKLRHAMEORPSQELLWDLOQERDLLQARVQELEVSVQEGKLHRNSPYIQVLEEDWRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169 ARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                          37;
      Length 536;
                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                          123;
Score 283.5; DB 1;
Pred. No. 1.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAR9_HUMAN STANDARD; PRT; 536 AA. 09H257; 09H854; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Caspase recruitment domain protein 9 (hCARD9)
                                                          58; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARD-CARD interaction. SUBCELLULAR LOCATION: Cytoplasmic.
19.4%;
29.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-492 FROM N.A.
                                                          Conservative
                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E--GRLKQQ 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284 EPPGVLKQE 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
                                                       91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
CAR9_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARD9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      410
                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>-</u>
```

```
Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176
  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its web y non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 EKGQKEVLLRRCQQLQEHL----GLAETRAEGLHQLEADHS------RMKREVSAH 62
TISSUE SPECIFICITY: Highly expressed in spleen. Also detected in liver, placenta, lung, peripheral blood leukocytes and in brain. SIMILARITY: CONTAINS 1 CARD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N -> S (IN REF. 3).
LSSGEPPEKER -> PAGLPGIGAVC (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 FHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 SRELKRCKEENYDLAMRLAHQSEEKGAALMRNRDLQLEIDQLKHSLMKAE--DDCKVERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 EQ-SLRTASDQESGDEELNRLKEE----NEKLRSLTFSLAEK------DILEQSLDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230 HTLKLRHAMEQRPSQELLWELQOEKALLQARVQELEASVQEGKLDRSSPYIQVLEEDWRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 ARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 VCELQKERDQAYSARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLRQLQAEPPGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 536;
                                                                 ç
                                                             CAUTION: Ref.2 sequence differs from that shown due frameshift in position 360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6EB1835315B83DE5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARD. COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.2e-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.8%; Score 274.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.
                                                                                                                                                                                                                                                                                          EMBL; AF311287; AAG28790.1; -. EMBL; AK024001; BAB14766.1; ALT_FRAME. EMBL; BC008877; AAH08877.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62267 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.4%;
                                                                                                                                                                                                                                                                                                                                                          Genew, HGNC:16391, CARD9.
InterPro, IPR001315, CARD.
PROSITE, PS50209, CARD: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fietz M.J., Rogers G.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                               98
277
419
12
492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 30, C
(Rel. 30, I
(Rel. 41, I
                                                                                                                                                                                                                                                                                                                                                                                                                                               6
117 2
332 4
12
482 4
536 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          407 LAVEGR 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  289 LKQEAR 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trichohyalin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1994
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRHY_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
      SO THE THE TENT OF THE TENT OF
```

```
THE INDER ROOT SHEATH (IRS) OF HAIR FOLLICLES AND MEDULLA, AND IN
THE TILIFORM PAPILLES OF DORRAL TONGUE EPITHELIUM (PROBABLE).
THE FILIFORM PAPILLES OF DORRAL TONGUE EPITHELIUM (PROBABLE).
THE EPITERMY.
THE EPIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ITS OWN CALCIUM-DEPENDENT POSTSYNTHETIC PROCESSING DURING TERMINAL
-:- FUNCTION: INTERMEDIATE FILAMENT-ASSOCIATED PROTEIN THAT ASSOCIATES IN REGULAR ARRAYS WITH KERATIN INTERMEDIATE FILAMENTS (KIF) OF THE INNER ROOT SHEATH CELLS OF THE HAIR FOLLICLE AND THE GRANULAR LAYER OF THE EPIDERMIS. IT LATER BECOMES CROSS-LINKED TO KIF BY ISODIPEPTIDE BONDS. IT MAY SERVE AS SCAFFOLD PROTEIN, TOGETHER WITH INVOLUCRIN, IN THE ORGANIZATION OF THE CELL ENVELOPE OR EVEN ANCHOR THE CELL ENVELOPE OF THE KIF NETWORK. IT MAY BE INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 VSAHFHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 LELQEQSLRTASDQESGDEELNRLKEENEKLRSLTFSLAEKDILEQSLDEARGSRQE--- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QEELNQEKGQK----EVLLRRCQQLQEHLGLAETRAEGLHQL-----EADHSRMKRE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    641 EQELROERERKLREEEQLLRREEQ-----ELROERERKLREEEQLLOEREERLRRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --LVERIHSLR-----ERAVAAERQR-----EQYWEEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: HOMODIMER (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P02633; 4ICB.
InterPro; IPR001751; CaBP_S100.
InterPro; IPR002048; EF-hand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z19092; CAA79519.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S28589; S28589.
                                                                                                                                                                                                                                                                                                                                                                                                                                     DIFFERENTIATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
```

```
PS50067; KINESIN_MOTOR_DOMAIN2; 1.
                                                                                       DOMAIN
DOMAIN
NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYHA_RAT
Q9JLTO;
  PROSITE;
                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MYH10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      996
                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                09
                                                                                                                                                                                                                                                                                                                                                                                                                                              167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MYHA_RAT
  QQ
                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chan G.K.T., Schaar B.T., Yen T.J.;

"Characterization of the kinetochore binding domain of CENP-E reveals interactions with the kinetochore proteins CENP-F and hBUBRI.";

J. Cell Biol. 143:49-63(1998).

- I- FUNCTION: MINUS-END DIRECTED MICROTUBULE MOTOR. PROBABLE KINETOCHORE MOTOR. ACCUMULATES JUST BEFORE MITOSIS AT THE G2 PHASE OF THE CELL CYCLE. PROBABLY IMPORTANT FOR CHROMOSOME MOVEMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBGNIT: INTERACTS WITH CENP-F AND BUBR1 KINASE.
SUBCELLULAR LOCATION: ASSOCIATES WITH KINETOCHORES DURING
CONGRESSION, RELOCATES TO THE SPINDLE MIDSONE AT ANAPHASE, AND IS
QUANTITATIVELY DISCARDED THE NED OF THE CELL DIVISION.
SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
                                                                        KLREEEQILQEREEERLRRQERERKLREEEQLLQEREEERLRRQERERKLREEEQLLRQE 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-93024922; PubMed-1406971;
Yen T.J., Li G., Schaar B.T., Szilak I., Cleveland D.W.;
"CENP-E is a putative kinetochore motor that accumulates just before
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thrower D.A., Jordan M.A., Schaar B.T., Yen T.J., Wilson L.; whitolic HeLa cells contain a CENP-E-associated minus end-directed mirroribile mofor ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                    247 OREISQSL··VEKDSLRRQVFE··LTDQVCELRTQLRQLQAEPPGVLKQE 292
                                                                                                                                                               Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                             01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-NMY-2000 (Rel. 39, Last annotation update)
Centromeric protein E (CENP-E protein).
                                           EQTLLQFQKSKMACQLYREKVNALQAQVCELQKERD----
                                                                                                                                                                                                                                                                                                  2663 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001752; kinesin_motor.
Pfam, PF00225; kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
SMART; SM00129; KISC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHĀRACTERIZATION.
MEDLINE=95196755; PubMed=7889940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARACTERIZATION.
MEDLINE-98437347; PubMed-9763420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND/OR SPINDLE ELONGATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; 215005; CAA78727.1; -. PIR; S28261, S28261. HSSP; P17119; 3KAR. Genew; HGNC:1856; CENPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       microtubule motor.";
EMBO J. 14:918-926(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 359:536-539(1992).
                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                           01-JUL-1993 (
01-JUL-1993 (
30-MAY-2000 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM; 117143;
                                                                                                                                                                                                                                                                                                    CENE_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mitosis.
                                                                                                                                                                                                                                                      RESULT 9
CENE_HUMAN
797
                                                                                       g
                                                                                                                                                                                                                                                                                                    HIDDRY REPAYED DESCRIPTION OF THE PROPERTY OF 
                                         ò
                                                                                                                                  ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAPPING.

-1-SUBUNT: WOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY
CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2
REGULAPORY LIGHT CHAIN SUBUNITS (MLC-2).

-1-DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CYCLES OF A 28-RESIDUE REPEAT PATTEN COMMOSED OF 4 HEPTAPEPTIDES,
CHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLS.

-1-SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----ATTQSNYKSTDQEFQNFKTLHMDFEQKYKMVLEENERMNQEIVNLSKE---AQK 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAHFHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCEL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELQEQSLRTASDQESGDEELNRLK-------EENEKLRSLTFSLAEKDILEQS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 LDEARGS------RQELVERIHSLRERAVAAERQREQYWEEKEQTLLOFQKSKMACQL 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 YREKVNALQAQVCELQKERDQAYSARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQ 277
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Sprague-Dawley, TISSUE-Brain;
MEDLINE=20483650; Pubmed=11027611;
Yam J.W.P., Chan K.W., Li N., Hsiao W.L.W.;
Molecular cloning and functional analysis of the promoter region of rat nonmuscle myosin heavy chain-B gene.";
Biochem. Biophys. Res. Commun. 276:1203-1209(2000).
-i- FUNCTION: CELLULAR WYOSIN APPEARS TO PLAY A ROLE IN CYTOKINESIS,
CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION AND
                                                                                                                                                                                                                                                                                                                                                            3 LAGAIGSLQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREV--- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2010 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Myosin heavy chain, nomuscle type B (Cellular myosin heavy chain, type B) (Nomuscle myosin heavy chain, type B) (Nomuscle myosin heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEELHIITSEKDKLFSEVVH-----KE---SRVQGLLEEIGKTKDDL------
Motor protein; Cell division; ATP-binding; Coiled coil; Mitosis;
                                                                                                                                                                                                                                                                                                    81;
                                                                                                                                                                                                                                         12.9%; Score 188.5; DB 1; Length 2663; 24.2%; Pred. No. 0.006;
                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                     ATP (BY SIMILARITY).
W; CEFC13880C8C8CB8 CRC64;
                                                           KINESIN-MOTOR.
COILED COIL (POTENTIAL).
GLOBULAR (POTENTIAL).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                    Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1976 AA.
                                                                                                                                                                              312087 MW;
                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     278 LRQLQAEPPGVLKQEART 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRNALES ---- LKOHOET 979
                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
                                                              335
2471
2663
93
                                  Cell cycle; Centromere.
DOMAIN 1 335
                                                                                   336 247
2472 266
86 9
2663 AA;
                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 77;
```

```
14;
between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         885 LLEEKNILAEQLQA-ETELFAEAEEMRARLAAKKQEL---EEILHDLESRVEGEEERNQI 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195 EQYWEEKEQTLLQFQKSKMACQLYREKV-----NALQAQVCELQ---KERDQAYSA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 LKEENEKLRSLTFSLAEKDILEQSLDEARGSRQEL-----VERIHSLRERAVAAERQR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  941 LONEKKKMQ-----AHIODLEEQLDEEEGAROKLQLEKVTAEAKIKKMEEEVLLLEDON 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 772 AGVLAHLEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQRNC---AAYLK 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 LAE-----TRAEGLHQLEADHSRMKREVSAHFHEVLRLKD-----EMLSLSLHYSN 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 ALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELELQEQSLRTASDQESGDEELNR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
16-CCT-3001 (Rel. 40, Last annotation update)
Plectin 1 (PLTM) (PCN) (300-kDa intermediate filament-associated protein) (IFAP300) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 1976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YLATION (SH-2) (POTENTIAL).
E32708BF9BF2B470 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COLLED COLLED ATP (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
**VATATION (SH-2) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 RDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLRQLQAEPPGVL 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50096; IQ; 1.
Myosin; ATP-binding; Calmodulin-binding; Actin-binding;
Coiled coil; Alkylation; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 186.5; DB : Pred. No. 0.0057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 4473 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cricetulus griseus (Chinese hamster).
                                                                                                                                                                                                                                                                               InterPro; IPR00048; IQ_region.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tall.
InterPro; IPR0012017; Spectrin.
InterPro; IPR001609; myosin_head.
Pfam; PF00063; myosin_head; 1.
Pfam; PF00612; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF02736; Myosin_N; 1.
PRINTS; PR00193; MYOSINHEAVY.
Probom; PD000035; myosin_head; 1.
SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228963 MW;
                                                                                                                                                                                                                           EMBL; AF139055; AAF61445.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.8%; 22.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1976
185
701
711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1976 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                               HSSP; P10587; 1BR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLE1_CRIGR
Q9JI55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLE1_CRIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLEC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ON DE CONTRACTOR DE CONTRACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
            ò
```

```
MADLINE-970212319; FULDMENG-10020314;

MADLINE-970212319; FULDMENG-10020314;

MADLINE-970212319; FULDMENG-1002014;

MADLINE-970210310; PLOSQHORY-100316.";

MADLINE-970310310; PLOSQHORY-100316.";

MADLINE-970310310; PLOSGHORY-100310; PLIAMENTS WITH MICROTUBULES AND AICHORY-100310; MAY BE INVOLVED NOT ONLY IN THE CROSSLINKING AND STABLIZANTION OF CYTOSKELFTAL INTERMEDIATE FILAMENTS OF DESMOSOMES OR HEMIDEANCOMES. MAY BE INVOLVED NOT ONLY IN THE CROSSLINKING AND STABLIZANTION OF THEIR DYNAMICS.

C. SUBMINT: HOMODIMER OR HOMOTETRAMER.

C. I- DOMAIN: THE N-TERMINUS GRAP, CYTOKERATINS, LAMIN B; WHEREAS BOTH THE N-TERMINUS CAN BIND INTEGRIN BETA-4.

C. I- DOMAIN: THE C-TERMINUS CAN BIND INTEGRIN BETA-4.

C. I- PIM: PHOSPHORYLATED BY CDC2: REGULATES DISSOCIATION FROM INTERMEDIATE FILAMENTS DURING MITOSTS.

C. I- SIMILARITY: CONTAINS 1 ACTIN-BINDING DOMAIN.

C. I- SIMILARITY: CONTAINS 32 PLECTIN REPEATS.

C. I- SIMILARITY: CONTAINS 32 PLECTIN REPEATS.

C. I- SIMILARITY: CONTAINS 32 PLECTIN REPEATS.

C. I- SIMILARITY: CONTAINS 4 SPECTRIN REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coiled coil; Repeat; Structural protein; Cytoskeleton; Actin-binding;
                                                                                                                                                  "The 300-kDa intermediate filament-associated protein (IFAP300) is a
Chordata, Craniata, Vertebrata, Euteleostomi;
Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                           MEDLINE-20334248; PubMed=10873583;
Clubb B.H., Chou Y.-H., Herrmann H., Svitkina T.M., Borisy G.G.,
Goldman R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROD DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECTRIN 3.
SPECTRIN 4.
COILED COIL (POTENTIAL).
                                                                                                                                                                                 Blochem. Biophys. Res. Commun. 273:183-187(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CENTRAL FIBROUS GLOBULAR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIN-BINDING.
CH 1.
CH 2.
SPECTRIN 1.
SPECTRIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLOBULAR 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLECTIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00019; ACTININ_1; PARTIAL. PROSITE; PS00020; ACTININ_2; FALSE_NEG. PROSITE; PS50021; CH; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro: IPR001789; Actbind_actnin.
InterPro: IPR001715; Calponin-11ke.
InterPro: IPR001701; Plectin_repeat.
InterPro: IPR002017; Spectrin.
Pfam: PF00307; CH; 2.
Spectrin. SMO0181; Plectin; 20.
SMART; SM00033; CH; 2.
SMART; SM00250; PLEC; 32.
SMART; SM00150; SPEC; 4.
                                                                                                                                                                                                                                 MEDLINE=96215219; PubMed=8626512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF260753; AAF70372.1; -.
                                                                                                                                                                      hamster plectin ortholog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1259
2544
4473
192
192
508
513
719
719
719
2548
     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; Q01082; 1BKR
                                                                                     SEQUENCE FROM N.A.
                                                 NCBI_TaxID=10029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <1
1260
2545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphorylation
                                                                                                                                                                                                                     PHOSPHORYLATION
                                       Cricetulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
```

σ

```
Plectin 1 (PLTN) (PCN) (Hemidesmosomal protein 1) (HD1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2552 KAEAELLQ------QQKELAQEQARRLQEDKEQMAQQIVEETGGFQRTLEVERQRGLEM 2304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2419 KSFLSEKDSLLQRERFIEQEKAKLEQLFQDEVAKAQQLREEQQRQQRQMEQEKQELVASM 2478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2192 LEEEAEKMKQVAERAARLSVAAQEAARLRQLAEEDLAQQRALAEKMLKEKMQAVQEATRL 2251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 KDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQEL--QRANMVSSCELELQEQ--- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 -----SLRTAS---DQESGDEELNRLKEE----NEKLRSLTFSLAEKDILEQSLDEAR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLECTIN 32.
BINDING TO INTERMEDIATE FILAMENTS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOEELNQEKGOKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAHFHEVLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAEAERLKLRMAEMSRAQARAEEDAQRFRKQAEEIGEKLHRTELATQEKVTLVQTLEIQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 GSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMAC----QLYREKVNALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --- DQAYSARDSAQREISQSLVEKDSLRRQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 X 4 AA TANDEM REPEATS OF G-S-R-X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.7%; Score 186; DB 1; Length 4473; 27.2%; Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38; Mismatches 137; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION (BY CDC2). W; E144615D361E3484 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY
                                                                             PLECTIN OF PLECTIN PLE
                                                                                                                                                                                                                      PLECTIN
PLECTIN
PLECTIN
PLECTIN
PLECTIN
PLECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                         PLECTIN
PLECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLECTIN
PLECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLECTIN
PLECTIN
                                       PLECTIN
PLECTIN
                                                                                                                                                                                PLECTIN
PLECTIN
                                                                                                                                                                                                                                                                                                                                                                                 PLECTIN
PLECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLECTIN
                                                                                                                                                               PLECTIN
                                                                                                                                                                                                                                                                                                                                                                 PLECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4328 PHO
AA; 509015 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2479 EEARRRQCEAEEAVRRKQEE 2498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265 FELTDQVCELRTQLRQLQAE 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 AOVCE----LOKER----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                               3646
                                                                                                                                                                                                                                                                                                                         3722
3760
3760
3834
3883
3927
3965
4003
4023
4272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4348
4386
4089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4429
                     2728
2766
2804
                                                                               2942
2980
3018
                                                                                                                                        3056
                                                                                                                                                                                                                                         3425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4310
                                                                                                                                                                                                   3349
                                                                                                                                                                                                                          3387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
es 87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                         REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
REPEAT
                                     REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

PLEI\_HUMAN STANDARD; PRT; 4684 AA. 015149; 016640; 015148; 16-007-2001 (Rel. 40, created) 16-007-2001 (Rel. 40, Last sequence update) 16-007-2001 (Rel. 40, Last annotation update)

DT DT

RESULT 12 PLE1\_HUMAN

```
RA MUSSE W., Hancher H.;

A wiche G., Uitto J., Hinther H.;

The plectin gene causes epidermolysis bullosa simplex with plectin and the plectin gene causes epidermolysis bullosa simplex with plectin and belectin gene causes epidermolysis bullosa simplex with plectin and belectin gene causes epidermolysis bullosa simplex with plectin and deficiency.";

Am. J. Pathol. 158:617-625(2001).

C. - I PUNCTION: INTERILINES INTERMEDIATE FILAMENTS TO DESMOSOMES OR HEMIDESMOSOMES. COULD ALSO BIND MUSCLE PROTEINS SUCH AS ACTIN TO COURSE. AND MUSCLE. MAY BE INVOLVED NOT ONLY IN THE ERBERGAL INTERMEDIATE FILAMENTS. IN THE ERBERGAL INTERMEDIATE FILAMENTS. IN THE ERBERGAL INTERMEDIATE FILAMENTS. BOWDINGRR. BUT ALSO IN THE REGULATION OF THEIR DYNAMICS.

C. - SUBUNT: HOMODINER OR HOMOTETRAMER.

C. - ALTERNATURE PRODUCTS: 3 ISOFORMS; I (SHOWN HERE), 2 AND 3; ARE PRODUCED BY ALTERNATIVE SPLICING;

C. - ALTERNATURE PRODUCTS: 3 ISOFORMS; I (SHOWN HERE), 2 AND 3; ARE PRODUCED BY ALTERNATIVE SPLICING;

C. - ALTERNATIVE PRODUCTS: 3 ISOFORMS; I (SHOWN HERE), 2 AND 3; ARE PRODUCED BY ALTERNATIVE SPLICING;

C. - DOMAIN: THE N-TERMINUS INTERACTS WITH ACTIN, THE C-TERMINUS WITH NITHER NITHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-96312447; PubMed-8698233;
McLean W.H.I., Pulkkinen L., Smith F.J.D., Rugg B.L., Lane B.B.,
Bullzich F., Burgeson R.E., Amac S., Hudson D.L., Owaribe K.,
McGrath J.A., McMillan J.R., Eady R.A.J., Leigh I.M., Christiano A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pulkkinen L., Smith F.J.D., Shimizu H., Murata S., Yaoita H., Hachksuka H., Mishikwa T., McLean W.H.T., Uitto J.; Mishikwa T., McLean W.H.T., Uitto J.; "Homozygous deletion mutations in the plectin gene (PLEC1) in patients with epidermolysis bullosa simplex associated with late-onset
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Loss of plectin causes epidermolysis bullosa with muscular dystrophy: {
m cDNA} cloning and genomic organization.";
                                                                            Euteleostomi;
                                                                                                                                                                                                                                                            Liu C.-G., Maercker C., Castanon M.J., Hauptmann R., Wiche G.; "Human Plectin: organization of the gene, sequence analysis, and chromosome localization (8q24)."; Proc. Natl. Acad. Sci. U.S.A. 93:4278-4283(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VAINTANT MD-EBS LEU-429 INS.
MEDLINE-21090821; PubMed=11159198;
Bauer J.W., Rouan F., Kofler B., Rezniczek G.A., Kornacker I.,
Muss W., Hametner R., Klausegger A., Huber A., Pohla-Gubo G.,
                                                                            Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                (ISOFORMS 2 AND 3), AND DISEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT MD-EBS 1003-GLN--ALA-1005 DEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hum. Mol. Genet. 5:1539-1546(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97049959; PubMed=8894687;
                                                                                                                                                                                                                                      MEDLINE=96210632; PubMed=8633055;
                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genes Dev. 10:1724-1735(1996).
                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            muscular dystrophy."
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                              TISSUE-Placenta;
                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Uitto J.;
```

```
CONTRIBUTE TO A SECOND TO A SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2463 KAEAELLQ------QQKELAQEQARRLQEDKEQMAQQLAEETQGFQRTLEAERQRQLEM 2515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQEEAEKMKOVAEEAARLSVAAQEAARLRQLAEEDLAQQRALAEKMLKEKMQAVQEATRL 2462
                                                     SIMILARITY).
MVAGMI,MPRDQLRAIYEVLFREGVMVAKKDRRPRSLHPHVP
                                                                          GVTNLQVMRAMASLRARGLVRETFAWCHFFWYLTNEGIAHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----SLRTAS---DQESGDEELNRIKEE----NEKLRSLTFSLAEKDILEQSLDEAR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQEL--QRANMVSSCELELQEQ--- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAHFHEVLRL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171 GSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMAC----QLYREKVNALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQVCE----LQKER-------DQAYSARDSAQREISQSLVEKDSL----
         BINDING TO INTERMEDIATE FILAMENTS (BY
                    SIMILARITY).
4 X 4 AA TANDEM REPEATS OF G-S-R-X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 4684;
                                           PHOSPHORYLATION (BY CDC2) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 185.5; DB 1; Length Pred. No. 0.015; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                   REF. 2).
                                                                                                                                                                                                                                 REF.
REF.
REF.
REF.
REF.
REF.
                                                                                                                                                                                                  -> F (IN I
PLECTIN 33
                                                                                                                                                                                                                       41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.7%;
27.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88; Conservative
                                                                                                                                                                                                                                                       4640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                         3408
                                                                                                                                                                                                                                                                                         321
334
534
662
688
767
789
                                                                                                                                                                                                                                                                                                                                                                    910
                               4625
                                                                                                                                                                                                                                                                                                             CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                            VARSPLIC
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                 VARSPLIC
                                DOMAIN
MOD_RES
                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                             VARIANT
REPEAT
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                 Colled coil; Repeat; Structural protein; Cytoskeleton; Actin-binding; Phosphorylation; Alternative splicing; Epidermolysis bullosa; Disease mutation.
                                                                                                                                                                                                                                                                                                                                     GLOBULAR 1.
CENTRAL FIBROUS ROD DOMAIN
GLOBULAR 2.
ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLECTIN 15.
PLECTIN 16.
PLECTIN 17.
PLECTIN 18.
PLECTIN 19.
PLECTIN 20.
                                                                                                                                                                                                                                                                                                                                                                                                     SPECTRIN 1.
SPECTRIN 2.
SPECTRIN 3.
SPECTRIN 4.
                                                                                                                                            InterPro; IPR001589; Actbind_actnin.
InterPro; IPR001715; Calponin-like.
InterPro; IPR001101; Plectin_repeat.
InterPro; IPR00101; Plectin_repeat.
InterPro; IPR003207; SiO_plectin.
Pfam; PF00307; CH; 2.
Pfam; PF00307; CH; 2.
Pfam; PF00501; SIO_plectin; 1.
SMART; SM0033; CH; 2.
SMART; SM00150; SPEC; 5.
PR05TE; PS00019; ACTININ_1; FALSE_NEG.
PROSITE; PS000109; ACTININ_1; FALSE_NEG.
PROSITE; PS000109; ACTININ_1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLECTIN 24.
PLECTIN 25.
PLECTIN 26.
PLECTIN 27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLECTIN 1.
PLECTIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLECTIN 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLECTIN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLECTIN 4.
PLECTIN 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLECTIN 3
PLECTIN 3
PLECTIN 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLECTIN E
PLECTIN 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLECTIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLECTIN
                                         EMBL; 254367; CAA91196.1; --
EMBL; U53204; AAB05427.1; --
EMBL; U63610; AAB05428.1; --
EMBL; U63609; AAB05428.1; --
EMBL; X97053; CAA65765.1; --
HSSP; Q01082; IBER.
                                                                                                  001082, 1BKR.
HGNC:9069, PLEC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1415
2756
2863
2901
                                                                                                                                                                                                                                                                                                                                                 1471 2756
                                                                                                                            601282;
                                                                                                                                     226670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                            MIM;
```

11;

Gaps

```
RESULT 14
CTRO_HUMAN
                                                                                                            448
Matches
                            11
                                                                                 62
                                                                                                                                                                                                                            557
                                                  Op
                                                                                                           оp
                                                                                                                                                                   g
                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                          Dp
                          δ
                                                                                δy
                                                                                                                                         δ
                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                        δy
                                                                                                                                                                                                                                                                                   엄
                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                             SPECIFICITY IN VIVO.
SUBUNT: HOMOIDIMER (PROBABLE).
TISSUE SPECIFICITY A MAJOR SIGNAL WAS OBSERVED IN TESTIS AND BRAIN, BUT IT WAS ALSO DETECTED IN THYMUS, SPLEEN, KIDNEY, HEART
                                                                                                                                                                                                                                                                                                                                                                  FEBS Lett. 377:243-248(1995).
-1- FUNCTION: PUTATIVE RHO/RAC EFFECTOR THAT BINDS TO THE GTP-BOUND FORMS OF RHO AND RAC1. IT PROBABLY BINDS P21 WITH A TIGHTER
                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 1 PH DOMAIN.
SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
                                                                                                                                                                                                                                                                                                                              .
G
                                                                                                                                    01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Citron protein (Rho-interacting, serine/threonine kinase 21).
                                                                                                                                                                                                                                                                                                                           Madaule P., Furuyashiki T., Reid T., Ishizaki T., Watanabe Morii N., Narumiya S.;
"A novel partner for the GTP-bound forms of rho and rac.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHORBOL-ESTER AND DAG BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SH3-BINDING (POTENTIAL)
MW; 7B7286C2305676DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coiled coil; Phorbol-ester binding; SH3-binding.

DOMAIN 1 845 COILED COIL (POTENTIAL).

DOMAIN 674 870 RHO/RAC BINDING.
                                                                                                            1597 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SW00036; CNH; 1.
SMART; SW00233; PH; 1.
PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
PROSITE; PS500003; PH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-LYS.
                                     2691 EARRROHEAEEGVRRKOEELQQLEQQ 2716
          -- RRQVFELTDQVCELRTQLRQLQAE 284
                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U39904; AAC52341.1; -. MGD; MCI:105313; Cit. InterPro; IPR001180; Citron. InterPro; IPR00219; DAG_PE-bind.
                                                                                                                                                                                                                                                                                                              MEDLINE-96128238; PubMed-8543060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00130; DAG_PE-bind; 1. Pfam; PF00169; PH; 1. Pfam; PP00169; PH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.7%;
26.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183448
                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001849; PH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ); CNH; 1.
09; C1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1526
                                                                                                                                                                                                            musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00780; CNH
SMART; SM00109; C1
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1011
1160
1521
1597
                                                                                                                                                                                                                                                                                                  TISSUE-Brain;
                                                                                                      CTRO_MOUSE
P49025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND LUNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                RESULT 13
CTRO_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SITE
                                                                                                                                                                                                             Mus
           õ
                                     qq
```

Score 185; DB 1; Length 1597; Pred. No. 0.0055;

Best Local Similarity

Query Match

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
   16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 LEQSLDEARGSRQELVE---RIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLY 218
                                                                                                                                                                                                                                                                                388 QEEMISELRQQKFYLETQAGKLEAQNRKLEEQLEKISHQDHSDKSRLLELETRLREVSLE 447
                                                                                           HFHEVLRLKDEMLSLSLHYSNALQEKE----LAASRCRSLQEELYLLKQELQRANMVSS 116
                                                                                                                                                                                                                                                                                                                EEQVLDLEALNDELLEKERQWEAWRSVLGDEKSQFECRVRELQRMLDTEKQSRARADQRI 665
                                                                                                                                                       117 CELELQEQSLRTASDQ------ESGDEELNRLKEENEKLRSLTFSLAEKDI 161
   92; Gaps
                                QEELNQE-KGQKEVLLRRCQQLQEHLGLAETRAEGL-HQLEADHSRM-----KREVS-A 61
                                                                                                                                                                         ----LDEASGANDEIVQLRSEVDHLRREIT----EREMQLTSOKQTM---EALKTTCTML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Citron protein (Rho-interacting, serine/threonine kinase 21)
   98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1286 AA
   54; Mismatches
                                                                                                                                                                                                                                                                                                                                             251 SQSLVEKDSLRRQVFELTDQVCELRTQLRQLQ 282
                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99246063; PubMed=10231032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Connell M., Goela D., Harper M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTRO_HUMAN STANDARD;
014578; Q9UP27;
30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AC002563; AAB71327.1; -. EMBL; AB023166; BAA76793.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 347-1286 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OR STK21 OR KIAA0949.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:1985; CIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Fragment)
```

```
RREWRY REWRY RREWRY REWRY RREWRY REWRY RREWRY REWRY RREWRY RREWRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----LDEASGANDEIVQLRSEVDHLRREIT----EREMQLTSQKQTM---EALKTTCTML 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 QEEMISELRQQKFYLETQAGKLEAQNRKLEEQLEKISHQDHSDKNRLLELETRLREVSLE 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 HFHEVLRLKDEMLSLSLHYSNALQEKE-----LAASRCRSLQEELYLLKQELQRANMVSS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 EEQVMDLEALNDELLEKERQWEAWRSVLGDEKSQFECRVRELQRMLDTEKQSRARADQRI 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CELELQEQSIRTASDQ ....----ESGDEELNRIKEENEKLRSLTFSLAEKDI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 QEELNQE-KGOKEVLLRRCQQLQEHLGLAETRAEGL-HQLEADHSRM-----KREVS-A 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, nonsuscle type B (Cellular myosin heavy chain,
type B) (Nonmuscle myosin heavy chain-B) (NMMHC-B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEQSLDEARGSRQELVE---RIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----SVCELQKERDQAYSARDSAQREI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Obara M., Ishiguro N., Shinagawa M.;
"Bos taurus nonmuscle myosin heavy chain B mRNA, complete cds.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.5%; Score 183; DB 1; Length 1286; 26.2%; Pred. No. 0.0057; ive 55; Mismatches 98; Indels 93
                                                                                                                                                                                                                                                                                                                                                                                          PHORBOL-ESTER AND DAG BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 SH3-BINDING (POTENTIAL).
146506 MW; 498101F79EA75E85 CRC64;
                                                                                                                                                                                                                                                                                                                            COILED COIL (POTENTIAL). RHO/RAC BINDING. POLY-LYS.
                                                                                                                   Pfam; PF00169; PH; 1.
Pfam; PF00780; CNH; 1.
SMART; SM00109; C1; 1.
SWART; SM00136; CNH; 1.
SWART; SM00233; PH; 1.
PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
PROSITE; PS50003; PH_DOMAIN; 1.
Coiled_coil; Phorbol-ester binding; SH3-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1976 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 SQSLVEKDSLRRQVFELTDQVCELRTQLRQLQ 282
MIM; 605629;
InterPro; IPR001180; Citron.
InterPro; IPR002219; DAG_PE-bind
InterPro; IPR001849; PH.
InterPro; IPR000861; REM_repeat.
                                                                                                    Pfam; PF00130; DAG_PE-bind;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REKVNALQA------
                                                                                                                                                                                                                                                                                                                                                                                                           822
1148
1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MYHA_BOVIN
Q27991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                         NON_TER
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local
                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYH10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYHA_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
THE STATE OF THE REPORT OF INSERTED SOFORMS OF VERTEBRATE NORMUSCLE MYOSIN HASY Chain II-8-1.

THOSIN CHEM. 270:14533-14540(1955).

THE STATE OF THE STATE OF THE SECRETION AND CAPPING (BY SIMILARITY).

CHELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION AND CAPPING (BY SIMILARITY).

CHAIN SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC.2).

CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC.2).

CHAIN SUBUNITS (CHAIN SUBUNITS (MLC.2).

CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

CHARACTERISTIC CONTAINS I MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               864 VKEKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEMRARLAAKKQELEEI 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRLKDEMLSLSLHYSNALQ-EKELAASRCRSLQEEL---YLLKQELQRANMVSSCELELQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | : : : || || : : : || 924 | HIDLESRVEEEEERRQILQNEKKMQAHIQDLEEGLDEEEGARQKLQLEKVTAEAKIKKM 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQSLRTASDQESGDEELNRLKEENEKLRSLTFSLAEKDILEQSLDEARGSRQELVERIHS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQEELNQEKGOKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSA---HFHEV 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.4%; Score 182; DB 1; Length 1976; 22.1%; Pred. No. 0.0099; tive 78; Mismatches 130; Indels 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 LRERAVAAERQREQYWEEK----EQTLLQFQKSKMACQLYREK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL)
ALKYLATION (SH-2) (POTENTIAL)
AMM, 6144354451C0F790 CRC64;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Calmodulin-binding; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coiled coil; Alkylation; Multigene family.
DOMAIN 1 785 MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000048; IQ_region.
InterPro; IPR000009; Myosin_N.
InterPro; IPR00228; Myosin_tail.
InterPro; IPR002017; Spectrin.
InterPro; IPR001609; myosin_head.
Promo Promo63; myosin_head.
Pfam; Pr00641; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01576; MY, 1.
Pfam; PF01576; Myosin_tail; 1.
Pfam; PR02736; Myosin_N; 1.
PRINTS; PR00193; MYOSINHEAVY.
SMART; SM00015; IQ; II.
SMART; SM00242; MYSC; 1.
                                                                                                      TISSUE=Brain cortex;
MEDLINE=95301542; PubMed=7782316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB022023; BAA36494.1; -.
                                                                     SEQUENCE OF 204-302 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U15716; AAA87715.1; -. HSSP; P10587; 1BR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00242; MYSC; 1. PROSITE; PS50096; IQ; 1. Myosin; ATP-binding; Cal
                                                                                                                                                                  Itoh K., Adelstein R.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         785
815
1976
185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29
```

6

Search completed: January 22, 2003, 08:53:32 Job time : 19.4987 secs

THIS PAGE BLANK (USPTO)

Oggye6 mus musculu O88317 mus musculu Q21022 caenorhabdi

09xvh4 caenorhabdi

29u0s7 mytilus gal

Q8txi4 methanopyru Q9pw73 xenopus lae O14812 homo sapien O60588 homo sapien Q9p450 homo sapien Q9p450 homo sapien Q96075 homo sapien Q96013 homo sapien Q96013 homo sapien Q96103 mus musculu Q97mh9 mus musculu Q97mh9 mus musculu Q63714 rattus norv Q63731 rattus norv Q63731 rattus norv

015738 dictyosteli Q21025 ceenorhabdi O20Kt9 leishmania 073732 xenopus lae Q912u8 mus musculu 042263 xenopus lae 042263 xenopus lae

Q9qx19 rattus norv Q8r1d2 mus musculu

Scoring table:

Searched:

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

OM protein

Run on:

```
: |::::||: :|::||: |: |: |: |: |: |: || |- || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QEQSLRTASDQES--GDEELNRLKEENEKLRSLTFSL-------AEKDILE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HFHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELEL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 LAGAIGSLOEELNOEKGOKEVLLRRCQQLQ-EHLGLAETRAEGLHQLEADHSRMKREVSA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohara O., Nagase T., Kikuno R., Okumura K.; "The nucleotide sequence of a long cDNA clone isolated from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 1171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1171 AA; 134966 MW; FA567ABBC8A703FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases EBBL, AK074049; BAB84875.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U1-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
FLJ00120 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.1%; Score 396.5; DB 4; 34.0%; Pred. No. 3.9e-14; tive 66; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1171 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                         090XE6
088317
020323
09XV14
08TXI4
08TXI4
08DW73
019DW73
090H25
099H25
099H25
099H25
099H25
099H25
099H29
099H29
09973
09973
088528
063731
063731
063731
063731
063731
063731
063731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                073732
091208
042263
025142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                    876
1335
2442
2442
2442
645
670
690
691
                                                                                                                                                                                                                                                                                                                                                                                    1641
2035
2035
3187
1999
746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=SPLEEN;
Best Local Sim
Matches 102;
189.5
1889.5
1889.5
1886.5
186.5
186.5
186.5
186.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185.5
185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLJ00120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             spleen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OSTES3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8TES3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 1
QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08743 rattus norv
095/12 homo sapien
075033 homo sapien
014981 homo sapien
096935 mus musculu
070365 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        drosophila
3 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9uqq7 homo sapien
O95287 homo sapien
Q8tba6 homo sapien
Q9u0s5 mytilus gal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8tes3 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homo sapien
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9vje5 drosophila
O44929 drosophila
                                                                                                                                                                                                                        (without alignments)
1321.544 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                     January 22, 2003, 08:49:36; Search time 45.9946 Seconds
                                                                                                                                                                                                                                                                                                                                                          1 ECLAGAIGSLQEELNQEKGQ.......TQLRQLQAEPPGVLKQEART 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9v587 d
Q61043 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        671580
                       5.1.3
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  671580 segs, 206047115 residues
                         GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                            US-09-767-215-2_COPY_126_420
1462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                    - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8TES3
Q8K443
Q96JV2
O75033
Q14981
Q14980
Q9D935
Q70365
Q9V365
Q9V365
Q9V365
Q9V365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9UQQ7
Q95287
Q8TBA6
Q9U0S5
                                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_fungi:*
sp_human:*
sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPTREMBL_21:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1171
691
691
1313
2101
2101
2238
1456
1690
1690
1690
1690
731
731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7: sp_mhc:*
8: sp_organe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.3.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
1.0.0
```

9

23;

396.5 198.5 198.5 195.5 194.5 193.5 193.5 191.5 191.5 191.5 191.5 191.5 191.5 191.5 191.5 191.5 191.5 191.5 191.5

Result Ş No

```
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heath P.;
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                075033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
075033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δý
qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2005, clone PLACE4000009, weakly similar to myosin heavy chain, nonmuscle type B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LONQLDESQQERNDLMQLKLQLEDQVTELRSRVQELEAALATARQEHSELTEQYKGLSRS 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 : : : : | | : : : | | : | : | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --QEELYLLKQELQRANMVSSCEL------ELQE----QSLRTASDQESGDE-- 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------ELNRLKEENEKLRSLTFSLAEK-DILEQSLDEARGSRQELVERIHS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     382 -RSRLEVAEVNGRLAELSLHMKEEKCQWSKERTGLLQSMEAE-----KDKILKLSAEIL 434
                                                                                                                                       384 TVMLQLEEVERERDQAFHSRDEAQTQYSQCLIEKDKYRKQIRELEEKNDEMRIEMVRREA 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 LQEELNQEKGQKEVLLR-----TRA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 REQEKLLGQLKEFQADKEQSEAELQTVREENCHLNTELQEAKGRQEEQGAQVQRLKDKVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 LRERAVAAE------RQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 ELQK----ERDQAYSARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLRQLQAEPP
                                                 QSLDEARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVN
                                                                                                                ALQAQVCELQKERDQAYSARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLRQLQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGLHQLEADHSRMKREVSAHFHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.6%; Score 198.5; DB 11; Length 691; 23.7%; Pred. No. 0.0015; Live 64; Mismatches 119; Indels 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=OFA-SD; TISSUE=CEREBELLUM;
Vie-Luton M.-P., Francon J.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY078385; AAL85572.1; -.
SEQUENCE 691 AA; 77276 WW; E4FF5AA1784377FE CRC64;
                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  612 AA.
                                                                                                                                                                                                                                                                            AA.
                                                                                                                                                                                                                                                                          691
                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
KIAA1536 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     495 ELLEYMRKLEAR 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVL----KQEAR 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
Les 88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     096JV2
096JV2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43
                                                                                                                                                                                                                             RESULT 2
Q8R443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                      g
                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                 Db
                                                                                                                    ò
```

```
235 ESEQK---EQLRRLKNEMENERWHLGKTIEKLOKEMADIVEAS----RTSTLELQNOLDE 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRE--RAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELELQ-EQSLRT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 ASDQESGDEELNRIKEENEKLRSLTFSLAEK-----DILEQSLDEARGSRQELVERIHS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137 LQEENEKLQGRSEELERRVAQLQRQ------IEDLKGDEAKAKETLKKYEGEIRQL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=BRAIN;
MEDLINE-98116662; PubMed=9455484;
Seki N., Ohlira M., Nagase T., Ishikawa K., Miyajima N., Nakajima D.,
Nomura N., Ohara O.;
"Characterization of cDNA clones in size-fractionated cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 LQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAHFHEVLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
                                                                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelé
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                     Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
13.4%; Score 196; DB 4; Length 61
Best Local Similarity 25.8%; Pred. No. 0.0018;
Matches 74; Conservative 62; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             00DC42FDE419EED1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 SARDSAQREISQSLVE-----KDSLRRQVFELTDQVCELRTQLRQ 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343 TKRQLLEQTLKDLEYELEAKSHLKDDRSRLVKQMEDKVSQLEMELEE 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases EMBL; AB007914; BAA32280.1; -. EMBL; AL049569; CAB96825.1; -. SEQUENCE 1313 AA; 148254 MW; 00DC42FDE419EED1 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 15, Last annotation update)
KIAA0445 protein (DJ37C10.5) (KIAA0445).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1313 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from human brain.";
DNA Res. 4:345-349(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                    NCBI_TaxID=9606;
```

586 ATAAE-EREASLRERDAALKQLEALEKEKA 247 QREISGSLVEKDSLRRQVFEL	DO 14980 PRELIMINARY; PRT; 2115 AA.  AC 014980; DT 01-NOV-1996 (TrEMBLrel. 01, Created) DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) DT 01-NOV-1996 (TrEMBLrel. 20, Last annotation update) DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) DF NUMA protein. OS Homo sapiens (Human). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		RA Maekawa T., Kuriyama R.;  RT "Primary Structure and microtubule-interacting domain of the SP-H RT antigen: a mitotic map located at the spindle pole characterized as a RT homologous protein to NuMA."; R. J. Cell Sci. 105:589-600(1993). BR EMBL: 211583; CAA77669-1; DR HSSP; P80220; IDIP. FT CONFLICT 124 124 0 -> P (IN REF. 2). FT CONFLICT 1587 0 -> H (IN REF. 2). SQ SEQUENCE 2115 AA; 238274 MW; DA5686215054DBEE CRC64;	Duery Match  13.3%; Score 194; DB 4; Length 2115;  Best Local Similarity 26.6%; Pred. No. 0.0081;  Matches 93; Conservative 49; Mismatches 104; Indels 104; Ga  10 LQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAH	AANNTOLOARVEMLETERGOÖBA ORANNVSSCELELOEQSLRT :: :           : EQASQAHGARLTAQVASLTSELTORKLRSLTFSLAEKDILE ::   :           ASOGLRHQVEQLSSSLKQKE	
Query Match Best Local Similarity 25.9%; Pred. No. 0.0042; Matches 83; Conservative 56; Mismatches 102; Indels 79; Gaps 12;  Qy I ECLAGAIGSLQEELNQEKGQKEVILRRCQQL	Db 270 ELMAQKLVQAEREAQASLREQRAHEEDLQRLQ	OY 216 QLYREKVNALQAQVCELQKERDQAYSARDSAQREISQSLVEKDSLRRQVFELTDQV 271  DD 410RSTVNALTSELRDLRAQREEAAAHAQEVRRLQEQARDLGRQRDSCLREAE 460  QY 272 CELRTQLRQLQAEPPGVLKQ 291	RESULT 5 Q14981 DD Q14981 AC Q14981; DT O1-NOV-1996 (TEMBLrel. 01, Created) DT O1-NOV-1996 (TEMBLrel. 01, Last sequence update) DT O1-NAR-2002 (TEMBLrel. 20, Last annotation update) DF NUMA protein. OS HOMO Sapiens (Human). OS ENARAÇOGA: Metazoa; Chordata; Craniata; Vertebrata: Euteleostomi;	NCBL_TaxID=966;  RN [1] TaxID=966;  RN [1] TaxID=966;  RN EDLINE-92176238; PubMed=1541636;  RA MEDLINE-92176238; PubMed=1541636;  RA Compton D.A., Szilak I., Cleveland D.W.;  RT "Primary Structure of NuMA, an Intranuclear protein that defines a RT Novel Pathway for Segregation of Proteins at Mitosis.";  RL J. Cell Biol. 116:1395-1408(1992).  REMBL, 211584; CAA77670.1; -  SQ SEQUENCE 2101 AA; 236297 WW; 2097F679D4E38E69 CRC64;	Ouery Match 13.3%: Score 194; DB 4; Length 2101; Best Local Similarity 26.6%: Pred. No. 0.008; Matches 93; Conservative 49; Mismatches 104; Indels 104; Ga 10 LQEELNOEKGOKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAH 11:	09 63 FHEVLRIKDEMISIS

Indels 104; Gaps 15;

```
48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09V587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δý
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                 CYRAIN-C57BL/65; TISSUE-PANCREAS;

KX Kawai J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Kawai J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Alzawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Andota K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Radota K., Matsuda H.A., Sabburner M., Batalov S., Casavant T.,

Radota K., Matsudo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Saki K., Okido T., Euruno M., Anno H., Baldarelli R., Barsh G.,

Brownstein M.J., Bult C., Pletcher C., Fullita M., Gariboldi M.,

Ruonstein M.J., Bult C., Pletcher C., Fullita M., Markoldi M.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Nyanawa M., Marchion K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nordone P., Marchion K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nordone P., Marchiola K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nordone P., Marchion K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nordone P., Marchion K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nordone P., Marchion K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 REQEKLLROLKEFQADKEQSEAELQTVREENCCLNTELEEAKSR----QEEQGAQVQRLKD 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVCELQK----ERDQAYSARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLRQLQA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LONGLDESQOERNDLMQLKLQLEDQVTELRSRVQELEAALATARQEHSELTEQYKGLSRS 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------ELNRLKEENEKLRSLTFSLAEK-DILEQSLDEARGSRQELVER 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LH--RSRLEVAEVNGRLAELSLHMKEEKCQWSKERTGLLQSMEAE-----KDKILKLSA 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QEELYLLKQ------ELQRANMVSSC-ELELQEQSLRTASDQESGDE----- 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGLHQLEADHSRMKREVSAHFHEVLRLKDEMLSLSLHYSNALQEKELAASRCRS----L 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 LQEELNQEKGQKEVLLR-----TRA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---ROREQYWEEKEQTLLQFQKSKMACQLYREKVNALQA
                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL: AKO07393; BAB25009.1;
MGD; MGI:1914738; 18100099806Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 11; Length 691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.2%; Score 193.5; DB 11; Length 22.9%; Pred. No. 0.0028; ive 66; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77280 MW; 4759E5478839D9B7 CRC64;
                Last sequence update)
Last annotation update)
   Created)
01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 1810009806fik protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 22.9
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | :| | | 1||
492 EKQELLEYMRKLEAR 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPPGVL----KQEAR 294
                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              691 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 IHSLRERAVAAE-
                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     070365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            õ
    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
```

2238 AA.

PRT;

PRELIMINARY;

070365

ΠD

```
553 ESLALEELELOKKAILTESENKLOELGOEAARYRTRILELETSLEKSLOESKTOSEHLAV 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SL-AEKD-----ILEQSLDEARGSRQE----LVERIHSL-RERAVAAERQREQYWEE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201 KEQTLLQFQKSKMACQLY-----REKVNALQAQVCELQKERDQAYSARDSAQREISQSL 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------LHYSN-ALQEKELA---ASRCRSLQEEL------YL-LKQELQRA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 NMVSSCELELQEQSLRTASD---QESGDE------EL----NRLKEENEKLRSLTF 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               373 NLIEQLEQDKGMVITETKRQMLETLELKEDEIAQLRSHIKQMTTQGEELREQKEKSERAA 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-BALBACT TISSUE-BRAIN; Gay D., Beiler B.M., Zhao H., Bhandoola A., Tomayko M.M., Murali R., Gay D., Beiler B.M., Zhao H., Bhandoola A., Tomayko M.M., Murks M.S., Greene M.L.; Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---HEVLRLKDEMLSLS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-BRAIN;
STRAIN-BALB/C; TISSUE-BRAIN;
SCOWAN D.A., Gay D., Beiler B.M., Zhao H., Yoshino A., Davis J.G.,
TOMMAYO M.M., Murzain R., Greene M.I., Marks M.S.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AR051337; AAC05573.2; -..
SEQUENCE 2238 AA; 257562 MW; 494EA2C111F0165B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 SLQEELNQEKGQ-----KEVLLRRCQ-----QLQEHLGLAETRAEGLHQ-----
                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUB-BRAIN;
COWAN D.A., GAY D., Beiler B.M., Zhao H., Yoshino A., Davis J.G.
TOMAYKO M.M., Murali R., Greene M.I., Marks M.S.;
"Characterization of mouse tGolgin-1 (golgin-245/ trans golgin-Characterization of mouse tGolgin-1 (golgin-245/ trans golgin-230/256kD golgin) and its upregulation during oligodendrocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.2%; Score 193.5; DB 11; Length 2238; 24.9%; Pred. No. 0.0091; ive 59; Mismatches 121; Indels 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 732 GDADKM-KOALE----AELEEORRHHOREVGSISEOOELT 766
                     01-JUN-2002 (TTEMBLTel. 21, Last sequence update) 01-JUN-2002 (TTEMBLTel. 21, Last annotation update) Golgi autoantigen golgin subtype a4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         255 VEKDSLRRQVFELTDQVCELRTQLRQLQAEPPGVLKQEART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
(TrEMBLrel. 07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Cell Biol. 0:0-0(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 13.2%
Best Local Similarity 24.9%
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                 Mus musculus (Mouse).
01-AUG-1998 (
01-JUN-2002 (
01-JUN-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9V587
Q9V587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DA LA
```

```
Ninein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9VJE5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9VJE5
   128
                                                                     178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                         RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9VJE5
                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
   δ
                                 g
                                                                   Qγ
                                                                                                 g
                                                                                                                                      ΩŊ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                           RAMEN SELEMBLEY;

RAMIN SELEMBLELEY;

RAMAN SELEMBLELEY;

RAMAN SELEMBLELEY;

RAMAN SELEMBLELEY;

RAMAN SELEMBLELEY;

RAMAN SELEMBLE S. E., Hill R.A., EVARIDS C.A., GOCGANG J.D.,

RAMAN S. CALINKER S.E., Richards S., Ashburner M., Henderson S.N.,

RAMA DAID G.C., WOTHOMAN J.R., Palazel R.G., Champe M., Pfeiffer B.D.,

RAMA Abril J.F., Agbayari A., An H.-J., Andrews Pfannkoch C., Baldwin D.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Basu A., Baxendale J., Brokstein P., Brottier P.,

RAMA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Deltakavo S.,

RAMA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RAMA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RAMA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RAMA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RAMA Cherry J.M., Cabbiellan A.E., Garg N.S., Gelbart W.M., Classer R.,

ROSTOR C., Gabriellan A.E., Garg N.S., Gelbart W.M., Classer R.,

RAMA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RAMAN A., Gong F., Gorrell J.H., Gu Z., Glabar W.M., Classer R.,

RAMAN A., Manch B., McIntosh T.C., McIeod M.P., McPherson D.L.,

RAMAN A., May M.M. Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RAMAN A., Mount S.M., Moy W., Murphy B., Murphy L., Muzny D.M., Nelson D.K.,

RAMAN A., Mount S.M., Moy W., Murphy B., Murphy L., Muzny D.M., Nelson D.K.,

RAMAN A., Mount S.M., Woday R., Murphy L., Muzny D.M., Nelson D.K.,

RAMAN A., Spier E., Spradling A.C., Stapleton M., Stupsk M., Sun E.,

Syriskas R., Moodage T., Worley K.C., Wu D., Yang S., Yang S., Yang A., Shang X.H., Zhong F.N., Zhong W., Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                 Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 GALTSLEEAI----GDKE---KQMAQLRDQRDRAE-----HEKQEERDLHEREVADYKI 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | | | | : | 1: DWESTKQRIARLELENERLKHDLERSQTTFGRTTMTTSQELDRAQERADKASAELRRTQA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAIGSLQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAHFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 KLRAAESEVEKLOTRLERAVTERERLEIKLEASOSELGKSKAELEKA----TCEMGRSSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1456 AA; 164239 MW; 49E04C6716443ECA CRC64;
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.1%; Score 192; DB 5; 25.1%; Pred. No. 0.0072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AE003833; AAF58930.1; -. FlyBase; FBgn0033420; CG1931. InterPro; IPR000533; Tropomyosin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00194; TROPOMYOSIN,
                 CG1931 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1618 ELSQKNSQN-----KEELKTLNQRLAEMLCQREEPGACTSEKWEQENASLKEELDHYK 1670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1671 VQTSTLVSSLEAELSRIKLQTHVMEQENLLLKDELERLKQLHRCPDLSDLQQKMSSVLSY 1730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1780 KSQLAVSQAKVQDLEDVLQNVNLQMAEIESDLQVTRQEKEAVKQEVMSLHRQLQNAIDKD 1839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 RMKREVSAHFHEVLRLKDEMLSLSLHYSNAL-QEKELAASRCRSLQEELYLLKQEL---- 108
                                                                                                                                        ----TASDQESGDEELNRLKEENEKLRSLTFSLAEKDILEQSLDEARGSRQEL-----V 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Belkaid Y., Milon G., Crocker P.R.; "Molecular characterisation of ninein, a new coiled-coil protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206 -LQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSAQREIS-----QSLVEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                333 ELRVTQSDAERAREEAAALQEKLEKSQGEVYRLKAK -- LENAQGEQESLRQELEKAQSGV
                                                                                                         ERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 NEKLRSLTFSLAEKDILEQSLDEARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bouckson-Castaing V., Moudjou M., Ferguson D.J.P., Mucklow M., Belkaid Y., Milon G., Crocker P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                   238 QAYSARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLRQLQAE 284
                                                                                                                                                                                                                                                  | | | : : | | : : | | 41 HLQDKLDKACTENRRLVLEKEKLTYDYDNLQSQLDKALGQAARMQKE 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249168 MW; FDB8EC0F240E58E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1840 ----WVSETAPHLSGLRGQQRRLSWDKLDHLMNEEPQLLCQESK 1879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 -QRANMVSSCELELQEQSLRT-ASDQES--GDEELNRLKE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259 SLRRQVFELTDQVCELRTQLRQ-----LQAEPPGVLKQEAR 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.1%; Score 192; DB 11; 24.4%; Pred. No. 0.011; iive 68; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 AIGSLQ-EELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:105108; Nin.
InterPro; IPR002048; EF-hand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01,
01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Cell Sci. 108:0-0(1996).
EMBL; U40342; AAA83234.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the centrosome."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                         Q61043
Q61043;
```

```
d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                óγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δλ
                                                                                                                                                                                                  ŏλ
                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                      δλ
                                                                                             g
                                                                                                                                                               q
                        g
                                                             ΟY
                                                                                                                                   δ
                                                                                                                                                                             RECEINING—SOURCE FOR A. A.

RECAILNE—SOURCE FOR A. A.

RECAILNE—SOURCE FOR A. B.

RECAIL F. R. A. B.

RECAIL J. F. A. A. DEWLS S. F. Richted S., Ashburner M., Henderson S.N.,

RA BALLEW R. B.

RESON K. M. BESU A., BARMANIA A., AN H. J., AN HALOS G.L.G.,

RA BALLEW R. M., BASU A., BARMANIA A., AN H. J., AN HALOS G.L.G.,

RA BALLEW R. M., BASU A., BARMANIA A., AN H. J., AN HALOS G.L.G.,

RA BALLEW R. M., BASU A., BARMANIA A., AN H. J., AN HALOS G.L.G.,

RA BALLEW R. M., BASU A., BARMANIA A., AN H. J., AN HALOS G.L.G.,

RA BALLEW R. C., BUSHAN M. R., BOURT J., RAGRESTOP D., BOLSHAROV S.,

RA BURLIS K.C., BUSHAN M. R., BOURT J., CARDER E., CORNET A., DOWLER P., BOLCHER A., DOWLER S., DUNOW B.C., DUNOW B.C., DOWN R., DOWLER S., CARLET B., DOWLES P.,

RA BALLEW R. J. BANGELLIA A.E., DOWNES M. DUGAN R. C., DUNOW B.C., DUNO P.,

RA HARTIS N.L., HARVEY D., HEMIAND T. J., HERTRANGE J. R., PRATIS N.L., HARVEY D., HEMIAND T. J., HERTRANGE J. R., ROHLEF S., MAN HARTIS M.,

RA HOSTID D., MOLE D. R., ROWLEND T. G., WOLLE D., WORLY D. M., NELSON D.L.

RA MERILIA M. KAINE B., MCINTOS T. C., NETHING T., WELL M., DOWLER S., MOLLE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     484 GALQEEIAKLQEKMTIQQKEVESRIAEQLEEEQRLRENVKYLNEQIATLQSELVSKDEAL 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        504 DSLESERVNKTDECEILQTEVRMRDEQIRELNQQLDEVTTQLNVQKADSSALDDMLRLQK 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --LGLAETRAEGLHQ----LEADHSRMKREVSAHFH------EVLRLKDEML----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D6F7916A9C532F16 CRC64;
 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.1%; Score 191.5; DB 5; 23.7%; Pred. No. 0.0088; ive 69; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -SLSLHYSNALQEKELAASRCRSLQEELYLLKQEL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSLQEELN--QEK---GQKEVLLRRCQQLQEH-----
                                                                     Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02; CAP_GLY; 2.
1690 AA; 189063 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FlyBase; FBgn0020503; CLIP-190.
InterPro; IPR000938; CAP-Gly.
01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17, CLIP-190 protein. CLIP-190 OR CG5020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE003655; AAF53604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                        Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Sim
Matches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

```
15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQKERDQAYSARDSAQREISQSLVEKDSLRRQV----FELTDQVCELRTQLRQLQAEPPG 287
----QRANMVSSCELEL----QEQSLRTASDQESGDEELNRLKE--ENEKL-RSLTFSL-- 156
                                                                                                                                                                   -----ERAVAA----ERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCE 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----LOAQVCELOKERD-------QAYSARDSAQREISQSLVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 SGDEELNRLKEENEK----LRSLTFSLAEKDILEQSLDEARGSRQELVERIHSLRERAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAERQ-----REQYWEEKEQTLLQFQKSKMACQLYREKVNA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --LGLAETRAEGLHQ----LEADHSRMKREVSAHFH------EVLRLKDEMLSLSLHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 SNALQEKELAASRCRSLQEELYLLKQELQRANM----VSSCELELQEQSLRTASD----OE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      720 NAINQIQLEKESIEQQLALKQNELEDFQKKQSESEVHLQEIKAQNTQKDLELVESGESLK
                        664 EGTEEKSTLLEKTEKELVQSKEQAAKTLNDKEQLEKQISDLKQLAEQEKLVREMTENAIN
                                                                                                                                                                                             ----EARGSRQ--ELVERIHSLR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189103 MW; BE4F48FD15F17A7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Microtubule binding protein D-CLIP-190.
CLIP-190 OR CG5020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 191.5; DB 5;
Pred. No. 0.0088;
1; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 GSLQEELN--QEK---GQKEVLLRRCQQLQEH-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lantz V.A., Miller K.G.;
J. Cell Biol. 0:0-0(1998).
ENBL; AF041382; AAB96783.1; -.
FlyBase; FB90000053; CLIP-190.
InterPro; IPR000938; CAP-Gly.
Pfam; PF01102; CAP_Gly?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.18; Scor
21.48; Pred
tive 71; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                   ---AEKDILEQSLD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1690 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=OREGON R;
                                                                                                                                                                                                                                                                                                                                            288 VLKQEAR 294
                                                                                                                                                                                                                                                                                                                                                                                  SLEEEAK 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
044929
ID 044929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                           232
                                                                                                                                                                                                                                                                                                     838
                                                                                                                                                                                                                                                                                                                                                                                      897
                                                                                        157
```

δ g ò q

```
516
                                                                                                                                                                                                                                                                                                                                                                                                                        293 AVAAKDSQLAVLKVRLQEADQLLSTRTEALEALQSEKSRIMQDQSEGN-----SLQNQ 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERAVAAERQR------EQYWEEKEQTLLQF-QKSKMACQLYREKVNAL----- 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------QAQVCELQKERDQAYSARDSAQREISQSLVEKDSLRRQVFE 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHS---RMKREVSAH---FHE 65
                                                                                                                                                                                    MEDLINE=99115642; PubMed=9915833;
Bascom R.A., Srinivasan S., Nussbaum R.L.;
"Identification and characterization of golgin-84, a novel Golgi integral membrane protein with a cytoplasmic coiled-coil domain.";
J. Biol. Chem. 274:2953-2962(1999).
EMBL; AF085199; AAD09753.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EELNQEKGOKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHS---RMKREVSAH---FHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 VLRLKDEMLS-LSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELELQEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLRTASDQESGDEELNRLKEENEKLRSLTFSLAEKDILEQSLDEARGSRQELVERIHSLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERKYSDEKKRVDELQQQVKLYKLNLESSKQELIDYKQKATRILQSKEKLINSLKEGSGFE
                                                                                  Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                    74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74;
                                                                                                                                                                                                                                                                                                                                  Length 731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 13.1%; Score 191; DB 4; Length 731
Local Similarity 26.5%; Pred. No. 0.0041;
nes 86; Conservative 43; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                              ; Score 191; DB 4; Length 73:
; Pred. No. 0.0041;
43; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: BC023021.1; -
SEQUENCE 731 AA, 82976 WW, 6661F19BA16425B0 CRC64;
                                                                                                                                                                                                                                                                                   19753.1; -.
82990 MW; E708D023C60B02BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Golgi autoantigen, golgin subfamily a, 5.
Homo sapiens (Human).
                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        731 AA
   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTDQVC-----ELRTQLRQLQAE 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  517 LHDQIAGQKASKQELETELERLKQE 541
                                                                  Homo sapiens (Human)
Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                              13.1%;
26.5%;
   10,
10,
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 26.5%
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                              731 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=PLACENTA;
                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                          TISSUE=TESTIS;
                                                   Golgin-84.
                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8TBA6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8TBA6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267
                                                                                                                                                                                                                                                                                                                                                                                                    12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OSTBA6
 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \dot{\Omega}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klugbauer S., Demidchik E.P., Lengfelder E., Rabes H.M.; "Detection of a novel type of Ret rearrangement (PTCS) in thyroid carcinomas after Chernobyl and analysis of the involved Ret-fused gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 AVAAKDSQLAVLKVRLQEADQLLSTRTEALEALQSEKSRIMQDQSEGN-----SLQNQ 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----QAQVCELQKERDQAYSARDSAQREISQSLVEKDSLRRQVFE 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  457 GLDSSTASSMELEELRHEKEMQREEIQKLMGQIHQLRSELQDMEAQQVNEAESAREQLQD 516
                                     125 SLRTASDQESGDEELNRLKEENEKLRSLTFSLAEKDILEQSLDEARGSRQELVERIHSLR 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 VLRLKDEMLS-LSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELELQEQ 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 EELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHS----RMKREVSAH----FHE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERAVAAERQR------EQYWEEKEQTLLQF-QKSKMACQLYREKVNAL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                 KDSLRRQ------VFELTDQVCELRTQLRQLQAE------PPGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 191; DB 4; Length 58;
; Pred. No. 0.0033;
43; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cancer Res. 58:198-203(1998).
EMBL; AJ132949; CAB36967.1; -.
SEQUENCE 585 AA; 66384 MW; FEEAF1F35F551681 CRC64;
                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     731 AA.
                                                                                                                                                                                                            ΑA
                                                                                                                                                                                                        585
                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIDQVC-----ELRTQLRQLQAE 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LHDQIAGOKASKQELETELERLKQE 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98103628; PubMed=9443391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 13.1%;
Best Local Similarity 26.5%;
Matches 86; Conservative 43
                                                                                                                                                                                                                                          13,
13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                        Q9UQQ7;
01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klugbauer S.;
Submitted (FEB-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. TISSUE-THYROID;
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                             LEEEAK 903
                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-THYROID;
                                                                                  LKQEAR 294
                                                                                                                                                                                                                                                                                                protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    095287
095287;
                257
                                                                                                                    868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
095287
ID 09528
AC 09528
                                                                                  289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267
                                                                                                                                                                      RESULT 13
                                                                                                                                                                                        09U007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
```

õ g ò QQ ò q οy g ò OD ò

13;

```
185 ERAVAAERQR----- EQYWEEKEQTLLQF-QKSKMACQLYREKVNAL----- 225
                                                                    125 SLRTASDQESGDEELNRLKEENEKLRSLTFSLAEKDILEQSLDEARGSRQELVERIHSLR 184
LTDQVC-----ELRTQLRQLQAE 284
                                                                                                                 | ||:
| LHDQIAGQKASKQELETELERLKQE 541
                                                                                                          267
                                                                         397
                                     Oy
Oy
Oy
                                                                                             pp
                                                                                                          ò
      QQ
                          QQ
```

Search completed: January 22, 2003, 08:56:38 Job time : 52.9946 secs

```
Human stomach canc
Human protein sequ
Human PKIN-13 prot
Novel human diagno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanog
Drosophila melanog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human caspase recr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human predicted ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        caspase recr
                                                                                                                                 (without alignments)
683.714 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS2/gcgdata/geneseq/jeneseqp-embl/AA1982.DAT:*
/SIDS2/gcgdata/geneseq-embl.AA1983.DAT:*
/SIDS2/gcgdata/geneseq-embl.AA1983.DAT:*
/SIDS2/gcgdata/geneseq-geneseqp-embl.AA1985.DAT:*
/SIDS2/gcgdata/geneseq-geneseqp-embl.AA1985.DAT:*
/SIDS2/gcgdata/geneseq-geneseqp-embl.AA1986.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl.AA1988.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl.AA1988.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl.AA1998.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl.AA1998.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl.AA1999.DAT:*
                                                                                                           2003, 08:49:35 ; Search time 18.125 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS2/gcgdata/geneseg/genesegp-embl/AA1997.DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA1998.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS2/gcgdata/geneseg/genesegp-embl/AA1999.DAT:
                                                                                                                                                                                                                      1 QVTMLAFQGDALLEQISVIG......GLLRRVDGFCCLSVKVNTDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS2/gcgdata/geneseq/genesegp-embl/AA1980.
/SIDS2/gcgdata/geneseg/genesegp-embl/AA1981.
                                                                                                                                                                                                                                                                                                                                                           908470
GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                    908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                      US-09-767-215-2_COPY_568_660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE07164
AAE07165
AAU01207
ABB64619
ABB62423
AAM93968
AAM93968
AAM93368
AAM93368
                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         П
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A_Geneseq_101002:*
                                                                                                                                                                                                                                                                                                                                                                                              length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11139
11445
11445
1916
1916
548
548
548
                                                                                                           January 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14:
15:
16:
19:
                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139
85.5
85.8
85
80
80
80
80
80
                                                                                                                                                                                                        Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ٠.
                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 9 8 4 3 2
                                                                                                             o
o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š.
                                                                                                             Run
```

novel ORFX 0	Human betal-syntro	polype	PDZ domain-contain	Neuron-associated	Mature protein con	Protein containing	Drosophila melanog	Protein containing	Amino acid sequenc	Protein containing	=	Arabidopsis thalia		· Arabidopsis thalia	Herbicidally activ	Drosophila melanog	Drosophila melanog	Human protein cont	Human protein tyro	Intracellular prot	Human PTPL1 phosph	Amino acid sequenc	Fly transducisome	Drosophila melanog	Amino acid sequenc	PD2P1	Novel signal trans	PDZ domain-contain	domain-c	uman diagn	Human P-dlg protei	prote			
ABG66725 AAB42658	AAB21149	AAM93296	AAY04741	AAB01383	AAY 04731	AAY 04730	ABB64459	AAY 04732	AAY53753	AAY04733	ABB62642	AAG05041	AAG05040	AAG05039	ABB93423	ABB57855	ABB67265	AAU87934	AAR71498	AAW75999	AAY90272	AAB19343	AAW92953	ABB59957	AAY24025	AAU87943	AAU17383	AAY04739	AAY04740	ABG09545	AAW72748	AAU87918		ALIGNMENTS	
23	21	22	20	21	20	20	22	20	21	20	22	21	21	21	23	22	22	23	16	19	21	21	20	22	20	23	22	20	20	22	13	23			
1651 1675	538	304	763	82	8	37	55	8	2037	0	974	229	280	327	503	871	87	1535	4	46	46	48	674	67	1881	96	158	272	319	658	674	1111			
17.0	v		ď.	ω.	'n.	Ď.	S.	'n.	ω.	ω.	S.	5	5.	S.	ъ.	S.	5	5.	5.	5.	Ŋ.	δ.	ъ.	5.	ω.	S.	5	5	ď.	5.	S.	Š.			
79.5	4.	, _	73	73	73	73	73	73	73	7	ς.	i.	ä	Ή.	Ξ.	ij	Ξ.	71.5	Ή.	1	ä	Ξ.	7.1	71	71	70	70	70	70	70	70	70			
111	13	12	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	38	40	41	42	43	44	45			RESULT 1

Human; caspase recruitment domain-14; CARD-14; chromosome 17; nuclear factor-kappa B; NF-kB; cell growth; cell death; cancer; therapy; autoimmune disorder; systemic lupus erythematosus; neurological disorder; Alzheimer's disease; Parkinson's disease; inflammatory disorder; anaemia haematological disorder; myelodysplastic syndrome; myocardial infarction; stroke; immune disorder; Crohn's disease; allergic rhinitis; infection; cell signalling disorder; cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antibacterial. 6..9 /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site" 18.21 /note= "Casein kinase II phosphorylation site" 25.27 /note= "Protein kinase C phosphorylation site" 12..15 /note= "Casein kinase II phosphorylation site" Human caspase recruitment domain-14 (CARD-14) AAE07164 standard; Protein; 1004 AA Location/Qualifiers 10..116 /label= CARD\_domain (first entry) Modified-site Modified-site Modified-site Modified-site sapiens 06-NOV-2001 AAE07164; Domain Homo AAE07164 

```
"CAMP- and cGMP-dependent protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Casein kinase II phosphorylation site"
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "N-myristoylation site"
1002..1004
/note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .844
.e= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..870
.te= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Casein kinase II phosphorylation site"
                                                                                                                     "Casein kinase II phosphorylation site"
                                                                                                                                                                                                              "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                          "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An isolated caspase recruitment domain polypeptide useful for
              .605
ce= "Casein kinase II phosphorylation site"
                                                          "Casein kinase II phosphorylation site"
                                                                                        "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Casein kinase II phosphorylation
                                                                                                                                                                                                                          .728
.e- "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                  "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .949
.e= "Peroxisomal targetting signal"
                                                                                                                                                                                                                                                                                                                                                                                                            'note= "Peroxisomal targetting signal"
96..799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'hote= "Protein ni...
370..872
'mote= "RGD cell attachment sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   326..1004
/label= Guanylate_kinase_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "N-myristoylation site"
                                                                                                                                                                                                                                                                        "N-myristoylation site"
                                                                                                                                                                                "N-myristoylation site"
"N-glycosylation site"
                                                                                                                                                                                                                                                                                                       "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                              nosphorylation site"
35..793
                                                                                                                                                     /label= SH3_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-FEB-2000; 2000US-0181159.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JAN-2001; 2001WO-US02087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , ...979
/note= "
                                                                                                                                                                                                                                    /note= "cu
                                                                                                                                                                                                                                                                                                                                  /note= "PJ
760..763
                                                                                                                                                                                /note= "N
725..727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "P
944..947
                                                                                                                                                                                                                                                                                                                                                                                                                                                        805
                                                                                                                                                                                                                                                                                                                  .761
                                                                                                      ..677
                                                                                                                                                                                                                                                                                         .740
                                                                                                                       /note=
                                                                                                                                                                                                                                                                             note=
                                                                                                                                                                                                                                                                                                                                                                                                                                             'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note=
                                                                                                                                                                                                                 'note=
                                                                                                                                                                                                                                                                                                                                                                   note=
                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-497073/54.
N-PSDB; AAD13447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200159065-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Addified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Addified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Addified-site
               Modified-site
                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Addified-site
                                            Modified-site
                                                                           Modified-site
                                                                                                         Modified-site
                                                                                                                                                                   Modified-site
                                                                                                                                                                                                 Andified-site
                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bertin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eptide
                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "Casein Kinase ..., 290..293
/note= "Casein Kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "Protein Aimese".
107..310

/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .472
e= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .504
e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                              note= "Casein Kinuse -- .
150..252
/note= "Protein Kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .283
e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .300
.e- "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .309
e= "Protein Kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .369
e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .386
e- "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      452
e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .465
e= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
262
e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Protein kinase C phosphorylation site"
                                               /note= "Protein kinase C phosphorylation site"
                                                                                                                                        "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                               "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                           /note= "N-myristograce...
165..168
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                     /note= "Tyrosine ^____.
221..224
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                 .243
.e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      365
.e= "Tyrosine kinase phosphorylation site"
                  /note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                       .227
.e= "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .381
.e= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .466
e= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                          .256
e- "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .406
e= "Leucine zipper pattern"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "N-myristoylation site"
589..592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .516
e= "N-myristoylation site"
                                                                                                                                                                                 ...135
:e= "N-myristoylation site"
                                                                                      117..122
/note= "N-myristoylation site"
121..123
                                                                             /note= "N-glycosylation site"
                                                                                                                                                                      'label Coiled_Coil_domain
                                                                                                                                                                                                                                                                                                                                                                                   'label= k-Box_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     label- PDZ_domain
                                                                                                                                                                                                                                  /note= "Ca
161..166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..592
                                                                                                                                                                                                    'note= "N
34..137
                                                              .117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note=
                                                                                                                                            'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
      Modified-site
                                  Modified-site
                                                              Modified-site
                                                                                            Modified-site
                                                                                                                          Modified-site
                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
```

site"

```
ò
                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; caspase recruitment domain-14; CARD-14; chromosome 17; nuclear factor-kappa B; Nr-kB; cell growth; cell death; cancer; therapy; autoimmune disorder; systemic lupus erythematosus; neurological disorder; Alzheimer's disease; Parkinson's disease; inflammatory disorder; anaemia haematological disorder; myelodysplastic syndrome; myocardial infarction; stroke; immune disorder; Crohn's disease; allergic rhinitis; infection; cell signalling disorder; cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antibacterial.
                                                     The present sequence is human caspase recruitment domain-14 (CARD-14). The CARD-14 gene is located on chromosome 17. The CARD-14 is used for the detection of modulators that modulates the ability of CARD-14 to bind to Bcl-10 and stimulates phosphorylation of Bcl-10 or activation of nuclear factor-kappa B (NF-kB). The CARD-14 is useful for regulating growth and cell death and useful for the treatment of cancer. It is also useful for the treatment of cancer. Stream is also useful for the treatment of autoimmune disorders (e.g., systemic lupus erythematosus), neurological disorders e.g., Alzheimer's and Parkinson's disease, inflammatory disorders, haematological disorders (e.g., amemia, myelodysplastic syndromes), myocardial infarctions, strokes, immune disorders (e.g., conformes), myocardial infarctions.
regulating growth and cell death and useful for the treatment of cancer
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                    1 QVTMLAFQGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLF 60
                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human predicted caspase recruitment domain-14 (CARD-14).
                                                                                                                                                                                                                                     Score 467; DB 22;
Pred. No. 2.2e-51;
                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                               628 KAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTDG 660
                                                                                                                                                                                                                                                                                                                                   KAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTDG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Encoded by TGG"
                                                                                                                                                                                                                                                                                                                                                                                                                  AAE07165 standard; Protein; 1139 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
700
                                 Claim 1; Fig 1A-1E; 109pp; English.
                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JAN-2001; 2001WO-US02087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-FEB-2000; 2000US-0181159
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                          Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-497073/54.
                                                                                                                                                                                                            1004 AA;
                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAD13448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200159065-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bertin J;
                                                                                                                                                                                                                Sednence
                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ношо
ò
                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                      g
```

```
ö
                                                                                                                                                     The present sequence is predicted human caspase recruitment domain-14 (CARD-14). The CARD-14 gene is located on chromosome 17. The CARD-14 is used for the detection of modulators that modulates the ability of CARD-14 to bind to Bol-10 and stimulates phosphorylation of Bol-10 or activation of nuclear factor-kappa B (NF-kB). The CARD-14 is useful for activation of nuclear factor-kappa B (NF-kB). The CARD-14 is useful for It is also useful for the treatment of autoimmune disorders (e.g., aystemic lupus erythematosus), neurological disorders e.g., Alzheimer's and Parkinson's disease, inflammatory disorders, haematological disorders (e.g., amemaia, myelodysplastic syndromes), myocardial infarctions, strokes, immune disorders (e.g., Crohn's disease, allergic rhinitis), cell signalling disorders and certain viral and bacterial infections.
An isolated caspase recruitment domain polypeptide useful for regulating growth and cell death and useful for the treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVTMLAFQGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; caspase recruitment domain; CARD-11; Bcl-10; NF-kappaB;
apoptosis; hyperproliferative disorder; autoimmune; neurological;
inflammatory disorder; viral infection; stress-related response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "cAMP- and cGMP-dependent protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 467; DB 22; Length 1139; 100.0%; Pred. No. 2.6e-51; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100..102
/note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /notes "Casein kinase II phosphorylation site"
168..171
175..183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note- "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162..165
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ...103
ce= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human caspase recruitment domain, CARD-11 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Coiled coil domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          678 KAVLEDITLEEAVGLLRRVDGFCCLSVKVNTDG 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KAVLEDITLEEAVGLLRRVDGFCCLSVKVNTDG
                                                                                                             Disclosure; Fig 2A-2C; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "CARD domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU01207 standard; Protein; 1147 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1139 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU01207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ношо
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU0120
```

/note= "Protein kinase C phosphorylation site"

```
/note= "cAMP- and cGMP-dependent protein kinase
 phosphorylation site"
                                                                                                                                                                                                                             /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                           /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.00-7.782
/Anote= "Casein kinase II phosphorylation site"
787..789
                                                                                                                                                    note= "Protein kinase C phosphorylation site" 71..474
note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                       008. 510
'note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                 /note= "Protein Aimac. - 578..581
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                  .689
e= "Protein Kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                           .25..728
"note= "Casein kinase II phosphorylation site"
61..766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ...767
ce= "Casein kinase II phosphorylation site"
                                                                              .289
e= "Casein kinase II phosphorylation site"
                                                                                            .292
.e- "Protein kinase C phosphorylation site"
                                                                                                                                                                                        . 479
te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                .695
.e= "Casein kinase II phosphorylation site"
                                                                                                                   site"
              "Casein kinase II phosphorylation site"
                                                           site"
"Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                    .641
.e= "Glycosaminoglycan attachment site"
                                                                                                          ..381
te= "Casein kinase II phosphorylation
                                                         "Protein kinase C phosphorylation
                             "Tyrosine kinase phosphorylation
                                                                                                                                                                                                                                                                               587..592
/note= "N-myristoylation site"
634..637
                                                                                                                                                                                                                                                                                                                                                                                                                                     "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                      "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "N-glycosylation site"
                                                                                                                                                                         .475
:e= "N-glycosylation site"
                                            'note= "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                            "N-myristoylation
                                                                        "Amidation site"
                                                                                                                                                                                                                                                                                                                                               "MAGUK domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..834
+e= "SH3 domain"
                                                                                                                                                                                                                                                                                                                                 "PDZ domain"
                                                         /note= "P<sub>J</sub>
282..285
                                                                                                                                                                                                                                                                                                                                                                                                         /note= "C.
698..703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     674..
                                                                                                                                                                                                                                                                                                                                                                                                                             ..715
                      .195
                                                  ..245
                                                                                                                                                                                                                      .513
                                                                                                                                                                                                                                                                                                                          748
                                                                                                                                                                                                                                                                                                                                        ..1147
        ..185
                                    . 244
                                                                                                                                               .461
                                                                                                                                                                                                                                            558..560
                                                                                                                                                                                                                                                                                                                                                /note=
638..64
                                                                                                                                                                                                  /note=
508..51
                                                                                                                                                                                                                                                                                                                                                                                                                        'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note=
                                                                                                                    note=
                                                                                                                                                                                   note=
                                                                                                                                                                                                                                                                                                                                                              note=
                note=
                                                                         'note=
                                                                                       note=
                                                                                                     'note=
                                                                                                                                                                                                                                                                                                                                                                             'note=
                                                                                                                                                                                                                                                                                                                                                                                           'note=
                                                                                                                                                                                                                                                                                                                          635.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                               Modified-site
                                                                                                                                                             Modified-site
                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
        Modified-site
                      Modified-site
                                    Modified-site
                                                  Modified-site
                                                                 Modified-site
                                                                               Modified-site
                                                                                             Modified-site
                                                                                                          Modified-site
                                                                                                                         Modified-site
                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
```

```
The present sequence represents novel human caspase recruitment
domain, CARD-11. The polynucleotide encoding this sequence was
isolated from a human T-cell DONA library. Also described are
novel human sequences for CARD-9 and CARD-10 (AAU01205, AAU01206)
and rat CARD-9 (AAU01204). CARD-9, CARD-10 and CARD-11 interact
with Bol-10 which is thought to activate nuclear factor (NF) kappaB
cond apoptosis. The sequences of the invention can be used for
treating a disorder associated with abnormal levels of apoptosis by
modulating the expression or activity of CARD-9, CARD-10, or CARD-11.
They can be used for the treatment of hyperproliferative disorders
(e.g. cancer), autoimmune disorders (e.g. systemic lupus erythematosus),
neurological disorders (e.g. Alzheimer's disease), inflammatory disorders
(e.g. cronn's disease), and viral infection (e.g. HIV). The CARD
polypeptide, polynucleotide and an antibody which selectively binds to
CARD can be used in screening and detection assays (e.g. chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel caspase recruitment domain (CARD) proteins, CARD-9, CARD-10, CARD-11, useful as targets for therapy, as immunogens, and in screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                  fnote= "Casein Kinase ...,
335..937
Anote= "Protein Kinase C phosphorylation site"
                                                                                                                                                                                                                                                            site"
                                                                                                                                                                                                                                                                                                                                                           site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "Casein kinase II phosphorylation site"
120..1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note≈ "Casein kinase II phosphorylation site"
                      "Casein kinase II phosphorylation site"
                                                                                                                  "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Tyrosine kinase phosphorylation site"
1050..1055
1080..1051
1088..1091
                                                                                                                                                                                                                           372..875
/note= "Casein kinase II phosphorylation : R82..1147
/note= "Guanylate kinase (GUK) domain" 897..900
                                                                                                                                                                                   .859
e= "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                            . 929
ce= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "Casein kinase II phosphorylation 1010..1018
                                                                                                                                                                                                                                                                                                                                                                                                          "N-myristoylation site"
                                       .828
e= "N-myristoylation site"
                                                                                                                                                                  "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Fig 14A-14C; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0168780.
2000US-0507533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0513904.
2000US-0685791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2000; 2000WO-US32716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35..
/note= .
^33..1006
                                                                                                                                                                                                                                                                                                                                                                            .922
                                                                                         .850
                                                                                                                                      858
                                                                                                                       /note=
853..85
                                                                                                                                                                       'note=
                                                                                                                                                                                                                                                                                                                                                                                                             'note=
                                                                                                                                                                                                                 'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-367809/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAS05389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200140468-A2
Modified-site
                                            Modified-site
                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                            Modified-site
                                                                                                                                           Modified-site
                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-FEB-2000;
10-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-DEC-1999;
18-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bertin J;
                                                                                                                                                                                                                                                                                       Domain
```

Length 1445;

S

Page

```
27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                       ABB62423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                ABB62423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
              Query Match
                                                                                                                          460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                         Best Loc
Matches
                                                        Ŋ
                                                                                                     65
                                                                                                                                                           RESULT 5
                                                                                                                                                                       ABB62423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dp
                                                         οy
                                                                            g
                                                                                                     δy
                                                                                                                         qq
                                                                                                                                                                                                        δy
                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
            The
mapping, tissue typing), predictive medicine (prognostic assays, monitoring clinical trials, and therapy, (treatment and prophylaxis). The modulate it. CARD polypeptide may be used to screen for drugs that bind to and/or modulate it. CARD sequences are potential targets for regulating inflammation. cancer, NF-KappaB signalling, stress related response and apoptosis in human disease. A host cell containing a polynucleotide encoding CARD can be used to create transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                       Gaps
                                                                                                                                                         9 GDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 20649; 21pp + Sequence Listing; English.
                                                                                                             Length 1147;
                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster polypeptide SEQ ID NO 20649
                                                                                                                                     37;
                                                                                                              Score 139; DB 22;
Pred. No. 1.3e-08;
                                                                                                     29 8%; Scor. 36.5%; Pred. No. 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Myers EW;
                                                                                                                                                                                                                                                                                    AA
                                                                                                                                                                                                                    726 KEEAHWTIQRCSGPVTLHYKVNHEG 750
                                                                                                                                                                                                     93
                                                                                                                                                                                                                                                                                   ABB64619 standard; Protein; 1445
                                                                                                                                                                                                     LEEAVGLLRRVDGFCCLSVKVNTDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-191637P
2000US-0614150
                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid
genes from Drosophila and
interactions -
                                                                                                                                   31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-656860/75.
N-PSDB; ABL08722.
                                                                                        1147 AA;
                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1445 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                       pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                               26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-2001
                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                          ABB64619;
                                                                                                              Query Match
                                                                                                                                                                                                     69
                                                                                                                                   Matches
                                                                                                                                                                                                                                                                      ABB64619
                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                              88888888888
                                                                                                                                                          ò
                                                                                                                                                                               q
                                                                                                                                                                                                     ò
                                                                                                                                                                                                                         ద
```

```
ä;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        įS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               409 ISFOKEGSV-GIRLIGGNEAGIFVTAVOPGSPASLOGLMPGDKILKVN-----DMDM 459
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 ISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVWVDYEASEPLFKAVLEDTTLEEAVGL 75
                                                                                                         64
                                                                                                            LAFQGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVWVDYEASEPLFKAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 14061; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.2%; Score 85; DB 22; Length 1916; 31.2%; Pred. No. 0.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster polypeptide SEQ ID NO 14061.
; Score 85.5; DB 22;
; Pred. No. 0.16;
11; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myers
                                                                                                                                                                                                                                                                                                                                                                                                         standard; Protein; 1916 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Li PWD,
                                                                                                                                                                                                                                                                      NGVTREEAVLFLLSLQDRID 479
  18.3%;
33.8%;
                                                                                                                                                                                                                   80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                   EDTTLEEAV - - - GLLRRVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid
genes from Drosophila and
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1916 AA;
                           Local Similarity
nes 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABL06526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-2002
```

```
N-PSDB; AAI93843
                                                                                                         WO200109317-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                dissemination
                                                                                                                                                                                     18-OCT-1999;
11-JAN-2000;
                                                                                                                                                                                                         17-FEB-2000;
02-MAY-2000;
                                                                                       Homo sapiens
                                                                                                                                                                                                                            09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JUN-2001
                                                                                                                                                                             27-AUG-1999;
                                                                                                                                                                  29-JUL-1999;
                  13-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                            08-FEB-2001
                                                                                                                                                                                                                                                                            Ishii S, S
Kodama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 L 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB93753
AAM93968;
                                                                                                                                                                                                                                                                  Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
AAB93753
QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ď
                                                                                                                                                                                                                                                                                                                                                                                                                            įs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from prosophila. The invention useful in developmental biology and in elucidating cell signalling and cell cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 ISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEAVGL 75
                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8;
                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 25059; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22; Length 1916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                              Drosophila melanogaster polypeptide SEQ ID NO 25059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.2%; Score 85; DB 22
llarity 31.2%; Pred. No. 0.28;
Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                           EW.
                                                                                                                                                                                                                                                                                                            Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM93968 standard; Protein; 548 AA.
                                                                      ABB66089 standard; Protein; 1916 AA
                                                                                                                                                                                                                                                                                                            PWD,
                                                                                                                                                                                                                                          23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                           23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                            Ľ
                                                                                                                                                                                 Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                            Adams M,
                                                                                                                                                                                                                                                                                                                              WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB57737 - ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1916 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity Matches 20; Conserv
                                                                                                                                                                                                                                                                                         (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                       N-PSDB; ABL10192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1564 ISKL 1567
                                                                                                                                                                                                  WO200171042-A2
                      1564 ISKL 1567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRRV 79
    76 LRRV 79
                                                                                                                                                                                                                      27-SEP-2001
                                                                                                                                                                                                                                                                                                            Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                         ABB66089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
AAM93968
                                                             ABB66089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   αq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      οy
                                                                                 ò
                      Сp
     õ
```

```
The invention relates to stomach cancer-expressed genes (AAI93842-AAI93917) and the encoded proteins (AAM93967-AAM94039). The genes can be used as markers in blood tests for screening for the early stages of the disease. The proteins and peptides can be used as targets for screening for compounds to treat the disease. They can also be used for predicting micro-metastases. The gene can predict peritoneal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stomach cancer-associated genes, useful as markers in blood tests
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; primer; detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 ISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEAVGL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saito K, Yamamoto J;
Otsuki T, Aburatani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .,
œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 548;
                                                                                    stomach cancer; marker; screening; micro-metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                         Human stomach cancer expressed polypeptide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for screening for the early stages of the disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 80; DB 22;
Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human protein sequence SEQ ID NO:13422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 67-69; 242pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ogai T, Nishikawa T,
Sugiyama T, Wakamatsu
Midorikawa Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB93753 standard; Protein; 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.18;
34.48;
                                                                                                                                                                                                                                                                                                                                                                                                              2000JP-0118776.
2000US-0183322.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                     99JP-0300253.
                                                                                                                                                                                                                                                                                                    28-JUL-2000; 2000WO-JP05063
                                                                                                                                                                                                                                                                                                                                                 99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                            peritoneal dissemination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-570287/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           548 AA;
```

ij

```
Human; kinase; enzyme; PKIN-13 protein; immune system disorder; anaemia; acquired immune deficiency syndrome; thymic hypoplasia; Crohn's disease; asthma; neurological disorder; epilepsy; Charcot-Marie-Trooth disease; AIDS; seizures; cell proliferative disorder; cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma; developmental disorder; Down's syndrome; gene therapy; protein therapy; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-AUG-2001; 2001WO-US27219
16-JUL-2002 (first entry)
                             Human PKIN-13 protein.
                                                                                                                                                                                                                                                                                                                                                                                                              WO200218557-A2.
                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-SEP-2000;
29-SEP-2000;
06-OCT-2000;
13-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                        07-MAR-2002
                                                                                                                                                                                                 Jomain
Jomain
                                                                                                                                                                                                                             Jomain
                                                                                                                                                                                                                                                         Jomain
                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                               Jomain
                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                    Key
 polynucleotide which comprises a 3'-end sequence, where the comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length convar. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 represent human man CDNA sequences; AAB92446 to AAH895893 represent human anino acid sequences; and AAH13629 to AAH13632 represent cligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligoral primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5 -end sequence and an oligonucleotide comprising a sequence complementary to a
                                                                                                                                                                                                                                                                                                          Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                          Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22; Length 548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 0.22;
*~hes 23; Indels
                                                                                                                                                                                                                                        Saito K, Ya
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; SEQ ID 13422; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                    Nagai K,
                                                                                                                                                                                                                                       sogaı T, Nishikawa T, Hayashi K,
Sugiyama T, Wakamatsu A, Nagai K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 80; DB 2
Pred. No. 0.22;
9; Mismatches
                                                                                                                                                                                                                                        Isogai T, Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.18;
34.48;
                                                                                                                                      27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                                             28-JUL-2000; 2000EP-0116126
                                                                                                                         99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 34.4
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the present invention.
                                                                                                                                                                                                             (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                  WPI; 2001-318749/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      548 AA;
                                                                                                                                                                                                                                                                                                                                                        full-length cDNAs
              Homo sapiens
                                       EP1074617-A2
                                                                                                                         29-JUL-1999;
                                                                   37-FEB-2001
                                                                                                                                                                                                                                                      Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
```

"Leucine zipper domain"

.754

/note= 733..75 /note= 2000US-234902P. 2000US-236499P. 2000US-238389P. 2000US-240542P.

2000US-231357P. 2000US-232654P.

2000US-229873P

"GLGF domain"

/note= "G 391..471 .439

"PDZ domain" "PDZ domain"

/note=

"GLGF domain" Location/Qualifiers

/note=

"PDZ domain" "PDZ domain"

/note=

.101

.280 .469

/note=

```
The present invention relates to human kinases (PKIN) and polynucleotides encoding such proteins. PKIN sequences of the invention are useful for diagnosing, treating or preventing disorders associated with aberrant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression of PRIN, particularly immune system disorders (e.g. acquired immune deficiency syndrome (AIDS), thymic hypoplasia, Crohn's disease, anaemia, asthma), neurological disorders (e.g. epilepsy, Charcor.Marie-Tooth disease or seizures), call proliferative disorders (e.g. cancers such as adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma), and developmental disorders (e.g. Down's syndrome). They are also used in gene therapy and protein therapy. The present sequence is human protein.
                                                                                                                                                                                                                                                                                                                                                                                                            New human kinases, useful for diagnosing, treating or preventing immune system disorders (e.g. Crohn's disease), neurological disorders (e.g. epilepsy), or cell proliferative disorders (e.g. cancers such as
                                                                   Gandhi AR
                                                                                            Patterson C, Yue H, Baughn MR, Tribouley
S, Lu Y, Ison CH, Au-Young J, Tang YT;
), Marcus GA, Zingler KA, Lu DAM, Lal PG;
), Kearney L, Policky JL, Thangavelu K;
                                                                   Yao MG,
                                                                Hafalia AJA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 68; Page 174-176; 218pp; English.
                                                                   Walia NK,
(INCY-) INCYTE GENOMICS INC.
                                                                                                    ?, Ding L, Pat
Elliott VS,
Burrill JD, N
Warren BA, R
                                                                   Nguyen DB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leukemia or lymphoma)
                                                                                                                                                                                                                                                                                                            WPI; 2002-329769/36.
                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAD34310
                                                                                                                                    Thornton M,
Azimzai Y, B
Ramkumar J,
                                                                                                       Gururajan R,
                                                                   Bandman O,
                                                                                                                                                                                                                                           Burford N;
```

ij

8; Gaps

ISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEAVGL 75 

16

ò

g ò g

г 76 L 75

92 75 AAE21718 standard; Protein; 928 AA.

AAE2171 RESULT

AAE21718;

but was obtained in electronic format directly from WIPO

```
Tang YT, GC
Yamazaki V,
                                                                                                                                                                                                                                                                               30-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUN-2002.
                                                                               21;
                                                                                                                                                                         L 558
                                                                                                                                                  76 L 76
                                                                                                                                                                                                                                                        ABG66725;
                                  Sequence
                                                          Query Match
                                                                                                                                                                         558
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
                                                                                 Matches
                                                                                                                                                                                                             RESULT 11
                                                                                                                                                                                                                         ABG66725
                                                                                                                                                                                                                                    g
                                                                                                                                                    ŏλ
                                                                                                                                                                        g
8 X C C
                                                                                                        οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a fock supplement. (II) and (II) are useful in medical anguing of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in cappositics, forensics, gene mapping, identification of mutations in the printed and sequences of data and products dependent on DNA and amino acid sequences ABGONOIO-ABG30377 represent novel human diagnostics amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed
                                                         ï
                                                                                                 16 ISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEAVGL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                         8;
                                  DB 23; Length 928;
                                  Score 80; DB 23
Pred. No. 0.45;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID No 52725; 103pp; English.
                                                                                                                                                                                                                                                                                Novel human diagnostic protein #22357.
                                                                                                                                                                                                             ABG22366 standard; Protein; 1037 AA.
                                   17.18;
                                                                                                                                                                                                                                                                                                                                                                                                              30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                           (first entry)
                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-639362/73.
N-PSDB; AAS86553.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu C,
                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
             Ä
                                                                                                                                                                                                                                                                                                                                                                 WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          biodiversity
                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                           18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drmanac RT,
                                      Ma.
Local St.
21;
                                                                                                                                                                                                                                                                                                                                                                                         11-OCT-2001.
                                                                                                                                                     455 L 455
                                                                                                                              76 L 76
                                                                                                                                                                                                                                    ABG22366;
             Sequence
                                   Query Match
                                                            Matches
                                                                                                                                                                                        RESULT 10
                                                                                                                                                                                                    ABG22366
                                                                                                                                                                                                                         X S
                                                                                                     q
                                                                                                                              ò
```

```
ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; inflammatory condition; shock: sepsis; immune response; cancer; wound healing; central nervous system disease; haematopoiesis; peripheral nervous system disease; amyotrophic lateral sclerosis; tendon; myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone; cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis; bone degeneralive disorder; periodontal disease; reperfasion injury; lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection; allergic condition; thrombolysis; thrombosis; coagulation disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to human novel polynucleotides and associated polypeptides. The polynucleotides and polypeptides are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses and cancer and for promoting wound healing. The sequences are used to brain tissue, and are useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's disease, sarkinson's disease and amyotrophic lateral sclerosis. The sequences are involved in chemotactic or chemokinetic activity, regulation of haematopoiesis, treatment of myeloid or lymphoid
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                   506 LRLAGGNDVGIFVSGVQAGSPADGQGIQEGDQILQVN------DVPFQNLTREEAVQF 557
                                                                                                                                                                                                                                                                                      16 ISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEAVGL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang
                                                                                                                                                                                                                       æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and polypeptides for diagnosis, treatment inflammatory, autoimmune, nervous system, myeloid or lymphoid disorders, cancer and promoting wound healing -
                                                                                                                                                          Length 1037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang J,
                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Asundi V,
                                                                                                                                                                                                                   23;
                                                                                                                                                             DB 22;
specification, but was obtained in electroni
at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                            Pred. No. 0.52
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ъ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 10; Page 629-632; 672pp; English.
                                                                                                                                                             Score 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu C, Zhou
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG66725 standard; Protein; 1651 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-NOV-2001; 2001WO-US47004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human novel polypeptide #60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-NOV-2000; 2000US-0028952.
                                                                                                                                                                 17.18;
                                                                                                                                                                                        34.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RW,
ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-508509/54.
N-PSDB; ABK94949.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goodrich
V, Ujwal
                                                                                                 1037 AA;
                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fungal infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200244340-A2.
```

```
э;
Э
              regeneration of bone, cartilage, tendon, ligament and/or never tissue growth, tissue repair, healing of burns, incisions, ulcers, treatment of osteoporosis, osteoarthritis, bone degenerative disorders and periodontal disease. The sequences of the invention are also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmuno disorders e.g. multiple sclerosis and myasthenia gravis, allergic conditions such as asthma, thrombolysis or thrombosis and coagulation disorders. Sequences ABG66666-ABG66758 represent human novel polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vulnerary; antipsoriatic; antiparkinsonian; notropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant, vasctropic; antidiabetic; hypotensive; dermatclogical; immunosuppressive; antidialamatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegeneralive disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autodimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                   Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                          QISVIGGNLT--GIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEA
                                                                                                                                                                                                                                                                                                                                       11;
disorders and platelet disorders such as thrombocytopenia,
                                                                                                                                                                                                                                                                                                  Length 1651;
                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human ORFX ORF2422 polypeptide sequence SEQ ID NO:4844.
                                                                                                                                                                                                                                                                                                                                       28;
                                                                                                                                                                                                                                                                                                  DB 23;
                                                                                                                                                                                                                                                                                                17.0%; Score 79.5; D 34.6%; Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                     12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB42658 standard; Protein; 1675 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | :|| : |:|| |
645 VEILRN-NTHLALTVKTN 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-2000; 2000WO-US08621
                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 VGLLRRVDGFCCLSVKVN 90
                                                                                                                                                                                                                                                                                       Query Match 17.0%
Best Local Similarity 34.6%
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shimkets RA, Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-602362/57.
                                                                                                                                                                                                                                                          1651 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAC76867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200058473-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-OCT-2000
                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB42658;
                                                                                                                                                                                                                                                                                                                                                                            15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB42658
                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
.;
                                                                                                 AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; antifungal; antirheumatic; antithyroid; and antibacterial; antiviral; antifungal; antirheumatic; antithyroid; conficience of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The proteins and nucleic acids may be used to treat cancers, vectors: the proteins and nucleic acids may be used to treat cancers.
                                                                                                                                                                                                                                                                                                                                 proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thomas G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QISVIGGNLT -- GIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEA 72
   reading frame X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1675;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Buee-Scherrer V,
                  useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; betal-syntrophin; SNT B1; PDZ domain; GLGF loop;
Novel nucleic acids and peptides derived from open
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 79.5; D
Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                     Claim 11; Page 4028-4032; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hasegawa M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB21149 standard; peptide; 538 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DHF domain; muscular dystrophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.0%;
34.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goedert M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-FEB-2000; 2000WO-GB00374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MEDI-) MEDICAL RES COUNCIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | :|| : |:|| |
668 VEILRN-NTHLALTVKTN 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99GB-0002696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 VGLLRRVDGFCCLSVKVN 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human betal-syntrophin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cohen P, Cuenda A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-558226/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1675 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spillantini MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200048002-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-AUG-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB21149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB21149
 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
```

```
Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nse
                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                              AAM93296
                                                                                                                                                                                                                                                                                                                                                                                                                                                         \mathcal{C}
                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                         QQ
                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                             4,
                                                                                          The present sequence is the protein sequence of human betal-syntrophin. It is described with reference to the methods of the invention, which involve the identification of compounds which are able to modulate the interaction between PDZ domains (also known as DHF or GLGF domains) and protein kinases. The invention also comprises peptide fragments derived from stress-activated protein kinases which are involved in protein phosphorylation. The compounds and peptides can be used in the treatment of muscular diseases, for example muscular dystrophy, or in cases where modulation of phosphorylation of proteins with PDZ domains or modulation of signalling via activin receptors or voltage gated channels is necessary, or in instances where the localisation of SARK3 at the neuromuscular junction or sarcolemma needs to be disrupted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is the protein sequence of human beta2-syntrophin. It is described with reference to the methods of the invention, which involve the identification of compounds which are able to modulate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for treating muscular protein kinase and PDZ
                                                                                                                                                                                                                                                                                                                                                                                                                              Thomas G;
Novel methods for identifying compounds useful for treating muscular dystrophy comprising identifying modulators of protein kinase and \rm PDZ domain binding -
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          8 QGDALLEQ-----ISVIGG--NLTGIFIHRVTPGSAADQ-MALRPGTQIVMVDYEASEP 58
                                                                                                                                                                                                                                                                                                                                                                             17;
                                                                                                                                                                                                                                                                                                                                           Length 538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Buee-Scherrer V,
                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nn; beta2-syntrophin; SNT B2; PDZ domain; GLGF loop; domain; muscular dystrophy.
                                                                                                                                                                                                                                                                                                                                            16.0%; Score 74.5; DB 21; 35.6%; Pred. No. 1.1; iive 10; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel methods for identifying compounds useful dystrophy comprising identifying modulators of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hasegawa M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 --GADLRDATHDEAVQALKRAGKEVLLEVK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 LFKAVLEDTTLEEAVGLLRRVDGFCCLSVK 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 12c; 102pp; English.
                                                                  Disclosure; Fig 12b; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB21150 standard; peptide; 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goedert M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-FEB-2000; 2000WO-GB00374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MEDI-) MEDICAL RES COUNCIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99GB-0002696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                            Local Similarity 35.69
nes 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human beta2-syntrophin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-558226/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ä
                                                                                                                                                                                                                                                                                                                538 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cuenda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  domain binding -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spillantini MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200048002-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB21150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cohen P,
                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human;
DHF dom
                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
```

á g ò g

```
molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the Oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                              .,
ش
interaction between PDZ domains (also known as DHF or GLGF domains) and protein kinases. The invention also comprises peptide fragments derived from stress-activated protein kinases which are involved in protein phosphorylation. The compounds and peptides can be used in the treatment of muscular diseases, for example muscular dystrophy, or in cases where modulation of phosphorylation of proteins with PDZ domains or modulation of signalling via activin receptors or voltage gated channels is necessary, or in instances where the localisation of SAPK3 at the neuromuscular junction or sarcolemma needs to be disrupted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    830 Primers useful for synthesizing full length cDNA clones and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 ISVIGG -- NLTGIFIHRVTPGSAADQ - MALRPGTQIVMVDYEASEPLFKAVLEDTTLEEA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H
                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kawai
                                                                                                                                                                                                                                                                                                                                                                   Length 540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; SEQ ID NO 2791; 1380pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 jai T, Hayashi K, Ishii S, Kawa
Nagai K, Kojima S, Otsuki T,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; full length cDNA; cDNA synthesis; oligo-capping.
                                                                                                                                                                                                                                                                                                                                                                      DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                              29;
                                                                                                                                                                                                                                                                                                                                                                      Score 73.5; Di
Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human polypeptide, SEQ ID NO: 2791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM93296 standard; Protein; 304
                                                                                                                                                                                                                                                                                                                                                                                                                                 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in genetic manipulation -
                                                                                                                                                                                                                                                                                                                                                                      15.7%;
36.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99JP-0194486.
2000JP-0118774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUL-2000; 2000EP-0114089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAY-2000; 2000JP-0183765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wakamatsu A, Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 VOALKRAGKEVLLEVK 195
                                                                                                                                                                                                                                                                                                                                                                         Query Match 15.7
Best Local Similarity 36.8
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 VGLLRRVDGFCCLSVK 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-524255/58.
                                                                                                                                                                                                                                                                                                                540 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAK94216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-JUL-1999;
11-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP1130094-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM93296;
                                                                                                                                                                                                                                                                                                                   Sequence
```

```
Ouery Match 15.6%; Score 73; DB 22; Length 304;
Best Local Similarity 31.2%; Pred. No. 0.77;
Matches 24; Conservative 14; Mismatches 25; Indels 14; Gaps
specification, but was obtained in CD-ROM format directly from EPO.
                                                      Sequence 304 AA;
S × S
```

Dp ò ρp

Οy

Search completed: January 22, 2003, 08:52:19 Job time: 21.125 secs

71 EAVGLLRRVDGFCCLSV 87

THIS PAGE BLANK (USPTO)

Sequence 2, A Sequence 31, Sequence 31, Sequence 52, Sequence 52, Sequence 52, Sequence 34, Sequence 34, Sequence 15, Sequence 23, Sequence 23, Sequence 23, Sequence 2, A Sequence 2, A

OM protein

Run on:

Sequence:

```
APPLICANT: GONEZ, LEONEL JORGE
APPLICANT: SARS, JAN
APPLICANT: SARS, JAN
APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: HELDIN, CARL-HENRIK
TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESS:
ADDRESSE: WOLF, GREENIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVIGG-----NLTGIFIHRV-TPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLE 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.6%; Score 73; DB 4; Length 2037; ilarity 31.2%; Pred. No. 1.4; Conservative 14; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Bartel, Paul L.
APPLICANT: Bartel, Paul L.
APPLICANT: Tavtiglan, Sean V.
TITLE OF INVENTION: MMSC2 - An MMAC1 Interacting Protein
TITLE OF INVENTION: MMSC2
CURRENT TILING DATE: 1999-05-07
CURRENT FILING DATE: 1999-05-08
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 3
LENGTH: 2037
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-306-998-3; Sequence 3, Application US/09306998; Patent No. 6291173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08596291
Patent No. 5821075
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2019 EAVAILKRTKGTVTLMV 2035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 EAVGLLRRVDGFCCLSV 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-09-306-998-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-596-291-3
                                                                                                                                                                                                                    58
58
57 . 5
57
57
57
   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Applisequence 16, Applisequence 16, Applisequence 2, Applisequence 3, Applisequence 25, Applisequence 20, Applisequence 20, Applisequence 20, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 2, Applisequence 3, Applisequence 2, Applisequence 2, Applisequence 2, Applisequence 3, Appli
                                                                                                                                                (without alignments) 429.229 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, A
Sequence 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                             January 22, 2003, 08:52:30 ; Search time 6.375 Seconds
                                                                                                                                                                                                                                      1 QVTMLAFQGDALLEQISVIG.....GLLRRVDGFCCLSVKVNTDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/Re_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                      GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-662-227-35
US-09-017-947-35
                                                                                                                                                                                                                                                                                                                               262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                  US-09-767-215-2_COPY_568_660
467
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                             · protein search, using sw model
                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                       seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 5 .. ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perfect score:
                                                                                                                                                                                                                                                                            Scoring table:
```

Minimum DB Maximum DB

Database

Result Š. Searched:

3;

Gaps

```
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: GONEZ, LEONEL JORGE
APPLICANT: SARAS, JAN
APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: HELDIN, CARL-HENRIK
TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 34
CONRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESSE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1071 EITLVNLKKDAKYGLGFQIIGGEKMETDLGIFISSVAPGGPADFHGCLKPGDRLISVNSV 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVTMLAFQGDALLE-QISVIGGNL----TGIFIHRVTPGSAAD-QMALRPGTQIVMVD-- 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
15.4%; Score 72; DB 2; Length 2465;
Best Local Similarity 28.9%; Pred. No. 2.5;
Matches 24; Conservative 15; Mismatches 30; Indels
                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/596,291
FILING DATE: 09-40(6.1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-58P-1993
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION UNMBER: 31,616
REGISTRATION UNMBER: 31,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Floppy disk
IBM PC compatible
PSYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                 LO461/7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/100,804 FILING DATE:
                                                                                                 E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1131 SLEGVSHHAAIEILQNAPEDVTL 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09100804 patent No. 6066472 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 -----YEASEPLFKAVLEDITL 69
                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: LO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 92-1742 EZEKIEL INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2465 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BOSTON
MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
COMPUTER: IBM PC comp
OPERATING SYSTEM: PC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-596-291-3
BOSTON
MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
US-09-100-804-3
                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Saras, Jan
APPLICANT: Franzn, Petra
APPLICANT: Fapenstru, Portus
APPLICANT: Hellman, Ulf
APPLICANT: Hellman, Ulf
APPLICANT: Hellinan, Ulf
APPLICANT: Hellinan, Ulf
APPLICANT: Hellin, UNGER: US/09/080, 855A
CURRENT APPLICATION NUMBER: US/09/080, 855A
CURRENT FILING DATE: 1999-05-18
BARLIER APPLICATION NUMBER: 08/805,583
BARLIER FILING DATE: 1997-02-25
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1071 EITLVNLKKDAKYGLGFQIIGGEKMGRLDLGIFISSVAFGGPADFHGCLKPGDRLISVNS 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1071 EITLVNLKKDAKYGLGFQIIGGEKMETDLGIFISSVAPGGPADFHGCLKFGDRLISVNSV 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVTMLAFQGDALLE-QISVIGGNL-----TGIFIHRVTPGSAAD-QMALRPGTQIVMVD- 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVTMLAFQGDALLE-QISVIGGNL----TGIFIHRVTPGSAAD-QMALRPGTQIVMVD-- 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3; Length 2465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
15.3%; Score 71.5; Di
Best Local Similarity 28.6%; Pred. No. 2.9;
Matches 24; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.4%; Score 72; DB: 28.9%; Pred. No. 2.5; tive 15; Mismatches
PRICRADITATION DATA:
APPLICATION NUMBER: US 08/596,291
FILING DATE: 09-AUG-1996
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-SEP-1993
PRIOR APPLICATION DATE:
APPLICATION NUMBER: PCT/US94/09943
FILING DATE: 01-SEP-1994
ATTORNEY-AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
                                                                                                                                                                                                                                                                                          LO461/7003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-080-855-12; Sequence 12, Application US/09080855A; Patent No. 6083721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1131 SLEGVSHHAAIEILQNAPEDVTL 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----YEASEPLFKAVLEDITL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 ----YEASEPLFKAVLEDITL 69
                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: LA TELECOMMUNICATION INFORMATION TELEPHONE: 617-720-3500 TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2465 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 15.4%
Best Local Similarity 28.9%
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: protein US-09-100-804-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
US-09-080-855-12
```

us-09-767-215-2\_copy\_568\_660.rai

```
NUMBER OF SEQ ID NOS: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                   SOFTWARE: Pater
SEQ ID NO 46
LENGTH: 2485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-100-804-16
                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-233-086-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    us-09-233-086-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
                                                                                                                                                                                                                              δλ
                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                         Qy
                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 46, Application US/09290640
Patent No. 6204055
GRAERAL INFORMATION:
GRAERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Elic G.
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-0351
CURRENT APPLICATION NUMBER: US/09/290,640
CURRENT FILING DATE: 1999-04-12
                                                                                                                                                                                                                            PRIMARY STRUCTURE AND FUNCTIONAL
EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
TYROSINE PHOSPHATASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVTMLAFQGDALLE-QISVIGGNL----TGIFIHRVTPGSAAD-QMALRPGTQIVMVD- 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.3%; Score 71.5; DB 5; Length 2466; 28.6%; Pred. No. 2.9; tive 15; Mismatches 30; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LO461/7000WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/115,573
FILING DATE: 01-SEP-1933
ATTORNEY/AGENT INFORMATION:
NAME: TWOMEY, MICHAEL J.
REGISTRATION NUMBER: P-38,349
REFERENCE/DOCKET NUMBER: LO461/7000W
TELECHONE: 617/720-3500
TELEPHONE: 617/720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 01-SEP-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER REAGABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09943
                                                                        PCT-US94-09943-2; Sequence 2, Application PC/TUS9409943; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1131 VSLEGVSHHAAIEILQNAPEDVTL 1154
1131 VSLEGVSHHAAIEILQNAPEDVTL 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 -----YEASEPLFKAVLEDTTL 69
                                                                                                                                                                                                                          TITLE OF INVENTION: PRIMARY STR
TITLE OF INVENTION: TYROSINE PH
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
STREET: 600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELERAX: 617/720-2441
TELEX: 92-1742 EZEKIEL
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2466 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 28.6 Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                           CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US94-09943-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
US-09-290-640-46
                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                            APPLICANT:
                                                                                                                                  APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                         RESULT 5
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16, Application US/09100804

Patent No. 6066472

GENERAL INFORMATION:
APPLICANT: GONEZ, LEONEL JORGE
APPLICANT: SARAS, JAN
APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: HELDIN, CARL-HERNIK
TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
                                                                                                                                                                                                                                                                                                                 1090 EITLYNLKKDAKYGLGFQIIGGEKMGRLDLGIFISSVAPGGPADLDGCLKPGDRLISVNS 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 SVIGG-----NLTGIFIHRV-TPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLE 70
                                                                                                                                                                                                                                                                               1 QVTMLAFQGDALLE-QISVIGGNL----TGIFIHRVTPGSAAD-QMALRPGTQIVMVD- 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                             15;
                                                                                                                                                                                DB 4; Length 2485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.2%; Score 71; DB 4; Length 1881; 32.5%; Pred. No. 2.3; tive 12; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bartel, Paul L.
APPLICANT: Bartel, Paul L.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
TITLE OF INVENTION: MMSCI - An MMACI Interacting Protein
FILE REFERENCE: MMSCI Gene
CURRENT FILING DATE: 1999-01-19
EARLIER APPLICATION NUMBER: US 60/071,861
EARLIER APPLICATION NUMBER: US 60/071,861
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C. STREET: 600 ATLANTIC AVENUE
                                                                                                                                                                           15.3%; Score 71.5; Di
28.6%; Pred. No. 2.9;
tive 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                1150 VSLEGVSHHAAIEILQNAPEDVTL 1173
                                                                                                                                                                                                                                                                                                                                                                                   53 -----YEASEPLFKAVLEDITL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09233086
Patent No. 6337192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :|| :|: | |:|
1864 QAVAILKHQRGTVTLTV 1880
                                                                                                                                                                                                                               Conservative
PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 EAVGLLRRVDGFCCLSV 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                              ; ORGANISM: Homo sapiens US-09-290-640-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                        Query Match
Best Local Similarity
Matches 24; Conserv
```

```
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEED VORSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/739,485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/71
FILING DATE:
CLASCYTT
                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: BAUMEISTER, Kirk
REGISTRATION NUMBER: 33,833
                                                                                                                                                                                 60/025436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER REALABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 173 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-terminal
                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 173 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                             ji single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Ph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE: 1
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
ANTI-SENSE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORIGINAL SOI
US-08-923-454A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-739-485-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 LGFQ------IIGGEKMGRLDLGIFISSVAPGGPADFHGCLKPGDRLISVNSVSLEG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 LAFQGDALLEQISVIGGNL----TGIFIHRVTPGSAAD-QMALRPGTQIVMVD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.9%; Score 69.5; DB 3; Length 77; 30.4%; Pred. No. 0.038; tive 10; Mismatches 22; Indels
                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DARA:
APPLICATION NUMBER: US/09/100.804
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08923454A
Patent No. 6004794
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Creasy, Caretha
APPLICANT: Livi, George
APPLICANT: Karran, Eric
APPLICANT: Rarnan, Eric
APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: SmithKline Beecham Corporation 709 Swedeland Road
                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 09-6404-1996
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09943
FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTATION NUMBER: 31,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LO461/7003
                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: LO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 --YEASEPLFKAVLEDITL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 VSHHAAIEILQNAPEDVTL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 30.45
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: King of Prussia
STATE: PA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19406
COMPUTER READABLE FORM:
      MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-923-454A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-100-804-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ρp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
```

```
Gaps
                                                                ë,
Ouery Match 14.2%; Score 66.5; DB 3; Length 173; Best Local Similarity 33.3%; Pred. No. 0.31; Matches 16; Conservative 11; Mismatches 18; Indels
                                                                                                                                                                  25 GIFIHRVTPGSAADQMALRPGTQIVMVD---YEASEPLFKAVLEDTTL 69
                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08739485
Patent No. 5863898
GENERAL INFORMATION:
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Jennifer L.
APPLICANT: Bandman, Jennifer L.
APPLICANT: Bandman, Jennifer L.
APPLICANT: Bandman, Jennifer L.
APPLICANT: BANDMAN IN NOVEL HUMAN LIM PROTEINS NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
```

Gaps

```
..
ش
                                                                                                                                                                               DB 3; Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3; Length 458;
                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                         25 GIFIHRVTPGSAADQMALRPGTQIVMVD---YEASEPLFKAVLEDTTL 69
                                                                                                                                                                                                                    11; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Livi, George
APPLICANT: Karran, Eric
APPLICANT: Clinkenbeard, Helen
APPLICANT: Clinkenbeard, Helen
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road
                                                                                                                                                                          Query Match
14.2%; Score 66.5; DE
Best Local Similarity 33.3%; Pred. No. 1.3;
Matches 16; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 66.5; Di
Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FSASLEGO VESTON 1.5
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25, Application US/08923454A
; Patent No. 6004794
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P50547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60/025436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: PSC
TELECOMMUNICATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.2%;
33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Creasy, Caretha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     458 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 610-270-5090
                                                                                            FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              King of Prussia
                    TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΡA
                                                                                                                                                                                                                                                                                                                                                                            US-08-923-454A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-923-454A-25
                                                                                                                                     US-08-923-454A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                              RESULT 12
                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                               20 GGNLTG-----IFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEA 72
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 14.2%; Score 66.5; DB 2; Length 316; Best Local Similarity 32.5%; Pred. No. 0.74; Matches 27; Conservative 12; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                       35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Creasy, Caretha
APPLICANT: Livi, George
APPLICANT: Karran, Eric
APPLICANT: Karran, Eric
APPLICANT: Clinkenbeard, Helen
APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
REFERENCE/DOCKET NUMBER: PF-0142 US TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555 TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARR: FastSBO Version 1.5
SURRENT APPLICATION DATA
APPLICATION NUMBER: US/08/923,454A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELECOMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/08923454A Patent No. 6004794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 VGLLRRVD-GFCCL-SVKVNTDG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 HOLCLKIDRGETHLWSPOVSEDG 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acids
TYPE: amino acid
                                                                                            INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
                                                                                                                                                                            single
                                                                                                                                                                                                                                  LIBRARY: Consensus
CLONE: Consensus
US-08-739-485-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM COMPOSERATING SYSTEM:
                                                                                                                                                                                             TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                        TYPE: amino and STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: King
STATE: PA
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-923-454A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
```

```
RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                οp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.2%; Score 66.5; DB 3; Length 458; 33.3%; Pred. No. 1.3; Live 11; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1: ||:| || || : ||| || : || || || 390 GVLIHKVILGSPAHRAGLRPGDVILAIGEQMVQNAEDVYEAVRTQSQL 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 GIFIHRVTPGSAADQMALRPGTQIVMVD---YEASEPLFKAVLEDTTL 69
 18; Indels
                                 25 GIFIHRVTPGSAADQMALRPGTQIVMVD---YEASEPLFKAVLEDTTL 69
                                                                                                                                                                                                                                                                                                                                                              E: SmithKline Beecham Corporation 709 Swedeland Road
 Mismatches
                                                                                                                                                                                                                                                            APPLICANT: Clinkenbeard, Helen
APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
CORRESPONDENCES: 40
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 Xaa = Arg or Cys
278 Xaa = Ala or Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
PRICA APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                  Sequence 31, Application US/08923454A Patent No. 6004794 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P50547
                                                                                                                                                                                                      Creasy, Caretha
Livi, George
Karran, Eric
Clinkenbeard, Helen
 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 458 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 33.3%
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acid
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                           CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  19406
                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-923-454A-31
                                                                                                                                         US-08-923-454A-31
                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
   16;
                                                                                                                                                                                                                                                                                                                                                                                  STREET:
   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                   a
                                       οy
```

RESULT 14 US-09-008-271A-11

```
METHODS FOR IDENTIFYINGHERBICIDAL AGENTS THAT INHIBIT DI PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 GIFIHRVTPGSAADQMALRPGTQIVMVD---YEASEPLFKAVLEDTTL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 33.3%; Pred. No. 1.3;
Matches 16; Conservative 11; Mismatches 18;
                                                                                                                                                                          Tang, Tom Y.
Shah, Purvi
INVENTION: HUMAN PROTEASE MOLECULES
                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,271A
FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIBRARY: SINIUCT01
CLONE: 2680548
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Mohan-Peterson, Sheela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20, Application US/08759581B; Patent No. 5876945; GENERAL INFORMATION:
                                                                APPLICANT: Bandman, Olga
Hillman, Jennifer L.
Sequence 11, Application US/09008271A Patent No. 6203979 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: CHISHOLM, DEXTER A.
APPLICANT: DINER, BRUCE A.
APPLICANT: DONDLOSON, GAIL K.
APPLICANT: JORDAN, DOUGLAS B.
APPLICANT: JORDAN, DOUGLAS B.
APPLICANT: TANG, XIAO-SONG
APPLICANT: TROST, JEFREX T.
APPLICANT: WANG, SHAOJIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 458 amino acids TYPE: amino acid
                                                                                                         Yue, Henry
Guegler, Karl J.
Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WARREN, PATRICK V.
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: WANG, SHAPPLICANT: WARREN, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                  STATE: CA
                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                         TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-008-271A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-759-581B-20
```

```
Query Match
14.1%; Score 66; DB 2; Length 539;
Best Local Similarity 24.7%; Pred. No. 1.9;
Matches 18; Conservative 16; Mismatches 25; Indels
NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:
ADDRESSE: E.I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: MILLINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
21P: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 3.1
SOFTWARE: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 3.1
SOFTWARE: MICROSOFT WORD 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,581B
FILING DATE:
CLASSIFICATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9964
TELECOMMUNICATION INFORMATION:
NAME: FLOYD, LINDA AZAMETHY
REGISTRATION NUMBER: GR-9964
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-92-8112
TELEFHONE: 302-773-0164
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARRATERISTICS:
LENGTH: 539 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
MOLECULE TYPE: protein
ONIGINAL SOURCE:
STRAIN: SETNACH DI PROTEASE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-759-581B-20
```

2; 9 GDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTT 68 14; ò qq

: || :|: || 287 IYEAANILQGPDG 299 69 LEEAVGLLRRVDG 81

δ

Search completed: January 22, 2003, 08:57:37 Job time : 8.375 secs

THIS PAGE BLANK (USPTO)

Sequence 3,

Sequence 60, Appl Sequence 119, App Sequence 2, Appl Sequence 22, Appl Sequence 24, Appl Sequence 26, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 32, Appl Sequence 519, Appl Sequence 619, Appl Sequence 619, Appl Sequence 812, Appl Sequence 813, Appl Sequence 813, Appl Sequence 813, Appl Sequence 813, Appl Sequence 811, Appl Sequen

```
1 QVTMLAFQGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INCORDATION:
APPLICANT: Bertin, John
TITLE OF INVENTION:
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-142001
CURRENT APPLICATION NUMBER: US/09/767,215
CURRENT FILING DATE: 2001-01-22
PRIOR FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
US-09-767-215-5
Sequence 5, Application US/09767215
Patent No. US2002008163641
GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION:
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 467; DB 10;
100.0%; Pred. No. 5.9e-48;
ative 0; Mismatches 0;
10 US-09-909-005-3

10 US-09-739-907-60

10 US-09-739-907-119

9 US-09-963-959-2

10 US-09-771-730-22

10 US-09-771-730-22

10 US-09-771-730-32

10 US-09-771-730-32

10 US-09-771-730-34

10 US-09-771-730-34

10 US-09-771-730-34

10 US-09-771-730-34

10 US-09-771-730-36

10 US-09-771-730-37

10 US-09-771-730-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         628 KAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTDG 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 KAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTDG 93
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09767215 Patent No. US20020081636A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93; Conservative
   TYPE: PRT
ORGANISM: Homo sapiens
US-09-767-215-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
   US-09-767-215-2
                                                                                                                                                     60.5
60.5
60.5
60.5
   63.5
62
62
61
61
61
61
61
61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Appl
Sequence 964, Appl
Sequence 5, Appli
Sequence 108, Ap
Sequence 2, Appli
Sequence 57, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Appli
Sequence 5, Appli
Sequence 14, Appl
Sequence 11, Appl
Sequence 3, Appli
Sequence 3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Appli
Sequence 46, Appl
Sequence 3, Appli
Sequence 20, Appli
Sequence 948, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 17, Appl
                                                                                                    (without alignments) 500.428 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                     January 22, 2003, 08:49:35; Search time 3.75 Seconds
                                                                                                                                                              1 QVTMLAFQGDALLEQISVIG......GLLRRVDGFCCLSVKVNTDG
                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
              GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-925-300-1508
US-09-911-826A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0 US-09-951-401-3
0 US-09-922-101-3
0 US-09-802-669-46
US-09-998-425-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-767-215-2
US-09-767-215-5
US-10-032-159A-14
US-10-032-159A-8
US-09-963-959-11
US-09-951-402-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-911-826A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-764-868-948
US-09-911-826A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-023-437-57
US-09-911-826A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-764-868-964
US-10-126-099-5
                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                           122226 seqs, 20178551 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                        US-09-767-215-2_COPY_568_660
467
                                                                                                                                                                                                                                                                                                                                                                    Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                             Maximum Match 100%
Listing first 45 summaries
                                                               - protein search, using sw model
                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                              seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1004
1138
11247
1247
2037
2037
2037
2037
1681
1681
163
173
1439
1439
1439
1439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                                            Minimum DB :
Maximum DB :
                                                               OM protein
                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                    Database
                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1184397100843371
118433710084351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š.
```

ALIGNMENTS

ö

Gaps

..

Indels

Length 1004;

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                Qγ
                                                                                                                                                                                                                                                                                                                                                                                                               QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                          δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                               9 GDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                            1 QVTMLAFQGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Reed, John C.
APPLICANT: Reed, John C.
APPLICANT: Reed, John C.
TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,
TITLE OF INVENTION: ENCODING NUCLEIC ACIDS, AND METHODS OF USE
FILE REPERENCE: P-LJ 5100
CURRENT APPLICATION NUMBER: US/10/032,159A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 60/257,457
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/10032159A
Patent No. US20020164703A1
Patent No. US20020164703A1
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Reed, John C.
APPLICANT: Godzik, Adam
TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,
TITLE OF INVENTION: ENCODING NUCLEIC ACIDS, AND METHODS OF USE
FILE REFERENCE: P-LJ 5100
                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                   Length 1138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.5%; Score 133; DB 9; Length 113; 36.6%; Pred. No. 4.8e-09;
                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                     DB 10;
                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                 Query Match 100.0%; Score 467; DB 10
Best Local Similarity 100.0%; Pred. No. 7e-48;
Matches 93; Conservative 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 4.86
16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  KAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTDG 93
FILE REFERENCE: 07334-142001
CURRENT APPLICATION NUMBER: US/09/767,215
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 60/181,159
PRIOR FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/10032159A Patent No. US20020164703A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 KEEAHWIIQRCSGPVTLHYKVN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 LEEAVGLLRRVDGFCCLSVKVN 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 36.6
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                             TYPE: PRT
CRCANISM: Homo sapiens
US-09-767-215-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-032-159A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
US-10-032-159A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-032-159A-8
                                                                                                                                                            LENGTH: 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 14
LENGTH: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                         677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                        δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                               ò
```

```
Sequence 11, Application US/09963959
Sequence 11, Application US/09963959
Sequence 11, Sequence 12, Sequence 13, Sequence 13, Sequence 13, Sequence 13, Sequence 12, Sequence 13, Sequence 12, Sequence 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 SVIGGNLTGIFIHRVTPGSAADOMA-----LRPGTQIVMVDYEASEPLFKAVLEDTTLE 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 GDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 SIVG----GIFVSSVVPGSPAAKAGRKSLGLLKVGDVILEVNGETS-----VEGLTHE 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Taviigian, Sean V.
TITLE OF INVENTION: MMSC2- An MMAC1 Interacting Protein
FILE REFERENCE: MMSC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.6%; Score 77.5; DB 9; 35.2%; Pred. No. 0.014; iive 10; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 28.5%; Score 133; DB 9; I Best Local Similarity 36.6%; Pred. No. 1.1e-07; Matches 30; Conservative 16; Mismatches 36;
CURRENT APPLICATION NUMBER: US/10/032,159A CURRENT FILING DATE: 2001-12-19 PRIOR APPLICATION NUMBER: US 60/257,457 PRIOR FILING DATE: 2000-12-21 NUMBER OF SEQ ID NOS: 37 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/951,402
CURRENT FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: US 09/306,998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Consensus sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09951402 Patent No. US20020168752A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        817 KEEAHWTIQRCSGPVTLHYKVN 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 LEEAVGLLRRVDGFCCLSVKVN 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Bartel, Paul L.
                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 EAVGLLRRVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EAVDLLKKAGG
                                                                                                                                                                                                                                                                                                                           LENGTH: 1247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-963-959-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-032-159A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-951-402-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 11
LENGTH: 80
```

```
NUMBER OF SEQ ID NOS: 72
                      SOFTWARE: Pater
SEQ ID NO 3
LENGTH: 2037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-802-669-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-802-669-46
                                                                                                                                                                                                                   24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
US-09-998-425-3
                                                                                           TYPE: PRT
                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QQ
                                                                                                                                                                                                                                                                δλ
                                                                                                                                                                                                                                                                                                      Dp
                                                                                                                                                                                                                                                                                                                                                δy
                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   э;
Э
                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                                                                  1967 SIVGGYGSPHGDLPIYVKTVFAKGAASEDGRLKRGDQIIAVNGQS------LEGVTHE 2018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.6%; Score 73; DB 10; Length 2037;
31.2%; Pred. No. 3.3;
tive 14; Mismatches 25; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 SVIGG----NLTGIFIHRV-TPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLE 70
                                                                                                                                                                                                                                                                                                                          17 SVIGG----NLTGIFIHRV-TPGSAADOMALRPGTQIVMVDYEASEPLFKAVLEDTTLE 70
                                                                                                                                                                                                                                       Query Match 15.6%; Score 73; DB 9; Length 2037; Best Local Similarity 31.2%; Pred. No. 3.3; Matches 24; Conservative 14; Mismatches 25; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Bartel, Paul L.
APPLICANT: Tavitigian, Sean V.
TILE OF INVENTION: MMSC2- An MMAC1 Interacting Protein
FILE REFERENCE: MMSC2- An MMAC1 Interacting Protein
FILE REFERENCE: MMSC2- An MMAC1 Interacting Protein
CURRENT APPLICATION NUMBER: US/09/951,401
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: US 09/306,998
PRIOR APPLICATION NUMBER: US 60/084,740
PRIOR FILING DATE: 1999-05-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bartel, Paul L.
APPLICANT: Tavtigian, Sean V.
TITLE OF INVENTION: MMSC2- An MMAC1 Interacting Protein
FILE REPERENCE: MMSC2-
CURRENT APPLICATION NUMBER: US/09/922,101
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/306,998
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 60/084,740
PRIOR FILING DATE: 1998-05-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09951401 Patent No. US20020115104A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-922-101-3
; Sequence 3, Application US/09922101
; Patent No. US20020146711A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         2019 EAVAILKRTKGTVTLMV 2035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||| :|:| | | | | 2019 EAVAILKRTKGTVTLMV 2035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 31.2%;
Matches 24; Conservative
                                                                NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO
LENGTH: 2037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO
LENGTH: 2037
                                                                                                                                                                                                                                                                                                                                                                                                              71 EAVGLLRRVDGFCCLSV 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 EAVGLLRRVDGFCCLSV 87
                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-951-402-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-951-401-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-951-401-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

```
APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
APPLICANT: Watt, Jacqueline
APPLICANT: Watt, Jacqueline
APPLICANT: Watt, Jacqueline
APPLICANT: Stang, Hong
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: 158H-345
CURRENT APPLICATION NUMBER: US/09/802,669
CURRENT FILING DATE: 2001-03-09
PRIOR PELICATION NUMBER: US 09/665,615
PRIOR PLICATION NUMBER: US 09/290,640
PRIOR PLING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ,
,
                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1967 SIVGGYGSPHGDLPIYVKTVFAKGAASEDGRLKRGDQIIAVNGQS------LEGVTHE 2018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVTMLAFQGDALLE-QISVIGGNL----TGIFIHRVTPGSAAD-QMALRPGTQIVMVD- 52
                                                                                                                                                                                                                                                                                                   17 SVIGG-----NLTGIFIHRV-TPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLE 70
                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BATTLIN.
APPLICANT: BATTLIN.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Mytiad Genetics, inc.
TITLE OF INVENTION: MMSC1 - An MMAC1 Interacting Protein
FILE REFERENCE: MMSC1 Gene
CURRENT APPLICATION NUMBER: US/09/998,425
CURRENT FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/233,086
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.3%; Score 71.5; DB 10; Length 2485; 28.6%; Pred. No. 6.4; tive 15; Mismatches 30; Indels 15;
                                                                                                                                                                                               Length 2037;
                                                                                                                                                                                                                                            25;
                                                                                                                                                                                         DB 10;
3.3;
                                                                                                                                                                                         15.6%; Score 73; DB 1
ilarity 31.2%; Pred. No. 3.3;
Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1150 VSLEGVSHHAAIEILQNAPEDVTL 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 46, Application US/09802669
; Patent No. US20020004490A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09998425 Publication No. US20030008346A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 -----YEASEPLFKAVLEDITL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2019 EAVAILKRTKGTVTLMV 2035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 15.3%
Best Local Similarity 28.6%
Matches 24; Conservative
Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                            71 EAVGLLRRVDGFCCLSV 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Homo sapiens
                                                                                                         ; ORGANISM: Homo sapiens US-09-922-101-3
                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
```

```
72 AVGLL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 ALEIL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-09-764-868-964
                                                                                                                                                                                                                                         ; OTHER INFORMAT
US-09-764-868-948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                          LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                      Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Rotin, Daniela and Pham, Nam
TITLE OF INVENTION: RAS Activator Nucleic Acid Molecules, Polypeptides and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: DDM-5001-US
CURRENT FORDICATION NUMBER: US/09/911,826A
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: PCT/CA00/00042
PRIOR FILING DATE: 2000-01-20
PRIOR PELICATION NUMBER: 2,259,830
PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                   17 SVIGG-----NLTGIFIHRV-TPGSAADQMALRPGTQIVWVDYEASEPLFKAVLEDTTLE 70
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/071,861; PRIOR FILING DATE: 1998-01-20; NUMBER OF SEQ ID NOS: 65; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 3; LEWGTH: 1881; TYPE: PRF. TYPE: PRF. TYPE: PRF. TYPE: NOR ARCH: 1881; OKCANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 948, Application US/09764868

Sequence 948, Application US/09764868

Setent No. US20020168711A1

GENERAL INFORMATION:

APPLICAMT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PT232

CURRENT PPLICATION NUMBER: US/09/764,868

CURRENT FILING DATE: 2001-01-17

Prior application data removed - refer to PALM or file wrapper

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .,
                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                   DB 9; Length 1881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10; Length 65;
                                                                                                                                                                                                                                                          26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 15.0%; Score 70; DB 10; L. Best Local Similarity 41.2%; Pred. No. 0.087; Matches 14; Conservative 7; Mismatches 13;
                                                                                                                                                                                                                 15.2%; Score 71; DB 9 ilarity 32.5%; Pred. No. 5.1; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 ISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIV 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 ISIVSGEKGGIYVSKVTVGSIAHQAGLEYGDQLL 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20, Application US/09911826A Patent No. US20020143164A1
                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
LENGTH: 65
                                                                                                                                                                                                                                                                                                                                                                                    71 EAVGLLRRVDGFCCLSV 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-09-911-826A-20
                                                                                                                                                                                                                                    Local Similarity
hes 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-09-764-868-948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-911-826A-20
                                                                                                                                                                                                                     Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                         Q
                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                              QQ
```

```
2,
                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                NAME/KEY: SITE
LOCATION: (149)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (157)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                            NAME/KEY: SITE LOCATION: (148)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Rotin, Daniela and Pham, Nam
TITLE OF INVENTION: RAS Activator Nucleic Acid Molecules, Polypeptides and
TITLE OF INVENTION: RAS Activator Nucleic Acid Molecules, Polypeptides and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: DDW-5001-US
CURRENT APPLICATION NUMBER: US/09/911,826A
CURRENT FILING DATE: 2002-02-26
PRIOR FILING DATE: 2002-01-20
PRIOR PLICATION NUMBER: 2,259,830
PRIOR APPLICATION NUMBER: 2,259,830
PRIOR APPLICATION NUMBER: 2,259,830
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 LEQISVIGGN-LTGIFIHRVTPGSAADQMALRPGTQIVWVDYEASEPLFKAVLEDTTLEE 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 LRGVAIATGNAAVGIYISHVEPGSKAQDVGLKRGDQIHEVNGQS------LDHVTSKR 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 964, Application US/09764868
Patent No. US20020168711A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT232
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT PILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER: OF SEQ ID NOS: 1510
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 14.7%; Score 68.5; DB 10; Length 77; Best Local Similarity 30.8%; Pred. No. 0.16; Matches 20; Conservative 13; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                     Length 158
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                                     DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 ISIVSGEKGGIYVSKVTVGSIAHQAGLEYGDQLL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 ISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIV 49
                                                                                                                                                                                                                                                                                                                                                                  Query Match 15.0%; Score 70; Best Local Similarity 41.2%; Pred. No. (Matches 14; Conservative 7; Mismatc)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-911-826A-16
; Sequence 16, Application US/09911826A
; Patent No. US20020143164A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Drosophila melanogaster US-09-911-826A-16
```

us-09-767-215-2\_copy\_568\_660.rapb

```
q
                                                                                                                                                  δλ
                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                               1 QVTMLAF---QGDALLEQISV-----IGGNLTG-----IFIHRVTPGSAADQM-ALR 43
                                                                                                                                                                                                                                                                                                                                                                         29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                Query Match 14.7%; Score 68.5; DB 9; Length 163; Best Local Similarity 29.2%; Pred. No. 0.43; Matches 31; Conservative 16; Mismatches 30; Indels 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 32.5%; Pred. No. 1.8;
Matches 27; Conservative 12; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 PGTQIVMVDYEASEPLFKAVLEDTTLEEAVGLLRRVDGFCCLSVKV 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Goll, Surya K.
Hillman, Jennifer L.
Bandman, Olga
TITLE OF INVENTION: NOVEL HUMAN LIM PROTEINS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARRE: FastSEO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/126,099
FILING DATE: 18-Apr-2002
CLASSIFICATION: CURNOWN>
PRIOR APPLICATION NUMBER: US/09/206,645
FILING DATE: CURNOWN>
APPLICATION NUMBER: US/09/39,485
FILING DATE: CUNROWN>
APPLICATION NUMBER: US/08/739,485
FILING DATE: CUNROWN>
TELEFONDMULCATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLONE: Consensus
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-126-099-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/10126099 Patent No. US20020170079A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 316 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
LIBRARY: Consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-868-964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-10-126-099-5
                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                       а
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
```

THIS PAGE BLANK (USPTO)

```
protein tyrosine-p
multiple PDZ domai
periplasmic trypsi
hypothetical prote
tcmN protein - Str
hypothetical prote
protein-tyrosine-p
                                                                                                                                                                                                                                                                                                                                                                                                      tamA protein - fru
tight junction pro
gene X104 protein
hypothetical prote
multi PDZ domain p
betal-syntrophin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical prote
proteinase hhoA (E
biphenyl dioxygena
biphenyl dioxygena
ribonuclease II-li
endopeptidase La (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein-tyrosine-p
hypothetical prote
different protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alpha-syntrophin -
3-hydroxyacyl-CoA
serine/threonine k
                                                  January 22, 2003, 08:49:35 ; Search time 7.125 Seconds (without alignments) 1254.807 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                            QVTMLAFQGDALLEQISVIG......GLLRRVDGFCCLSVKVNTDG
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                          283224 seqs, 96134422 residues
                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                  US-09-767-215-2_COPY_568_660
467
                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                     - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                     T113703
TE0366
1146336
11294336
11294336
11294336
1296251
1296255
1231255
1231255
1231255
1231255
1231255
1231255
1231255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167629
A54971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T20145
AB1581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E42409
F41858
T48246
AF3361
T22159
T14765
S62894
                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                               seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                  %
Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                       1367
1163
775
1116
853
2054
2450
2055
387
717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22294
22944
229466
2172
21172
11336
1231
408
408
7233
7253
682
682
                                                                                                                                                                                                                                                              PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                          Title:
Perfect score:
                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                           76.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB s
Maximum DB s
                                     OM protein
                                                                                                             Sequence:
                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                 Database
                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                        Result
```

			K.; Miya extramad						cons		
tth p p tth tth in in in in in in in in in in in in in					3;				highly		4
flagellar biosynth hypothetical prote farboxy-terminal protection by the flagellar biosynth different proteins dynein heavy chain proteinse (EC 3.4 topolsomerase IV, vacB protein - The nitrate reductase IV intrate reductase aminopeptidase Atu proteinase DO VCO5 throonine ammonia-fluss SpovG subtilis SpovG		2000	Kondo, way of	PID:91498137	S.	64 459		-2000	a)	20580	sd
r bic teal teal ical ical tor eavy eray fruy eras () eras tein tein tein tein tein tein		Nov-	A.; Kon pathway	:g14	Gaps			-Jul-	2, ar	PID:9382058	Gaps
flagellar biosyn hypothetical pro carboxy-terminal flagellar biosyn hypothetical pro different protei dyneln heavy cha probable fructok proteinase (EC I) topolsomerase IV vacB protein T		17-			.67; 13;	PLFK		21	-02		 
flag carbo carbo flag hypo diff dyne prob topo vacs nitr amin prot		nange	Murayama, activating	23.1;	ch 13 els	EASE		ıange	protein,	59.1;	1163 els
		#text_change 17-Nov-2000		A1193	Length Indels	VMVD)		#text_change		C954(	Length 1 ; Indel
		_	M. the 823	DDBJ PIDN:BAA11923	2; 29;	GTQI   :  GDKI	•		, 1998 ht junction PMID:9837755	PIDN: AAC95469	; Le 20;
	S	ster) -1999	yashi nt of ID:86	\	0.63; thes	MALRE     QGLME		-1999	1998 Junc IID:96	; PII	۸.,
	ALIGNMENT	melanogaster) n 13-Aug-1999	.; Kobayashi, component of 452; PMID:869	GB/EMBL/DDBJ	re 85.5; d. No. 0.6 Mismatches	SAADQ     SPASL		23-Jul-1999	522, cight ); PM	20579	re 81; DB d. No. 1.6 Mismatches
AE0745 AC3202 JH0263 B55546 T72166 AH1227 AH1227 AH1227 AG0433 AG0434 AG044 AG044 AG044 AG044 AG044 AG04 AG0	ALIGN	mela on 13	i, T.; Kobaya , a component 6312452; PMID	from GB/EMBL NID:91498136;	Score E Pred. N	VTPG8       VQPG8		en on 23	617-6 the t 5755(	:9383	Score E Pred. N
AEO AC3 JHO BB55 T225 AH11 BB54 F71 AG0 AB7 H72 S16 AE3 F82 F82 F82 AD1		hila er visi	Suzuki, 6 gene, UID:963	d fr NID	Sc Pr 11;	FIHR  :  FVTA	80 479	chicken en) evision	.52, of :990	NID	; Sc ; Pr 16;
00000000000000000		osop gast e_re	Suzuki 996 ou gene, MUID:96	late 477; FBqn	18.3%; 33.8%; ive	LTG1    EAG1		icke e_re	J. n. 2 ains MUID	184;	* *
692 323 539 692 11034 11136 4367 457 695 710 982 384 456 456 845 695 710 982 102		y (Dre elanoe quence	S.; 5, 19 tamo 700; 1	y; translated from A A TAK> EMBL:D83477; NID:91	18. larity 33. Conservative	LAFQGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVWDYEASEPLFKAVL 	EDTTLEEAVGLLRRVD               :   NGVTREEAVLFLLSLQDRID	ZO-2 s (ch:	Commun Gommun Goms 366; 1	AF085	17.38 Larity 35.38 Conservative
~		fl. # m # See	179 179 111a 217	TAK TAK EMB	tity	SOIS	LFLL	ein, allu #se	ss. sdin JEO JEO	COC CB:	ity
		fruit ophil	Toga 1783- osoph ber:	3703 minar : mRh 367 < ces: tam)	ch 1 Similarity 27; Conserv	AFQGDALLE :  ::: SFQKEGSV-	EEAV      EEAVI	junction protein, junction protein, ites: Gallus gallu :: 23-Jul-1999 #se	s. Riz s. Re n-bir ber: 0366 minar	163 <	Ē
66 65 65 65 65 65 65 65 65 65 65 65 65 6		.n - Dros	M.; 10, 10, ne Dr	n: Tl breli type 1-1 eren	ch 1 si 27;	LAFQG ::   ISFQK	EDTTLEEAV          NGVTREEAV	tion Gall Jul-	J.R. ophy otei num n: JE reli type	l-1 eren	
		1 otej es:	ev.	sior ule ules: lues: ref	Mat Loca les	5	65	2 unct es: 23-	ns, I. Bi ence sior sior iule	lues:	Match Local
0.10.00.00.00.00.00.00.00.00.00.00.00.00		RESULT 1 T13703 Tand protein - fruit fly (Drosophila me C;Species: Drosophila melanogaster C;Date: 13-Aug.1999 #sequence_revision	Takah Takah enes D Title	A.Accession: T13703 A.Status: preliminary; translated fi A.Molecule type: mRNA A.Residues: 1-1367 <tak> A.Cross-references: EMBL:D83477; NII C.Genetics: A.Gene: tamou (tam) A.Gross-references: FlvBase:FBan0000</tak>	Query Match Best Local S Matches 27	y b	У d	RESULT JE0366 tight j C;Speci C;Date:	R;Collins, J.R.; Rizzolo, L.J. 252, 617-622, 1996 Blochem. Blochyes. Res. Commun. 252, 617-622, 1996 A;Title: Protein-binding domains of the tight jur A;Reference number: JE0366; MUID:99057550; PMID:9454. A;Stetus: preliminary A;Molecule type: _mRNA	;Resid ;Cross	Query Ma Best Loc Matches
		8 日 日 り り り り り	) K O K K	ৰৰৰৰ একৰ		Qy D <b>b</b>	Qy	# F + O O O	RWAAAAA	A A	

```
A;Introns: 41/3; 110/1; 151/2; 194/1; 232/1; 342/3; 390/3; 528/1; 551/2; 628/1; 674/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-2054 <ULL>
A;Cross-references: EMBL:AJ001320; NID:q2959978; PIDN:CAA04681.1; PID:g2959979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-853 <SAN
A;Cross-references: EMBL: 041035; PIDN: AAB37028.1; GSPDB:GN00028; CESP:T10A3.1
A;Experimental source: strain Bristol N2; clone T10A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        multi PDZ domain protein 1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 21-Jul-2000
C;Accession: T46612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein T10A3.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RiUlhmer, C.; Schmuck, K.; Figge, A.; Lubbert, H. FEBS Lett. 424, 63-68, 1998
A;Title: Cloning and characterization of MUPPI, a novel PDZ domain protein. A;Reference number: 223104; MUID:98196865; PMID:9537516
A;Accession: T46612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVIGG-----NLTGIFIHRY-TPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLE 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 AFQGDALLEQISVIGGNLT----GIFIHRVTPGSAADQMA-LRPGTQIV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Sansone, J.; Nhan, M. submitted to the EMBL Data Library, November 1995 A;Description: The sequence of C. elegans cosmid T10A3. A;Reference number: Z20675 A;Accession: T29736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.4%; Score 76.5; DE 34.2%; Pred. No. 3.5; tive 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 76; DB Fred. No. 11; 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.3%;
ilarity 32.5%;
Conservative 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 TYEOVYDSIAASRYDTSVE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EAVAILKRIKGTVTLMV 2052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DYEASEPLFKAVLEDTTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: brain C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 EAVGLLRRVDGFCCLSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                betal-syntrophin - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 27; Conserv
                                          567 VREDAVL 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Genetics:
A;Gene: CESP:T10A3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: T29736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: MUPP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
                                                                                                                                                                                                  RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of two novel genes and reduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZO-2, a tight junction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          July protein - human
C; Species: Homo sapiens (man)
C; Accession: 154378
R; Duclos, F.; Rodius, F.; Wrogemann, K.; Mandel, J.
H; Min. Mol. Genet.; 3, 909-914, 1994
A; Title: The Friedrich ataxia region: characterization of two novel genes and re A; Reference number: 154378; MUID:95038744; PMID:7951235
A; Accession: 154378
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Mosicule type: mRNA
A; Mosicule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tight junction protein - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 16-Dec-1998
C:Accession: 146236
B:Jesaitis, L.A.; Goodenough, D.A.
J. Cell Biol. 134, 949-961, 1994
A:Title: Molecular characterization and tissue distribution of ZO-2, a tight jun A; Reference number: A54475; MUID:94179414; PMID:8132716
A:Accession: 146236
A:Ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>ښ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |: | :||: | : ||: | : ||: | : ||: | : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 MLAF-QGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKA 62
62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 MLAF-QGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKA 62
                                                    MLAF-QGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 16.5%; Score 77; DB 2; Length 1116; Best Local Similarity 34.3%; Pred. No. 4.3; Matches 23; Conservative 15; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.5%; Score 77; DB 2; Length 775; Larity 34.3%; Pred. No. 2.8; Conservative 15; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
es 23; Conserv
                                                                                                                                                                                                                                                            :: || |
IVREDAVL 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152 VREDAVL 158
                                                                                                                                                                                                  63 VL-EDITL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 VLEDITL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 VLEDITL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                 a
```

4

Gaps

ä

14;

10:56:41

Wed Jan, 22

```
C.Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homolog C.Superfamily: phosphoric monoester hydrolase; transmembrane protein; ty F;566-860/Domain: protein 4.1 membrane-binding domain homology <B41> F;1089-1165/Domain: GLGF domain homology <GLG1> F;1361-1137/Domain: GLGF domain homology <GLG1> F;1455-1574/Domain: GLGF domain homology <GLG2> F;1455-1574/Domain: GLGF domain homology <GLG3> F;1769-1840/Domain: GLGF domain homology <GLG3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Accession: T30259
R.Simpson, E.H.; Suffolk, R.; Jackson, I.J.
Genomics 59, 102-104, 1999
A.Title: Identification, sequence, and mapping of mouse multiple PDZ domain protein A.Reference number: 220797; MUID:99326529; PMID:10395806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2055 <312.
A;Cross-references: EMBL:AJ131869; NID:94150877; PIDN:CAA10523.1; PID:94150878
A;Experimental source: strain C57/BL6 X CBA F1; whole brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1094 LGFQ-----IIGGEKMGRLDLGVFISAVTPGGPADLDGCLKPGDRLISVNSVSLEG 1144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Accession: $40290
A,Molcoule type: mRNA
A,Residues: 2266-2372 <HEN>
A,Cross-references: EMBL:223059; NID:9438155; PIDN:CAA80594.1; PID:9438156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 IFIHRV-TPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEAVGLLRRVDGFCC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;1863-1937/Domain: GLGF domain homology <GLG5>
F;2203-2422/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;2374/Active site: Cys (phosphocysteine intermediate) #status predicted
F;2380/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 LAFQGDALLEQISVIGGNL----TGIFIHRVTPGSAAD-QMALRPGTQIVMVD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.7%; Score 73.5; D
34.9%; Pred. No. 21;
ive 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 74.5;
Pred. No. 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 multiple PDZ domain protein - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1145 VSHHAAVDILQNAPEDVTL 1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.0%;
30.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 --YEASEPLFKAVLEDTTL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 30.**
The 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
A; Reference number: S40280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2051 LMV 2053
                                                                                                                                                                                                                                                                                            A; Map position: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSV 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: mpdz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
G97295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 а
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross references: GB:L34582; NID:g806297; PIDN:AAC42056.1; PID:g806298
A;Cross references: GB:L34582; NID:g806297; PIDN:AAC42056.1; PID:g806298
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: mRNA
A;Melecule type: mRNA
A;Residues: 1338-1354, K',1356-1447, R',1449-1454 <RE2>
A;Cross references: GB:L34581; NID:g806295; PIDN:AAC42055.1; PID:g806296
A;Cross references: GB:L34581; NID:g806295; PIDN:AAC42055.1; PID:g806296
A;Cross references: GB:L34581; NID:g806296
A;Cross references: GB:L34581; NID:g806296; DIDN:AAC42055.1; Mieringa, B.
Submitted to the EMBL Data Library, June 1993
A;Description: Assessment of the expression levels of murine protein-tyrosine phosphatas
                                                             C. Accession: 159291
R.Ahn, A.H.: Yoshida, M.; Anderson, M.S.; Feener, C.A.; Selig, S.; Hagiwara, Y.; Ozawa, M.S.; Accession: 159291
R.Ahn, A.H.: Yoshida, M.; Anderson, M.S.; Feener, C.A.; Selig, S.; Hagiwara, Y.; Ozawa, M.S.; Leener, C.A.; Selig, S.; Hagiwara, Y.; Ozawa, M.S.; Leener, Sci. 108.A.; Al. 4446-4450, 1994
A.Title: Cloning of human basic Al, a distinct 59-kba dystrophin-associated protein encomplement of human basic Al, adistinct 59-kba dystrophin-associated protein encomplement in the selection of human basic Al, adistinct 59-kba dystrophin-associated protein encomplement in the selection in the se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A. Molecule type: MRNA
A. Residues: 1-2450 cCHI>
A. Crossreferences: EMBL:D83966; NID:g1232103; PIDN:BAA12158.1; PID:g1232104
A: Crossreferences: EMBL:DB3966; NID:g1232103; PIDN:BAA12158.1; PID:g1232104
A: Experimental source: strain DBA/2; cell line MEL 745A
R: Wolf, B.B.; Brown, M.D.
FBBS Lett. 376, 177-180, 1995
A:Title: Epidermal growth factor-binding protein activates soluble and receptor-bound : A:Reference number: S67987; MUID:96105375; PMID:7498536
A:Accession: S67987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 13 - mouse
N;Alternate names: epidermal growth factor-binding protein; serine proteinase
C;Species: Mus musculus (house mouse)
C;Date: 27-Nov-1997 #sequence_revision 12-Dec-1997 #text_change 21-Jun-2002
C;Accession: 371625; 867987; 181210; 181209; 840290
R;Chida, D.; Kume, T.; Mukouyama, Y.; Tabata, S.; Nomura, N.; Thomas, M.L.; Watanabe, FBBS Lett. 358, 233-239, 1995
A;Title: Characterization of a protein tyrosine phosphatase (RIP) expressed at a very A;Reference number: S71625; MUID:95145716; PMID:7843407
                                       Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Residues: 1098-1102 < WOL>
A; Residues: 1098-1102 < WOL>
A; Experimental source: submaxillary glands
R; Sato, T.; Irie, S.; Kitada, S.; Reed, J.C.
Science 268, 411-415, 1995
A; Title: FAP-1: a protein tyrosine phosphatase that associates with Fas.
A; Reference number: 159595; MUID:95232528; PMID:7536343
A; Accession: 181210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 QGDALLEQ-----ISVIGG--NLTGIFIHRVTPGSAADQ-MALRPGTQIVMVDYEASEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 16.0%; Score 74.5; D Best Local Similarity 35.6%; Pred. No. 3.4; Matches 32; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --GADLRDATHDEAVQALKRAGKEVLLEVK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 LFKAVLEDTTLEEAVGLLRRVDGFCCLSVK 88
Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

4

Gaps

23;

Length 2450;

```
periplasmic trypsin-like serine protease (with PDZ domain), HtrA subfamily (imported) C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 16-Aug-2002 C;Accession: G97295 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L
```

3

6

Indels

Length 2055;

.,

29;

Length 494;

```
R.Mackawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.
FEBS Lett. 337, 200-206, 1994
A;Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membr
A;Reference number: I53483; MUID:94116679; PMID:8287977
A;Accession: I67630
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                        A;Cross-references: GB:M80674; NID:g15348B; PIDN:AAA6751B.1; PID:g153499
A;Note: sequence extracted from NCBI backbone (NCBIN:87744, NCBIP:87747)
B;Bibb, M.J.; Biro, S.; Motamedi, H.; Collins, J.F.; Hutchinson, C.R.
EMBO J. 8, 2727-2736, 1989
A;Title: Analysis of the nucleotide sequence of the Streptomyces glaucescens tcml gen
A;Reference number: S05972; MUID:90060035; PMID:2684656
A;Accession: S05976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein T30N20_90 - Arabidopsis thaliana (C;Specias: Arabidopsis thaliana (mouse-ear cress) (C;Specias: Arabidopsis thaliana (mouse-ear cress) (C;Date: 21-3u1-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000 (C;Accession: T50791 FS) (S;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; submitted to the Protein Sequence Database, July 2000 (A;Reference number: 225240)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 29-May_1998 #sequence_revision 29-May-1998 #text_change 30-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 LADDOGMERFSRIADLGGGGGWFLAQILRRHPHATGLLMDLPRVAASAGPVLEEAKVADRV 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 SVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEAVGLL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----NLTGIF--IHRVTPGS------AADQM 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:AL365234
A;Experimental source: cultivar Columbia; BAC clone T30N20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                380 TVLPGDFFTDPVPTGYDAY -- LFKGVLHNWSDERAVTVLRRV 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.3%; Score 71.5; DB 2; 28.4%; Pred. No. 6.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 ALRPG---TQIVMVDYEASEPLFKAVLEDTTLEEAVGLLRRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.3%; Score 71.5; Dl
30.4%; Pred. No. 6.6;
Live 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 LAFQGDALLEQISVIGG------
                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL:X15312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Map position: 5
A, Introns: 220/3; 255/3; 312/3
A, Note: T30N20_90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-503 <BEV>
                                                  A; Molecule type: DNA
A; Residues: 1-494 <SUM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-17 <BIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 VAVKGMC 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 RRVDGFC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: 167630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: T50791
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
I67630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                òγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   temn protein - Streptomyces glaucescens
C;Species: Streptomyces glaucescens
C;Species: Streptomyces glaucescens
C;Species: O'Peb-1995 #sequence_trevision 20-Peb-1995 #text_change 22-Oct-1999
C;Accession: B42276; S05976; S27696
R;Summers, R.G.; Wendt-Pienkowski, E.; Motamedi, H.; Hutchinson, C.R.
A; Bacteriol. 174, 1810-1820, 1992
A;Title: Nuclectide sequence of the tcmII-tcmIV region of the tetracenomycin C biosynthe dehydratase-O-methyl transferase.
A;Reference number: A42276; MUID:92193265; PMID:1548230
                                                                               Solvent-Producing Bacterium Cld
                                                                                                                                                                                                                                                                                                                                                             A;Gene: CAC3218
C;Superfamily: Escherichia coli trypsin-like proteinase; GLGF domain homology; trypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: 221316
A; Reference number: 221316
A; Reference number: 221316
A; Reference number: 221316
A; Status: T324
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-717 <GGI>A; CGEI>
A; Cross-references: EMBL: AF068716; PIDN: AAC17752.1; GSPDB: GN00023; CESP: F26D11.11
A; Experimental source: strain Bristol N2; clone F26D11
C; Genetics: A; Genetics: Strain Bristol N2; 368/3; 376/2; 623/2
A; Introns: 34/2; 119/2; 226/1; 302/3; 368/3; 576/2; 623/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  э;
Э
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bact
A; Reference number: A96900; MUID:21359325; PMID:21359325
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-387 < KURA
A; Cross-references: GB:AE001437; PIDN:AAK81154.1; PID:g15026290; GSPDB:GN00168
A; Experimental source: Clostridium acetobutylicum ATCC824
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F26D11.11 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T32295
R;Geisel, C.; Bradshaw, H.
submitted to the EMBL Data Library, May 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 GKVIKPFVGIVGGDIKVRSQDNMKGVYVKEVVPGSGAAKAGLRPSDIILELNGQ----- 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 GDALLEQISVIGG-----NLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 LAFQGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVD----YEASEPL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 15.4%; Score 72; DB 2; Length 387; Best Local Similarity 23.7%; Pred. No. 4.4; Matches 22; Conservative 17; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.4%; Score 72; DB : 29.1%; Pred. No. 9; :ive 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            342 -RILSTNDIGSIVSSSKIGDKVPC---KVNRNG 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTDG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 FKAVLEDTTLEEAVGLLRR 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 29.1% nes 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
```

form 3

ij

Gaps

1;

Length 503; Indels

```
Protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice form 2 - protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice form 2 - C:Species: Homo sapiens (man)
C:Accession: 167629
R:Maekawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.
A:Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane A; Reference number: 153483; MUID:94116679; PMID:8287977
A; Reference number: 153483; MUID:94116679; PMID:8287977
A; Reterence number: 153483; MUID:94116679; PMID:8287977
A; Reterence number: 153483; MUID:94116679; PMID:8287977
A; Molecular type: mRNA
A; Molecule type: mRNA
A; Reterences: GB:DD1210; NID:9452191; PIDN:BAA04751.1; PID:9452192
C; Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology; C; Keywords: phosphatia: noncester hydrolase
F; 574-868/Domain: GLGF domain homology <GLG2>
F; 2218-2437/Domain: protein-tyrosine-phosphatase homology <PTP>
F; 2218-2437/Domain: protein-tyrosine-phosphatase homology <PTP>
A;Residues: 1-2294 <RES>
A;Cross-references: GB:D21211; NID:9452193; PIDN:BAA04752.1; PID:9452194
A;Cross-references: GB:D21211; NID:9452193; PIDN:BAA04752.1; PID:9452194
C;Superfamilty: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology; C;Reywords: phosphoric monoester hydrolase
F;574-868/Domain: protein 4.1 membrane-binding domain homology <B41>
F;1187-1258/Domain: GLGF domain homology <GLG2>
F;2046-2265/Domain: protein-tyrosine-phosphatase homology <PTP>
                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     899 EITLVNLKKDAKYGLGFQIIGGEKMGRLDLGIFISSVAPGGPADLDGCLKPGDRLISVNS 958
                                                                                                                                                                                                                                                                                                                                                                                                            1 QVTMLAFQGDALLE-QISVIGGNL----TGIFIHRVTPGSAAD-QMALRPGTQIVMVD- 52
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVTMLAFQGDALLE-QISVIGGNL----TGIFIHRVTPGSAAD-QMALRPGTQIVMVD- 52
                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
                                                                                                                                                                                                                                                                                DB 2; Length 2294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.3%; Score 71.5; DB 2; Length 2466; 28.6%; Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30; Indels
                                                                                                                                                                                                                                                                                Query Match 15.3%; Score 71.5; D
Best Local Similarity 28.6%; Pred. No. 39;
Matches 24; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: January 22, 2003, 08:54:39
Job time: 10.125 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1131 VSLEGVSHHAAIEILQNAPEDVTL 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----YEASEPLFKAVLEDTTL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----YEASEPLFKAVLEDTTL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local
Matches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ολ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                       à
```

HIS PAGE BLANK (USPTO)

```
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

January 22, 2003, 08:49:35 ; Search time 3.625 Seconds (without alignments) 1064.082 Million cell updates/sec

US-09-767-215-2\_COPY\_568\_660 467

1 QVTMLAFQGDALLEQISVIG......GLLRRVDGFCCLSVKVNTDG 93 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Q9bx16 homo sapien	mus m	homo	homo	canis	-	hom		mus	P16559 streptomyce		P37337 burkholderi			Q8xzi4 ralstonia s	P40729 salmonella	P45443 neurospora	059128 pyrococcus			_	Q9wzil thermotoga	P08619 neurospora	P55196 homo sapien	P80150 xanthomonas	-	Q13009 homo sapien		_	37	622	4936	026819 methanobact
SUMMARIES	ID	CARE_HUMAN	CARE_MOUSE	CARB_HUMAN	ZO3_HUMAN	ZO3_CANFA	ZO2_CANFA	ZO2_HUMAN	ZO2_MOUSE	ZO3_MOUSE	TCMN_STRGA	PTND_HUMAN	BPHG_BURCE	LON_BRUAB	HRA2_HUMAN	YE11_RALSO	FLHA_SALTY	DYHC_NEUCR	YE59_PYRHO	HRA2_MOUSE	AI75_HUMAN	PARE_CAUCR '	RNR_THEMA	NIA_NEUCR	AF6_HUMAN	HRC2_XANCV	NIFJ_ANASP	TIAM_HUMAN	GLMS_THEMA	PRAX_HUMAN	FLHA_YEREN	DLG2_RAT	YAEL_HAEIN	CIMA_METTH
	DB		Н	٦	~	٦	7	П	П	7		•		Н		•													Н			-	-	П
	Query Match Length	1004	666	1147	933	868	1174	1190	1167	902	494	2485	408	812	458	462	692	4367	310	458	552	695	710	982	1816	645	1199	1591	605	1461	692	852	443	496
ð	Query Match	100.0	81.6	29.8	17.1	16.7	16.5	16.5	16.1	15.6	15.3	15.3	14.7	14.7	14.2	14.1	14.1	14.1	14.0	14.0	14.0	13.9	13.9	13.9	13.7	13.6	13.5	13.5	Э.			13,3	13.2	13.2
	Score	467	381	139	80	78	77	77	75	73	71.5	71.5	68.5	68.5	66.5	99	99	99	65.5	65.5	65.5	65	65	65	64	63.5	63	63	62.5	62.5	62	62	61.5	61.5
	Result No.	-	7	3	4	<sub>S</sub>	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

34 61.5 13.2 906 1 CADO_XENLA CO7984 archaeoglob   35 61 13.1 298 1 DHY2_ARCFU	SULT 1  CARE_HUMAN STANDARD; PRT; 1004 AA.  CARE_HUMAN STANDARD; PRT; 1004 AA.  COBXL6; 099VB5;  15-JUN-2002 (Rel. 41, Last sequence update)  15-JUN-2002 (Rel. 41, Last annotation update)  15-JUN-2002 (Rel. 41, Last annotation update)  2 Caspase recruitment domain protein 14 (CARD-containing MAGUK protein 2).  2) (Carma 2).  CARD14 OR CARMA2.  Homos appleas (Human).  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	SEQUENCE FROM N.A.  SECURINE FROM N.A.  MEDLINE-21192234; PubMed=11278692;  MEDLINE-21192234; PubMed=11278692;  MEDLINE-21192234; PubMed=11278692;  Stinivasula S.M., Merriam S., DiStefano P.S., Alnemri E.S.;  Stinivasula S.M., Merriam S., DiStefano P.S., Alnemri E.S.;  Stinivasula S.M., Merriam S., DiStefano P.S., Alnemri E.S.;  (CARD)/membrane-associated guanjlate kinase (MAGUK) family members that interact with Boll ond activate NF-kappaB.";  J. Biol. Chem. 276:11877-11882(2001).  SEQUENCE FROM N.A.  MEDLINE-21255663; PubMed=11356195;  Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.;  Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.;  Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.;  Gaide O., Martinon and NF-kappaB activation.";	onnet D., Thome M., Tschopp J.;  Bank/DDBJ databases.  a Bcl10 and IKK. Stimulates the o each other by CARD-CARD  c. placenta. Also detected in HeLa ancer cell lines tested.  IN. (KINASE-LIKE DOMAIN. H3 domain which is not detected by It is produced through a collaborat nformatics and the EMBL outstatic	the buildhoun brointonmarks instructs. There are no restrictions on the use by non-profit institutions as long as its content is in no way
	RESUI LID AC DT DT DE DE OC OC	R R R R R R R R R R R R R R R R R R R	3 C C C C C C C C C C C C <b>S S S S S S S </b>	38

```
CONFLICT
                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                        DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                           CARB_HUMAN
                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
qq
                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                ·;
    noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 14 (Bcll0-interacting MAGUK protein
                                                                                                                                                                                                      DYEASEPLEKAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTD
GYKRLLQDLEAK -> SRARPLLSPGLLMGTVAAGGVTQAD
FTSPRRCRSTLGWASALSWADVKRSAHL (IN REF. 2;
                                                                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                                  1 QVTMLAFQGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLF 60
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Α.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Bimpl, a MAGUK family member linking protein kinase C activation
Bcll0-mediated NF-kappa B induction.",
J. Biol. Chem. 276:30589-30597(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Benito
   and for
                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 467; DB 1; Length 1004; 100.0%; Pred. No. 1e-42; 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=21391892; PubMed=11387339;
MCALLISter-Lucas L.M., Inchara N., Lucas P.C., Ruland J., Be
MCALLISter-Lucas L.M., Inchara N., Lucas P.C., Ruland T.W.,
Li Q., Chen S., Chen F.F., Yamacka S., Verma I.M., Mak T.W.
Nunez G.;
                                                                                                                                                                                                                                             7469B8B56BE06073 CRC64;
                                                                                                                                                                             COILED COIL (POTENTIAL).
                                                                                            SMART: SMO072: GUKC: 1.
SMART: SM00072: GUKC: 1.
PROSTTE: PS50209; CARD: 1.
PROSTTE: PS00086: GUANYLATE_KINASE_1; FALSE_NEG-PROSTTE: PS50052; GUANYLATE_KINASE_2; 1.
PROSTTE: PS50106; PDZ: 1.
                                                                                                                                                                                                 GUANYLATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                            999 AA
   modified and this statement is not removed. entities requires a license agreement (See Por send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                    628 KAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTDG 660
                                                                                                                                                                                                                                                                                                                                          KAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTDG 93
                                                                                                                                                                                                                                       AAH01326
                                      EMBL; AF322642; AAG53403.1; --
EMBL; AY032927; AAK54453.1; --
EMBL; BC018142; AAH18142.1; --
EMBL; BC01326; AAH01326.1; ALT_INIT.
InterPro; IPR00019; Guanylate_kin.
InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 82-743 FROM N.A.
                                                                                                                                                                                                                                                                          100.08;
                                                                                                                                                                                                                                               1004 AA; 113299
                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                     107
409
658
990
671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2) (Bimp2).
CARD14 OR BIMP2.
                                                                                                                                                                     15
128
568
858
858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Breast;
                                                                                                                                                                                                                                                                                                                                                                                                              CARE_MOUSE
                                                                                                                                                            Coiled coil
                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                    099KF0;
                                                                                                                                                                                        DOMAIN
                                                                                                                                                                       DOMAIN
                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                    CARE_MOUSE
                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                             g
       ò
                                                                                                                                                                                                                                                                                                                         a
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
-!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
-!- SIMILARITY: CONTAINS 1 GUANYLATE KINASE-LIKE DOMAIN.
-!- CAUTION: Supposed to contain a SH3 domain which is not detected by PROSITE, Pfam or SMART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 11 (CARD-containing MAGUK protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVTMLAFQGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIJNE-21255663; PubMed=11356195; Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.; Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.; "Carmal, a CARD-containing binding partner of Bc110, induces Bc110 Phosphorylation and NF-kappaB activation."; FEBS Lett. 496:121-127(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE-21192234; Pubmed-11278692; M.D., Poyet J.-L., MEDIINE-21192234; Pubmed-11278692; M.D., Poyet J.-L., Srinivasula S.M., Merriam S., DiStefano P.S., Alnemri E.S.; Srinivasula S.M., Merriam S., DiStefano P.S., Alnemri E.S.; "CARDII and CARDI4 are novel caspase recruitment domain "CARDI membrane associated quanylate kinase (MAGUK) family members that interact with Bcll0 and activate NF-kappaB."; J. Biol. Chem. 276:11877-11882(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           743 QAQQQLLA -> HLLEDHRS (IN REF. 2).
113496 MW; D18350DA12430255 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.6%; Score 381; DB 1; Length 99
79.6%; Pred. No. 2.1e-33;
.ive 12; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BC004692; AAH04692.1; -.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR00178; PDZ.
InterPro; PFR00178; PDZ.
Pfan; PF00595; PDZ; 1.
PROSITE; PS50209; CARD; 1.
PROSITE; PS50062; GUANYLATE_KINASE_1; FALSE_NEG-PROSITE; PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GUANYLATE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1147 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARD.
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF363457; AAK60137.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 79.6
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             411
655
986
743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                999 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3) (Carma 1).
CARD11 OR CARMA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15
125
572
854
736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARB_HUMAN
Q9BXL7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coiled coil
```

```
16 L 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203_CANFA

ID 203_C,

AC 06268

DT 16-0C

DT 16-0C

DT 15-JU

DE Tight

DE 0cclu

GN TJP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                    -:- SUBCELLULAR LOCATION: Cytoplasmic.
-:- TISSUE SPECIFICTAY: Detected in adult peripheral blood leukocytes, trysue Spelen and liver. Also found in promyelocytic leukemia HL-60 cells, chronic myelogenous leukemia K562 cells, Burkitt's lymphoma Raji cells and colorectal adenocarcinoma SW480 cells. Not detected in HeLa Si, Molt-4, A549 and G431 cells. Not detected in HeLa Si, Molt-4, A549 and G431 cells.
-:- SIMILARITY: CONTAINS I CARD DOMAIN.
-:- SIMILARITY: CONTAINS I PDZ/DHR DOMAIN.
-:- SIMILARITY: CONTAINS I GUANYLATE KINASE-LIKE DOMAIN.
-:- SUBPOSCE to contain a SH3 domain which is not detected by PROSITE, Pfam or SWART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 GDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTT 68
                                       Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.;
FEBS Lett. 505:198-198(2001).
-!- FUNCTION: Activates NF-kappaB via Bcl10 and IKK. Stimulates the
phosphorylation of Bcl10.
-!- SUBUNIT: CARD11 and Bcl10 bind to each other by CARD-CARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Washaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tight junction protein 20-3 (Zonula occludens 3 protein) (Zona occludens 3 protein) (Tight junction protein 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 1147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 103 CARD.
123 442 COILED COIL (POTENTIAL).
673 748 PDZ.
866 1133 GUNYLATE KINASE.
808 808 P -> L (IN REF. 2).
1147 AA; 132641 MW; 913A4B015D2B36CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.5%; Pred. No. 3.7e-07;
live 17; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genew; HGNC:16393; CARDII.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PD2.
SMART; SM00228; PD2.
PROSTTE; PS50209; CARD; 1.
PROSTTE; PS50052; GUANYLATE_KINASE_1; FALSE_NEG.
PROSTTE; PS500106; PD2; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         933 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.8%; Score 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          726 KEEAHWTIQRCSGPVTLHYKVNHEG 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 LEEAVGLLRRVDGFCCLSVKVNTDG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF322641; AAG53402.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 36.5
nes 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                        interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZO3_HUMAN
095049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                       ERRATUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203_HUMAN
1D 203_H
1D 203_H
1D 203_H
1D 16-0C
1D 16-0C
1D 15-0C
1D 15-0C
1D 179-0C
1D 
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
16 ISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEAVGL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tight junction protein ZO-3 (Zonula occludens 3 protein) (Zona cocludens 3 protein) (Tight junction protein 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 80; DB 1; Length 933;
Pred. No. 0.72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 93 PDZ 1.

195 272 PDZ 2.

394 460 PDZ 3.

489 563 SH3.

675 775 GUANYLATE KINASE.

933 AA; 102800 MW; 680298CFD0615B47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00856; GUANYLATE_KINASE_1; FALSE_NEG. PROSITE; PS50052; GUANYLATE_KINASE_2; 1. PROSITE; PS50002; SH3; 1. PROSITE; PS50106; PDZ; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tight junction; SH3 domain; Repeat; Membrane.
DOMAIN 11 93 PDZ 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         898 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AC005954; AAC72274.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew; HGNC:11829; TJP3.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PD2.
Pfam; PF00595; PD2; 3.
Pfam; PF00595; Guanylate_kin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00072; GUKC; 1
SMART; SM00228; PDZ; 3.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P31016; 1BFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZO3_CANFA
O62683;
```

```
551 VREDAVL 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 VLEDITL 69
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
ZO2_HUMAN
 οp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its web y non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                        16 ISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVWYDYEASEPLFKAVLEDTTLEEAVGL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 42, Last annotation update)
15-JUN-2002 (Rel. 43)
15-JUN-2002 (Rel. 44)
15-JUN-2002 (Rel. 45)
15-JUN-20
                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBL_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 898;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GUANYLATE KINASE.
8091D6132DB9F15D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             interPro; IPR000619; Guanylate_Kin.
InterPro; IPR001478; PDZ.
InterPro; IPR001478; PDZ.
InterPro; IPR001478; PDZ.
InterPro; IPR001452; SH3.
Pfam; PF00652; Guanylate_Kin; 1.
SMART; SM00072; GuKc; 1.
SMART; SM00328; PDZ; 3.
SMART; SM00328; PDZ; 3.
SMART; SR00326; SH3; 1.
PROSITE; PS50055; GUANYLATE_KINASE_1; FALSE_NEG.
PROSITE; PS500105; PDZ; 3.
PROSITE; PS50106; PDZ; 3.
PROSITE; PS50106; PDZ; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat; Membrane.
PDZ 1.
PDZ 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1174 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.7%; Score 78; 34.4%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF023617; AAC39177.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98414 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tight junction; SH3 domain;
DOMAIN 11 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
       Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                369 4
464 5
650 7
898 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P31016; 1BFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZOZ_CANFA
Q95168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          435 L 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 L 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
ZOZ_CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ñ,
                                                                                                                                                                                                                        N 123

N PARTIAL SEQUENCE FROM N.A.

X MEDLINE-94179414; PubMed-8132716;

A Jesaitis L.A., Goodenough D.A.;

T "Molecular characterization and tissue distribution of 20-2, a tight at monecular characterization and tissue distribution of 20-2, a tight at "Molecular characterization and tissue distribution of 20-2, a tight at "molecular characterization and tissue distribution of 20-2, a tight at "molecular characterization and tissue distribution of 20-2, a tight at "molecular characterization and tissue distribution brotein ";

T. Call Biol 124'949-961(194).

C. -- SUBCELULAR ROCE IN TIGHT JUNCTIONS AND ADHERENS JUNCTIONS.

C. -- SUBCELLULAR LOCATION: PERPERSAM EMBRANE. CYTOPLASMIC SIDE.

C. -- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE

PRODUCED BY ALTERNATIVE SPLICING.

C. -- SIMILARITY: CONTAINS 3 PEZ-DHR DOMAINS.

C. -- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

C. -- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
              MEDLINE-96421547; PubMed=8824195; Beatch M., Jesaitis L.A., Gallin W., Goodenough D.A., Stevenson B.R.; Beatch M., Jesaitis L.A., Gallin W., Goodenough D.A., Stevenson B.R.; "The tight junction protein 20-2 contains three PDZ (PSD-95/Discs-Large/ZO-1) domains and an alternatively spliced region."; J. Biol. Chem. 271:25723-25726(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 MLAF-QGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tight junction; SH3 domain; Repeat; Membrane; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 77; DB 1; Length 1174;
Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45AB836BBDDB1226 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE: PS00856; GUANYLATE_KINASE_1; FALSE_NEG. PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GUANYLATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY - GLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00625; Guanylate_kin; 1.
SMART; SM00072; GuKc; 1.
SMART; SM00228; PDZ; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132085 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.5%;
34.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L27152; AAC37332.1; -. HSSP; P31016; 1BE9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 34...
Loca 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001478; PDZ. InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50106; PDZ; 3.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00018; SH3; 1.
Pfam; PF00595; PDZ; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00326; SH3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1146 114
1174 AA;
SEQUENCE FROM N.A.
```

Ŋ

```
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                  Duclos F., Rodius F., Wrogemann K., Mandel J.L., Koenig M.; "The Friedreich ataxia region: characterization of two novel genes and reduction of the critical region to 300 kb."; Hum. Mol. Genet. 3:909-914(1994).
                                                                                                                                                                                                                                                                                                                                                      Chlenski A., Ketels K.V., Korovaitseva G.I., Talamonti M.S., Oyasu R., Scarpelli D.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.
-:- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-:- SIMILARITY: CONTAINS 1 GUANYLATE RINASE-LIKE DOMAIN.
-:- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROFEINS.
-:- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITION 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY.

-1- ALTENNATIVE PRODUCTS: 4 ISOFORMS; Al (SHOWN HERE), Cl, A2 AND C2;

-1- ALTENNATIVE PRODUCTS: 4 ISOFORMS; Al (SHOWN HERE), Cl, A2 AND C2;

-1- TISSUE SPECIFICITY: THIS PROTEIN IS FOUND IN EPITHELIAL CELL

JUNCTIONS. ISOFORM ALIS ABUNDANT IN THE HEART AND BRAIN WHEREAS

ISOFORM CL IS EXPRESSED AT HIGH LEVEL IN THE KIDNEY, PANCREAS,

HEART AND PLACEMYA. IN BRAIN AND SKELETAL MUSCLE, ONLY ISOFORM AL

IS DETECTABLE. ISOFORM CL IS FOUND IN NORMAL AS WELL AS IN MOST

IN NORMAL TISSUES.
                                                                                                                                                                                                                                                                                                                                                                         "Organization and expression of the human zo-2 gene (tjp-2) in normal and neoplastic tissues.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams L.D., Werny I., Schwartz S.M.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: PLAYS A ROLE IN TIGHT JUNCTIONS AND ADHERENS JUNCTIONS.
--- SUBBUNIT: INTERACTS WITH OCCLUDIN.
--- SUBGELLULAR LOCATION: PERIPHERAL MEMBRANE. CYTOPLASMIC SIDE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlenski A., Ketels K.V., Tsao M.-S., Talamonti M.S., Anderson M.R., Oyasu R., Scarpelli D.G.; "Tight junction protein Zo-2 is differentially expressed in normal pancreatic ducts compared to human pancreatic adenocarcinoma."; Int. J. Cancer 82:137-144(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlenski A., Ketels K.V., Engeriser J.L., Talamonti M.S., Tsao M.-S. Koutnikova H., Oyasu R., Scarpelli D.G.;
"Lo-2 gene alternative promoters in normal and neoplastic human pancreatic duct cells.";
                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
202_HUMAN STANDARD; PRT; 1190 AA. 090UDY2; 015883; 0510DY1; 090UDY3; 099839; 16-0CT-2001 (Rel. 40, created) 16-0CT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update) cocludens 2 protein Z0-2 (Zonula occludens 2 protein) (Tight junction protein Z0-2 (Zonula occludens 2 protein) (Tight junction protein Z). TJP2 OR ZO2 OR X104.
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-104 FROM N.A. (ISOFORMS A1 AND C1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARTIAL SEQUENCE FROM N.A. (ISOFORMS A1 AND C1).
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORMS A1; C1; A2 AND C2)
                                                                                                                                                                                                                                                                                                                                                                                                            Biochim. Biophys. Acta 1493:319-324(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Pancreas;
MEDLINE-99426875; Pubmed=10495427;
                                                                                                                                                                                                                                                                                                                                       MEDLINE-20472048; PubMed=11018256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-99287578; Pubmed-10360833;
                                                                                                                                                                                                                     MEDLINE=95038744; PubMed=7951235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Int. J. Cancer 83:349-358(1999).
                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM A1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1047-1167 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ONWARD DUE TO A FRAMESHIFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Aortic smooth muscle;
                                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                         TISSUE-Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Pancreas;
                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                          TISSUE-Brain;
```

```
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                     EMBL, AF177533, AAA20387.2; EMBL, AF043195, AAD20387.2; EMBL, AF043195, AAD20387.2; JOINED. EMBL, AF043195, AAD20387.2; JOINED. EMBL, AF177519, AAD20387.2; JOINED. EMBL, AF177529, AAD20387.2; JOINED. EMBL, AF177521, AAD20387.2; JOINED. EMBL, AF177521, AAD20387.2; JOINED. EMBL, AF177523; AAD20387.2; JOINED. EMBL, AF177524, AAD20387.2; JOINED. EMBL, AF177524, AAD20387.2; JOINED. EMBL, AF177524, AAD20387.2; JOINED. EMBL, AF177525; AAD20387.2; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                      JOINED.
JOINED.
JOINED.
JOINED.
JOINED.
JOINED.
                                                                            EMBL; L27476; AAA61300.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOINED.
JOINED.
JOINED.
                                                                                                                                                                                             JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                          JOINED.
                                                                                                                                                                                                                                                                            JOINED.
                                                                                                                                                                                                                                                                                                                                               JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOINED.
                                                                                                                                                                                                                                                                 JOINED
                                                                                                                                                                                                                                                                                                   JOINED
                                                                                                                                                                                                                                                                                                                         JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOINED
                                                                                                                                                                                                                                                                                                                                       JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD56219.2;
AAD56219.2;
AAD56219.2;
AAD56219.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD56218.2;
AAD56218.2;
AAD56219.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD56218.2;
AAD56218.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD56218.2;
AAD56218.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD56219.2;
AAD56219.2;
                                                                                                                                                                                                                                                                                                                         AAC02527.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD56218.2;
AAD56218.2;
                                                                                                                                                                                                                              AAD20387.2;
                                                                                                                                                                                                                                                                                                                                                                       AAC02527.2;
                                                                                                                                                                                                                                                                                                                                                                               AAC02527 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC02527.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD56218.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD56219.2;
AAD56219.2;
                                                                                                                                                                                                                                                                            AAD20387.2;
                                                                                                                                                                                                                                                                                                                                                           AAC02527.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD56218.2;
                                                                                                                                                                                                                                                                                                             AAC02527.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD56218.2
AAD56218.2
AAD56218.2
AAD56218.2
                                                                                                                                                                                                                                                     AAD20387.
                                                                                                                                                                                                                                                                                                   AAD20387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC02527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD56218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD56219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD56218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD56219.
                                                                                                                                                                                                                              AF177526;
                                                                                                                                                                                                                                                     AF177528;
                                                                                                                                                                                                                                                                                                                         AF043196;
                                                                                                                                                                                                                                                                                                                                                           AF177519;
                                                                                                                                                                                                                                                                                                                                                                       AF177520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF177528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF177529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF177531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF177532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF043195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF043196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF043197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF177519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF177521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF177522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF177529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF177533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF043196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF177518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF177519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF177521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF177525;
                                                                                                                                                                                                                                                                                                                                                                                                                               AF177525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF177523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF043197
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF177527
between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                   EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                       EMBL;
```

```
occludens 2 protein) (Tight junction protein 2). TJP2 OR 202.
                                                                                                                                                                                                                                                                                                                                                                                Tight junction; SH3
DOMAIN 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                            HSSP; P31016; 1BE9
                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     547 VREDAVL 553
                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                        1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 VLEDITL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZO3_MOUSE
Q9QXY1;
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZO3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
 QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 MLAF-QGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKA 62
                                                                                                                                                                                      right junction; SH3 domain; Repeat; Membrane; Alternative splicing;
                                                                                                                                                                                                             A1/A2.
TIGHT JUNCTION PROFEIN ZO-2, ISOFORMS
C1/C2.
POR ISOFORMS C1/C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202_MOUSE STANDARD; PRT; 1167 AA.
0920U1;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 1190;
                                                                                                                                                                                                      TIGHT JUNCTION PROTEIN 20-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                 EYR -> IRS (IN REF. 5).
MW; BE2BE6F181467058 CRC64;
                                                                                                                                                                                                                                                                           GUANYLATE KINASE.
POLY-GLU.
MISSING (IN ISOFORM A2/C2).
                                                                                                                                                                                                                                                                                                                                                                                S -> N (IN REF. 5).
GSYG -> RSFC (IN REF. 5).
EYR -> IRS (IN REF. 5).
                                                                                                                            SMART; SM00072; Gukc; 1.
SMART; SM00028; PD2; 3.
SMART; SM00326; SH3; 1.
PROSITE; PS00856; GUANYLATE_KINASE_1; FALSE_NEG.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 77; DI
Pred. No. 2;
 AR177526, AAD56219.2; JOINED.
AR177527, ABD56219.2; JOINED.
AR177528; AAD56219.2; JOINED.
AR177529; AAD56219.2; JOINED.
AR177523, AAD56219.2; JOINED.
AR083892; AAC33121.1; --
                                                                      GGGNEW, HGNC:11828; TJP2.
InterPro: IPR001619; Guanylate_kin.
InterPro: IPR001478; PD2.
InterPro: IPR001478; PD2.
Fem: PF0018; SH3:
Pfam: PF00595; PD2; 3.
Pfam: PF00595; PD2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                        16.5%;
                                                       U84581; AAB41794.1; -. P31016; 1BE9.
                                                                                                                                                                                                                                                                                                                                                                                                         133971
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                1136
1158
1167
                                                                                                                                                                                                                      1190
                                                                                                                                                                                              Alternative initiation
                                                                                                                                                                                                                                                                                                                                                                                                           AA:
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        567 VREDAVL 573
                                                                                                                                                                                                                                                                                                                                                                                                1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 VLEDTTL 69
                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                  CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                      INIT_MET
                                                                                                                                                                                                                                                                                            VARSPLIC
                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
ZOZ_MOUSE
                          EMBL;
EMBL;
EMBL;
                                                 EMBL;
EMBL;
                                                                 HSSP;
                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC AC DIT DIT DIT DIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
     ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
                                                                                                                                                                                       STRAIN=CS7BL/6 X CBA;

X MEDLINE=99150392; PubMed=10026224;

X MEDLINE=99150392; PubMed=10026224;

TIOH M., Morita K., Tsukita S.;

TIOH M., Morita K., Tsukita S.;

Toccludin M. Banderens junctions with a binding affinity to coccludin and alpha catenin...;

Toccludin and alpha catenin...;

SIGLI Chem. 274:598-5986(1999).

SIGLI Chem. 274:598-5986(1999).

SIGLI CHEM. STATES A ROLE IN TIGHT JUNCTIONS AND ADHERENS JUNCTIONS.

SUBJURIT: INTERACTS WITH OCCLUDIN.

SUBJURIT: INTERACTS WITH OCCLUDIN.

SUBJURITY: CONTAINS 3 PDZ/DHR DOMAINS.

SIMILARITY: CONTAINS 1 SH3 DOMAIN.

SIMILARITY: CONTAINS 1 GUANNICATE RIABSE-LIKE DOMAIN.

SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 MLAF-QGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKA 62
                       Craniata, Vertebrata, Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.1%; Score 75; DB 1; Length 1167; 34.3%; Pred. No. 3.2; Live 15; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1142 POLY-GLU.
AA; 131614 MW; F15DA3EBC3F9434F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00856; GUANYLATE_KINASE_1; FALSE_NEG-PROSITE; PS50052; GUANYLATE_KINASE_2; 1. PROSITE; PS50106; PD2; 3. PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat; Membrane.
PDZ 1.
PDZ 2.
PDZ 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SH3.
GUANYLATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   905 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD: MGI:1341872; Tjp2.
Interpro; IPR000619; Guanylate_kin.
Interpro; IPR001452; SH3.
Interpro; IPR001452; SH3.
Interpro; IPR001452; SH3.
Interpro; IPR001452; SH3.
Interpro; IPR00148; SH3.
Interpro; IPR00518; PDZ; 3.
Interpro; IPR00723; Guanylate_kin; I.SWART; SW00272; Guanylate_kin; I.SWART; SW00228; SH3; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF113005; AAD19964.1; -.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
```

```
01-FEB-1995 (Rel. 31, Last sequence update)
   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and a stis content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                   LRLAGGNDVGIFVSGVQAGSPADGQGIQEGDEILQVN-----GMPFRNLTREEAVQF 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 ISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEAVGL 75
                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN t junction protein 20-3 (Zonula occludens 3 protein) (Zona occludens 3 protein) (Tight junction protein 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.6%; Score 73; DB 1; Length 905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.8%; Pred. No. 4;
Live 9; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B787BA1592661FEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SH3.
GUANYLATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tight junction; SH3 domain; Repeat; Membrane.
DOMAIN 11 93 PDZ 1.
DOMAIN 187 264 PDZ 2.
DOMAIN 368 434 PDZ 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  494 AA
                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00856; GUANYLATE_KINASE_1; PROSITE; PS50052; GUANYLATE_KINASE_2; PROSITE; PS50002; SH3; FALSE_NEG. PROSITE; PS50106; PDZ; 3.
                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PD2.
InterPro; IPR001478; PD2.
InterPro; IPR001455; SH3.
Ffam; PF00625; Guanylate_kin; 1.
SMART; SM007275; Guanylate_kin; 1.
SMART; SM00228; PD2; 3.
SMART; SM00328; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                           MEDLINE-20069797; PubMed-10601346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     434 PI
540 SI
754 GI
99324 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCMN_STRGA STANDARD; P16559; Ol-AUG-1990 (Rel. 15, Created)
                                                                                                                                                                                                                                                                                                            EMBL; AF157006; AAF24175.1; -. HSSP; P31016; 1BFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 32.8
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                            MGD; MGI:1351650; Tjp3.
                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      368
467
654
905 AA;
                                                                                                         SEQUENCE FROM N.A.
                                                                                    NCBI_TaxID=10090;
                                                                                                                   STRAIN-BALB/c;
                                                 TJP3 OR ZO3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                г 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCMN_STRGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  434
  DA PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M80674; AAA67518.1; -.
EMBL; M80674; AAA67518.1; -.
PIR; B42276; B42276.
PIR; S27696; S27696.
PIR; S05976; S05976.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 LADOGMERFSRIADLGGGDGWFLAQILRRHPHATGLLMDLPRVAASAGPVLEEAKVADRV 379
                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=AFCC 13032 / ETH 22794 / GLA.0;
MEDLINE=92193265; PubMed=1548230;
Summers R.G., Wendt-Pienkowski E., Motamedi H., Hutchinson C.R.;
"Nucleotide sequence of the tcmII-tcmIV region of the tetracenomycin C. biosynthetic gene cluster of Streptomyces glaucescens and evidence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 LAFQGDALLEQISVIGG------AADQM 40
                                                                                   Bacteria; Actinobacteria: Actinobacteria (class); Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                  Multifunctional cyclase-dehydratase-3-0-methyl transferase tomN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001601; Methyltransf.
InterPro; IPR001077; O_Metransf2.
InterPro; IPR001077; SAM_bind.
InterPro; IPR000051; SAM_bind.
Antibiotic biosynthesis; Multifunctional enzyme; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              494 AA; 55930 MW; 6E153D32782F66B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                              that the tcmN gene encodes a multifunctional cyclase-dehydratase-O-methyl transferase."; J. Bacteriol. 174:1810-1820(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.3%; Score 71.5; 30.4%; Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
                                                                 Streptomyces glaucescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Methyltransferase.
                                                                                                                               NCBI_TaxID=1907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Si
Matches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
```

ů

œ

```
Saras J., Claesson-Welsh L., Heldin C.-H., Gonez L.J.;
"Cloning and Characterization of PTPLI, a protein tyrosine phosphatase
with similarities to cytoskeletal-associated proteins.";
J. Biol. Chem. 269:24082-24089(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99329089; PubMed-10400701; Mutthy K.K., Clark K., Fortin Y., Shen S.-H., Banville D.; "ZRP-1, a zytin-related protein, interacts with the second PDZ domain of the cytosolic protein tyrosine phosphatase hPTPIE."; J. Biol. Chem. 274:20679-20687(1999).
                                                                                    PTND_HUMAN STANDARD; PRT; 2485 AA.
012923; 015263; 016826; 015265; 015159;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
(Protein tyrosine phosphatase IE) (PTP-E1) (hPTPE1) (PTP-EAS)
(Protein-tyrosine phosphatase IE) (PTP-E1) (hPTPE1) (PTP-EAS)
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-94116679; PubMed-8287977;
MacKawa K., Inangawa N., Nagamatsu M., Harada S.;
"Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane-binding domain and GLGF repeats.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein tyrosine + phosphate.
-:- SUBUNIT: Interacts with TRIP6 and FAS receptor through its second
                                                                                                                                                                                                                                                                                                                   Banville D., Ahmad S., Stocco R., Shen S.-H.;
"A novel protein-tyrosine phosphatase with homology to both the
cytoskeletal proteins of the band 4.1 family and junction-associated
guanylate kinases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kozlov G., Gehring K., Ekiel I.;
"Solution structure of the PD22 domain from human phosphatase hPTP1E
                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor.";
Biochemistry 39:2572-2580(2000).
-!- FUNCTION: BINDS TO A NEGATIVE REGULATORY DOMAIN IN FAS THAT INHIBITS FAS-INDUCED APOPTOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and its interactions with C-terminal peptides from the Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -! - SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
              380 TVLPGDFFTDPVPTGYDAY--LFKGVLHNWSDERAVTVLRRV 419
ALRPG---TQIVMVDYEASEPLFKAVLEDTTLEEAVGLLRRV 79
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem. 269:22320-22327(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRUCTURE BY NMR OF 1361-1456.
MEDLINE=20170882; Pubmed=10704206;
                                                                                                                                                                                                                                                                                          TISSUE-Breast carcinoma;
MEDLINE-94350988; PubMed-8071359;
                                                                                                                                                                                         phosphatase 1) (FAP-1).
PTPN13 OR PTP1E OR PTPL1 OR PNP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE-Fibroblast;
MEDLINE-95014139; Pubmed-7929060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1216-2490 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEBS Lett. 337:200-206(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERACTION WITH TRIP6.
                                                                                                                                                                                                                    Homo sapiens (Human).
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Leukemia;
                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDZ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang H.Y
                                                                                        QC
  ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                      TISSUE SPECIFICITY: PRESENT IN MOST TISSUES WITH THE EXCEPTION OF THE LIVER AND SKELETAL MUSCLE. MOST ABUNDANT IN LUNG, KIDNEY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50106; PDZ; 5. — PROSITE; PS00383; TYR_PHOSPHATASE_1; FALSE_NEG. PROSITE; PS50056; TYR_PHOSPHATASE_2; 1. PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1. STS0055; TYR_PHOSPHATASE_PTP; 1. Structural protein; Cytoskeleton; Hydrolase; Repeat; 3D-structure;
ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISSING (IN ISOFORM 2).
MISSTNG (IN ISOFORM 3).
LD -> FH (IN REP. 3).
KDHHWSRGTLRHIS -> DLSRSHCHVYLAHL (IN
                                                                                        -!- SIMICARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 5 PDZ/DHR DOMAINS.
-!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN-TYROSINE PHOSPHATASE.
COLLED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -> TVLFDK (IN REF. 1).
-> A (IN REF. 3).
-> K (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REF. 4).
GL -> A (IN REF. 4).
S -> P (IN REF. 4).
KP -> RS (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDZ 1.
PDZ 2.
PDZ 3.
PDZ 4.
PDZ 5.
POLY SER.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BAND 4.1-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IRR001478; PDZ.
InterPro; IRR000387; TYR_phosphatase.
InterPro; IRR000342; Tyr_Pp.
Fam; PF00102; Y_phosphatase; 1.
Pfam; PF00373; Band_41; 1.
Pfam; PF00595; PDZ; 5.
PRINTS; PR00935; BAND41.
PRINTS; PR00700; PRTYPHPHTASE.
SMART; SM00228; PDZ; 5.
SMART; SM00228; PDZ; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00660; BAND_41_1; FALSE_NEG-
PROSITE; PS00661; BAND_41_2; FALSE_NEG-
PROSITE; PS50057; BAND_41_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-LEU.
                    PRODUCED BY ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coiled coil
                                                                                                                                                                                                                                                                                                                                        EMBL; U12128; AAB60339.1; --
EMBL; D21209; BAA04750.1; --
EMBL; D21211; BAA04752.1; --
EMBL; X80289; CAA56563.1; --
EMBL; X79676, CAA56124.1; --
PDB; 3PDZ; 17-MAR-00.
Genew; HGNC:9646; PTPN13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR000299; Band_4.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1804
2085
2085
1178
1452
1588
1868
1965
1749
2408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1239
1357
1363
1383
1538
1649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00661;
PROSITE; PS50057;
                                                                            FETAL BRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1238
1357
1362
1383
1538
1649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    379
469
1775
2057
1093
1368
1501
1742
2408
884
884
1134
1134
1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 600267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
```

InterPro; IPR000205; NAD\_binding

σ

```
DR KW KW DR BET WAR SO FIT
                                                                                                                                                                                                                                                               Q
                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                     ::|:: :|| ::|| | ::|| | 1090 EITLVNLKKDAKYGLGFQIGGEKMGRLDLGIFISSVAPGGPADLDGCLKPGDRLISVNS 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COFACTOR: FAD.

PATHWAY: BIPPHONI and POLYCHLOLINATED biphenyl degradation.

BATHWAY: BIPPHONI AND A VERNASE SYSTEM CONSISTS OF FOUR PROTEINS: THE SUBUNIT: THIS DIOXYGENASE SYSTEM CONFOUND (BPHA AND BPHE), A FERREDOXIN (BPHE) AND A FERREDOXIN REDUCTASE (BPHG).

SIMILARITY: TO OTHER BACTERIAL RING-HYDROXYLATING DIOXYGENASE PERREDOXIN REDUCTASE COMPONENTS.
KSQEDTICTMFYYPQKI -> RVKKIPFVPCFTILRKR
                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1994 (Rel. 30, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Biphenyl dioxygenase system ferredoxin--NAD(+) reductase component (EC 1.18.1.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Erickson B.D., Mondello F.J.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PART OF THE ELECTRON TRANSFER COMPONENT OF BIPHENYL
DIOXYGENASE, TRANSFERS ELECTRONS FROM FERREDOXIN (BPHF) TO
                                                                                                                                                                                                 1 QVTMLAFQGDALLE-QISVIGGNL----TGIFIHRVTPGSAAD-QMALRPGTQIVMVD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Erickson B.D., Mondello F.J.; "Nucleotide sequencing and transcriptional mapping of the genes "Nucleotide sequencing and transcriptional mapping of the genesenceding biphenyl dioxygenase, a multicomponent polychlorinated-biphenyl-degrading enzyme in Pseudomonas strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burkholderia cepacia (Pseudomonas cepacia).
Bacteria: Proteobacteria: beta subdivision; Burkholderia group;
Burkholderia.
NCBI_TaxID=292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: Reduced ferredoxin + NAD(+) = oxidized
                                                                                                                                  DB 1; Length 2485;
                                                                                                                                                               30; Indels
                                                                               DQ -> VARS (IN REF. 4).
8D1B31597C66962B CRC64;
               (IN REF. 4).
G -> A (IN REF. 3).
AA -> G (IN REF. 4).
A -> S (IN REF. 4).
GLLDQ -> VARS (IN REF
                                                                                                                                                                                                                                                                                                                                                                                    408 AA.
                                                                                                                                15.3%; Score 71.5; C
28.6%; Pred. No. 18;
tive 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001327; FAD_pyr_redox
                                                                                                                                                                                                                                                                                                1150 VSLEGVSHHAAIEILQNAPEDVTL 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriol. 174:2903-2912(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-92234948; PubMed-1569021;
                                                                                                   Ψ¥;
                                                                                                                                                                                                                                                                 -----YEASEPLFKAVLEDTTL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M86348; AAB63429.1; -.
                                                                                                 276903
                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                              1857
                                 1797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ferredoxin + NADH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; F41858; F41858.
                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                 1797
1856
2069
2206
2485
                                                                                                                                       Local St. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-LB400
                                                                                                                                                                                                                                                                                                                                                                                BPHG_BURCE
P37337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REVISIONS.
                                                              CONFLICT
CONFLICT
SEQUENCE
CONFLICT
                                                                                                                                Query Match
                                 CONFLICT
                                                CONFLICT
                                                                                                                                                                 Matches
                                                                                                                                                                                                                              qq
FIFE
                                                                                                                                                                                                                                                                 ò
```

```
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between the Swiss Institute of Bioinformatics and the EMBL outstation—
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                          11 ALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTOIV-----MVDYEASEPLFKAVLE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella.
                                                                                                                                               5.
                                                                                                                     Length 408;
Pfam; PF00070; pyr_redox; 1.
PRINTS: PR00368; FADPNR:
ProDom: P000139; FAD_pyr_redox; 1.
Aromatic hydrocarbons catabolism; Plavoprotein; FAD; NAD;
                                                                                                                                               35; Indels
                                                                FAD (ADP PART) (POTENTIAL).
NAD (ADP PART) (POTENTIAL).
8A52BB01688667A9 CRC64;
                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DUN-2002 (Rel. 41, Last annotation update)
ATP-dependent protease La (EC 3.4.21.53).
                                                                                                                                                                                                                                                                                                                           812 AA
                                                                                                                                   Pred. No. 5.1;
                                                                                                                                               12; Mismatches
                                                                                                                     14.7%; Score 68.5; 31.6%; Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00382; AAA; 1.
SMART; SM00464; LON; 1.
TGRFAMS; TGR000763; lon; 1.
PROSITE; PS01046; LON SER; 1.
Hydrolase; Serine protease; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003959; AAA_ATPase_centr.
                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ron_endopep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003593; AAA_ATPase.
                                                                                            42953 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF042348; AAB97420.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00830; ENDOLAPTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR004815; Lon_fam
                                                                                                                                               24; Conservative
                                                                                                                                                                                                                                              66 DITLEEAVGLLRRVDG 81
                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                  35
173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00004; AAA; 1.
Pfam; PF02190; LON; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003111;
                                                                                             408 AA;
                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                    Brucella abortus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S16.001;
                                                      Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=235;
                                                                 NP_BIND
NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                          LON_BRUAB
                                                                                                                     Query Match
                                                                                                                                   Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEROPS;
                                                                                                                                               Matches
                                                                                                                                                                                                 109
                                                                                                                                                                                                                                                                                                          LON_BRUAB
```

```
CHAIN
    3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    βy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gray C.W., Ward R.V., Karran E.H., Turconi S., Rowles A., Viglienghi D., Southan C., Barton A., Fantom K.G., West A., Savopoulos J.W., Hassan N.J., Clinkenbeard H., Hanning C., Amegadzie B., Davis J.B., Dingwall C., Livi G.P., Creasy C.L., "Characterization of human HtrA2, a novel serine protease involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                       "Characterization of a novel human serine protease that has extensive homology to bacterial heat shock endoprotease HtrA and is regulated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Faccio L., Fusco C., Viel A., Zervos A.S.;
"Tissue-specific splicing of Omi stress-regulated endoprotease leads
to an inactive protease with a modified PDZ motif.";
Genomics 68:343-347(2000).
                                                                          Gaps
                                                                                                13 LEQISVIGGNLTG-------IFIHRVTPGSAADQMALRPGTQIVMVDYEA-- 55
                                                                                                                      4 IEOKTPVGGSETGGADGLYAVLPLRDIVVFPHMIVPLFVGREKSIRALEEVMGVDKOILL 63
                                                                                                                                                                                                                             HRA2_HUMAN STANDARD; OPPOY4; 458 AA.
043464; O9PBZ4; Q9POY3; OPPOY4;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine protease HTRA2, mitochondrial precursor (EC 3.4.21.-) (High temperature requirement protein A2) (HtrA2) (Omi stress-regulated endoprotease) (Serine proteinase OMI).
                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 134-458, INTERACTION WITH BIRC4, AND MUTAGENESIS OF
                                                                         29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS 1; 3 AND 4), AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20112822; PubMed=10644717;
Faccio L., Fusco C., Chen A., Martinotti S., Bonventre J.V.,
Zervos A.S.;
                                                   Length 812;
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1), AND MUTAGENESIS OF SER-306.
MEDLINE-20112822; Pubmed-10644717;
                                                                         33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Chen F., Do A., Do T., Meisler M., Roe B.A.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                            -----SEPLFKAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTDG 93
               Y SIMILARITY. B9D07E9F0D7DFDBB CRC64;
                                                  Score 68.5; DB 1;
ATP (POTENTIAL).
BY SIMILART#V
                                                                         20; Mismatches
                                                               Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the mammalian cellular stress response.";
Eur. J. Blochem. 267:5699-5710(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biol. Chem. 275:2581-2588(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Brain;
MEDLINE-20428457; PubMed-1097<u>158</u>0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Kidney;
MEDLINE-20453195; PubMed-10995577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-21468395; PubMed-11583623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
                             89859 MW;
                                                  14.78;
                                                               22.68;
                                                                           24; Conservative
                 689
                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
      367 3
689 6
812 AA;
                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ischemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rissue-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.
      NP_BIND
ACT_SITE
SEQUENCE
                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kidney
                                                                                                                                               99
                                                                             Matches
                                                                                                                                                                                                                                 g
                                                                                                                                               δ
        FT
```

```
Proteans Expr. Purif. 19:227-234(2000).

Protein Expr. Purif. 19:227-234(2000).

Protein Expr. Purif. 19:227-234(2000).

I protein Expr. Purif. 19:227-234(2000).

a nonspecific substrate beta-casein. Promotes or induces cell death either by direct binding to and inhibition of BIRC proteins (also called inhibitor of apoptosis proteins, IAPS), leading to an increase in caspase activity, or by a BIRC inhibition-independent acaspase independent and serine protease activity-dependent, mechanism. Isoform 2 seems to be proteolytically inactive.

SUBUNIT: Interacts with Mxi2. The mature protein, but not the precursor, binds to BIRC2, BIRC3 and BIRC4/XIAP.

PRECURSORY INGS to BIRC2, BIRC3 and BIRC4/XIAP.

Intermembrane space. Released into the cytosol following apoptotic stimuli, such as UV treatment, and stimulation of mitochondria with caspase-8 truncated BID/BID.

I ALTERNATIVE PRODUCTS: 4 isoforms; 1/13B (shown here), 2/D-Omi, 3/P) and 4/P4; are produced by alternative splicing.

I PIN: Autoproteolytically activated.

I SIMILARITY: BELONGS TO PEPTIPASE FAMILY S2C.

I SIMILARITY: BELONGS TO PEPTIPASE FAMILY S2C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                              CHARACTERIZATION.
MEDLINE-20334437; PubMed=10873535;
Savopoulos J.W., Carter P.S., Turconi S., Pettman G.R., Karran E.H.,
Gray C.W., Ward R.V., Jenkins O., Creasy C.L.;
Expression, purification, and functional analysis of the human serine
Suzuki Y., Imai Y., Nakayama H., Takahashi K., Takio K., Takahashi R.; "A serine protease, HtrA2, is released from the mitochondria and interacts with XIAP, inducing cell death."; Mol. Cell 8:613-621(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50106; PD2; 1.
Hydrolase; Protease; Serine protease; Zymogen; Mitochondrion; Transit peptide; Transmembrane; Apoptosis; Alternative splicing TRANSIT 1 MITOCHONDRION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM.
MISSING (IN ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SERINE PROTEASE HTRA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IAP-BINDING MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
Pfam; PF00595; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF184911; AAG13126.1; -.
EMBL; AC006544; -; NOT_ANNOTATED_CDS.
EMBL; BC000096; AAH00096.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF141305; AAF66596.1; -. EMBL; AF141306; AAF66597.1; -. EMBL; AF141307; AAF66598.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF020760; AAB94569.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00834; PROTEASES2C. SMART; SM00228; PD2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew; HGNC:14348; PRSS25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEROPS; S01.278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32
1134
1105
1166
3364
1138
2228
238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 606441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
ACT_SITE
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROPEP
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license gireement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                            ÷
L -> LARELGAVSLQ (IN ISOFORM 3).
MISSING (IN ISOFORM 2 AND ISOFORM 3).
GEVICAVINTKVTAGISFAIPSDRIREFLHRGEKKNSSGI
SGSORRYICWMALTLEPSILAELQLREPSPPVQHGWLHKK
VILGSPAHRAGIRPGDVILAIGEQHWQNAEDVYEAVRTQSQ
LAVQIRRGRETLILYVPPENTE -> VSETSFLPRIPAPGQ
CGKGRRPLIGGCLWRFLSSSLLAISQYPTRSPQHILVLFG
CPHPLLFV (IN ISOFORM 4).
A->M: LOSS OF INTERACTION WITH BIRC4;
LOSS OF INHIBITION OF BIRC4 ACTIVITY.
A->M: LOSS OF INTERACTION WITH BIRC4 AND
OF INHIBITION OF BIRC4 ACTIVITY.
S->M: LOSS OF PROTESSES
S->M: LOSS OF PROTESSES
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- COFACTOR: Zinc (Probable).-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Remard C., Cunnacc S., Demange N., Saptier M., Moissan A., Robert C., Saurin W., Schiex T., Siquier P., Thebault P., Whalen M., Wincker P., Levy M., Reissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502(2002).
                                                                                                                                                                                                                                                                                            ٠.
ښ
                                                                                                                                                                                                                                                          DB 1; Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                             18; Indels
                                                                                                                                                                                                                                                                                                                           GIFIHRVTPGSAADQMALRPGTQIVMVD---YEASEPLFKAVLEDTTL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical zinc metalloprotease RSc1411 (EC 3.4.24.-).
RSC1411 OR RSO5281.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (By similarity).
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M50B.
SIMILARITY: CONTAINS 1 PD2/DHR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001478; PDZ.
InterPro; IPR004387; Zn_Mprotease.
InterPro; IPR0004387; Zn_Mprotease.
InterPro; IPR000130; Zn_MTpeptdse.
SMART; SM00228; PDZ; 1.
TIGREAMS; IIGR00054; mem_zinc_metalprot; 1.
                                                                                                                                                                                                                                                       14.2%; Score 66.5; Di
33.3%; Pred. No. 9.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                               462 AA
                                                                                                                                                                                                                                                                                          11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50106; PDZ; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-GMI1000;
MEDLINE-21681879; PubMed-11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2002 (Rel. 41, Created)
                                                                                                                                                                                                                       48840 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AL646064; CAD15113.1;
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
     313
403
458
                                                                                                                                       134
                                                                                                                                                                      134
                                                                                                                                                                                                                                                                   Local Similarity
es 16; Conserv
                                                                                                                                                                                                                       458 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEROPS; M50.004;
                                                                                                                                       134
                                                                                                                                                                    134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                                             YE11_RALSO Q8XZI4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ralstonia
                   VARSPLIC
VARSPLIC
     VARSPLIC
                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                          Query Match
                                                                                                                                       MUTAGEN
                                                                                                                                                                      MUTAGEN
                                                                                                                                                                                                        MUTAGEN
                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                          25
     FT FT FT FT SO SET
                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                       g
```

```
ä
Hypothetical protein; Hydrolase; Metalloprotease; Zinc; Transmembrane;
                                                                                                                                        Gaps
                                                                                                                                        .;
8
                                                                                                                                                                             12 LLEQIS -- VIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKA 62
                                                                                                            14.1%; Score 66; DB 1; Length 462; 37.7%; Pred. No. 11; tive 10; Mismatches 15; Indels
                       (CATALYTIC) (POTENTIAL).
                                             ZINC (CATALYTIC) (POTENTIAL).
                                                                                    3F2818F8B0C1121B CRC64;
                                                                                                                                                                                                                             Search completed: January 22, 2003, 08:53:35
Job time : 6.625 secs
                                      POTENTIAL
             Complete proteome.
                         ZINC
                                                                                    49613 MW;
                                                                                                                                        Conservative
                                                                                    462 AA;
                                                                                                                          Similarity
             Inner membrane;
                                                                                                                Ma.
Local Sim.
20;
                                 ACT_SITE
METAL
TRANSMEM
                                                                          DOMAIN
SEQUENCE
                                                                                                              Query Match
                       METAL
                                                                                                                            Best Loc
Matches
KW
FT
FT
SO
```

THIS PAGE BLANK (USPTO)

```
008783 mus musculu 055164 rattus norv 088bbx6 mus musculu 08bbx6 mus musculu 08bbx6 mus musculu 04912 homo sapien 05512 mus musculu 05214 rhizobium m 09bx84 homo sapien 051345 homo sapien 051345 homo sapien 051345 homo sapien 09x31 homo sapien 09x33 drosophila 075970 homo sapien 095018 drosophila 075970 homo sapien 095018 drosophila 075970 rattus norv 094191 mus musculu 09502 rattus norv 085930 rattus norv 088999 oryctolagus
P70625 rattus norv
Q22366 caenorhabdi
Q28006 bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 GDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohara O., Nagase T., Kikuno R., Okumura K.; "The nucleotide sequence of a long cDNA clone isolated from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.8%; Score 139; DB 4; Length 1171; 36.5%; Pred. No. 2.3e-06; tive 17; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1171 AA; 134966 MW; FA567ABBC8A703FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         spleen.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK074049; BAB84875.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1171 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                022366
028006
028006
055164
08VBXO
08
                                                                                                                                                                                                  Q9W283
Q9BY09
Q61235
Q13425
Q9Z1K3
Q43798
                                                                                                                                                                                                                                                                                         Q8WX31
Q921G9
Q9VMF3
Q95V18
Q75970
                                                                                                                                                                                                                                                                                                                                                            Q91Y70
Q9JHL1
Q920G2
Q8SQG9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEEAHWTIQRCSGPVTLHYKVNHEG 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 LEEAVGLLRRVDGFCCLSVKVNTDG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLJ00120 protein (Fragment).
FLJ00120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          t Local Similarity 36.5
ches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
 TISSUE=SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
SEQUENCE
 73
73
73
73
72.5
72.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8TES3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
Q9BKL2

\begin{array}{c}
1 & 1 & 1 & 1 \\
1 & 1 & 1 & 1 \\
1 & 1 & 1 & 1
\end{array}

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OBTUMO METHANODYIN
Q9yhv2 gallus gall
Q96kb4 homo sapien
O43386 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09bkl2 hydra atten
0960n4 drosophila
094880 drosophila
09vk4 drosophila
09vkq8 drosophila
09fd11 aeromonas h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapien
sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8tes3 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapien
                                                                                              January 22, 2003, 08:49:36; Search time 14.5 Seconds (without alignments) 1321.544 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ношо
Ношо
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           рошо
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pomod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                     1 OVTMLAFQGDALLEQISVIG......GLLRRVDGFCCLSVKVNTDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9uhv4
Q8teu6
Q96pc1
Q8teu7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08tea3
              GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                           671580 segs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                          US-09-767-215-2_COPY_568_660
                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                      - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8TES3
Q9BKL2
Q960N4
Q94880
Q9VKG8
Q9FD11
Q8TVM0
Q9TVW2
Q9KB4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8TEA3
Q9UHV4
Q8TEU6
Q96PC1
Q8TEU7
                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_human:*
sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_rodent:*
sp_virus:*
sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                       SPTREMBL_21:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1171
1695
974
1367
1445
1916
453
334
1163
579
1113
1113
1204
1391
1601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229.8
222.3
118.3
118.3
118.3
118.3
117.3
117.3
117.0
117.0
117.0
117.0
117.0
117.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perfect score:
                                                                                                                                                                                                                   Scoring table:
                                                                      OM protein
                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No.
                                                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Result
```

ö

```
FlyBase; FBgn0003177; pyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CANTON-S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               094880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              094880
                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 094880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
DR
DR
DR
DR
SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 ISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVM---VDYEASEPLFKAVLEDTTLEEA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BERKELEY;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Y. C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21025768; PubMed-11225567;
Fei K., Yan L., Zhang J., Sarras M.P. Jr.;
Fei K., Yan L., Zhang J., Sarras M.P. Jr.;
Fei K., Yan L., Zhang J., Sarras M.P. Jr.;
Four land bloological characterization of a zonula occludens-1 homologue in Hydra vulgaris, named HZO-1.";
Dev. Genes Evol. 210:611-616(2000).
EMBL; AFK28122.1;
HSSP; P29476; 1DAV.
InterPro; IPR001619; Guanylate_kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
                                                                                                                                                                                                                  Hydra attenuata (Hydra) (Hydra vulgaris).
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
Hydridae; Hydra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.3%; Score 104; DB 5; Length 1695; 40.6%; Pred. No. 0.024; ive 9; Mismatches 15; Indels 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190878 MW; AE0E7D09007316F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            974 AA.
      PRT; 1695 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PDZ; 3.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PP00625; Guanylate_kin; 1. Pfam; PP00655; PD2; 3. Pfam; PP00791; ZU5; 1. SMART; SM00072; GuKc; 1. SMART; SM00228; PD2; 3. SMART; SM00226; SH3; 1. SMART; SM00216; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                              Tight junction protein ZO-1.
                                                                 (TrEMBLrel. 17, (TrEMBLrel. 17, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 40.6
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001452; SH3
InterPro; IPR000906; ZU5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1695 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYD OR CG9763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 :|
735 VLIL 738
                                                                 01-JUN-2001 (
01-JUN-2001 (
01-DEC-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 VGLL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0960N4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q960N4
         TD DTT DDT TD DTT 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DT ACCOCO ON THE BEACH OF THE B
```

```
3;
                                                                                                                                                                                                                                                .,
3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-96312452; PubMed-8698238;
Takahisa M., Togashi S., Suzuki T., Kobayashi M., Murayama A., Rondo K., Miyake T., Ueda R.;
Rondo K., Miyake T., Ueda R.;
"The Drosophila tamou gene, a component of the activating pathway of extramacrochaetae expression, encodes a protein homologous to mammalian cell-cell Junction-associated protein 20-1.";
Genes Dev. 10:1783-1795(1996).
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 LAFQGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVL 64
                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                              5 LAFQGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVWVDYEASEPLFKAVL 64
                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 33.8%; Pred. No. 1.9;
Matches 27; Conservative 11; Mismatches 29; Indels 13.
                                                                                                                                                                                             Length 974;
                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148347 MW; 571C4566C6B6BBF8 CRC64;
                                                                                                                                   DZ; 3.
107338 MW; 5FA3A7D7D0922C2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                             29;
                                                                                                                                                                                                DB 5;
                                                                                                                                                                                                                                                27; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1367 AA
                                                                                                                                                                                                18.3%; Score 85.5; Di 33.8%; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50052; GUANYLATE_KINASE_2; 1. PROSITE; PS50106; PDZ; 3. SEQUENCE 1367 AA; 148347 MW; 571C456
InterPro, IPR000619; Gudnylate_kin.
InterPro, IPR001478; PDZ.
Pfam; PF00625; Guanylate_kin; 1.
Pfam; PF006595; PDZ; 2.
PROSITE: PS50052; GUANYLATE_KINASE_Z; 1.
PROSITE: PS50106; PDZ; 3.
SEQUENCE 974 AA; 107338 MW; 5FA3A7D71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro, IPR000619; Guanylate_kin.
InterPro, IPR001478; PDZ.
InterPro, IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00625; Guanylate_kin; 1.
Pfam; PF00595; PD2; 2.
SMART; SM00072, GuKc; 1.
SMART; SW00228; PD2; 3.
SMART; SW00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   460 NGVTREEAVLFLLSLQDRID 479
                                                                                                                                                                                                                                                                                                                                                                                                                                              631 NGVTREEAVLFLLSLODRID 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 EDTTLEEAV----GLLRRVD 80
                                                                                                                                                                                                                                                                                                                                                                                              65 EDTTLEEAV----GLLRRVD 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FlyBase; FBgn0003177; pyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1997 (TrEMBLrel. 01-FEB-1997 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYD OR TAMOU OR CG9763.
                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; Q12923; 3PDZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
```

1445 AA; 156723 MW; A5675FB66676A40E CRC64;

```
SEQUENCE
                                                                                                                                                                                                                       RESULT 6
g
                                                                                                                g
                                                                                                                                              ò
                                                                                                                                                                          Ωp
                                                                                                                                                                                                                                                                  RAIN STAIN PERKREEFEY;

RAIN PEDETRIEFEY;

RAIN PEDETRIEFEY;

RAIN MEDILINE-20196006; PubbMed=10731132;

RAIN MEDILINE-20196006; PubbMed=10731132;

RAIN MEDILINE-20196006; PubbMed=10731132;

RA Amanatides P.G., Scherer S.E., Hilp W., Hoskins R.A., Galle R.F.;

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C.R., Bladvin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RADORON R., Deucham M.R., Bouck J., Brokstein P., Brottler P.,

RA Cherry J.M., Cawley D.A., Buller H., Caddeu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Glodek A., Gody E., Gorrell J.H., Calvar R., Calbart M.M., Classer R.,

RA Glodek A., Gody F., Gorrell J.H., Se Z., Kenlson J.A., Retrien S., Fleischman W.,

RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,

Alali M., Kalush F., Karpen G.H., Ke Z., Kenlson J.A., Retrommer B.E.,

Lasko P., Lei Y., Levitsky A.A., Li J.J., Li Z., Liang Y., Lin Z.,

Liu X., Mattei B., McIntosh T.C., McLeod M.P., Morbreron D.L.,

RA Shue B.C., Sorden Klamos I., Simpson M., Stupski M.P., Smith T.,

Spitskas R., Moyan W. Murphy B., Murphy L., Murany D.M., Nelson D.K.,

RA Shue B.C., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,

Spitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang Z.Y., Wassaman D.A., Weilsenbach J.,

RA Shue B.C., Shaden Klamos I., Simpson M., Stupski M.P., Smith M.P.,

RA Shene S., Stapleton G. W., Venter J.C.,

RA Shene S., Shaden Klamos I., Sandows W., Subay S., Zhu X., Smith H.O.,

RA Shene S., Shaden C., Turner R., Venter B., Wang Z.-Y., Wassaman D.A., Weilsea R., 
                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                         PRT; 1445 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PDZ; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; 012923; 3702.
FlyBase; FBGn000317; pyd.
InterPro: IPR000619; Guanylate_kin.
InterPro: IPR000478; pp2.
InterPro: IPR001452; SH3.
InterPro: IPR001452; SH3.
InterPro: IPR001906; ZU5.
Pfam: PF00625; Guanylate_kin; 1.
Pfam: PF00791; ZU5; 1.
SWART; SW00228; PDZ; 3.
SWART; SW00228; SH3; 1.
SWART; SW00228; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE003680; AAF54300.1;
HSSP; Q12923; 3PDZ.
                                         PRELIMINARY;
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                 STRAIN-BERKELEY,
                                                                                                                PYD protein.
PYD OR CG9763
                                         Q9VHK4
            RESULT 5
                           09VHK4
```

```
REP STOURNEE FROM N.A.

RADDIANE-STREED:

RADDIANE
RADDIA
                                                                      .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                  Gaps
                                                                                                                                             5 LAFQGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVL 64
                                                                      13;
   Length 1445;
                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2002 (TrEMBLrel. 11, Last annotation update)
CG5509 protein (LD32687p).
                                                               29;
   DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1916 AA.
18.3%; Score 85.5; Di
33.8%; Pred. No. 2.1;
                                                                      Mismatches
                                                                   11;
                                                                                                                                                                                                                                                                                                                                                          460 NGVTREEAVLFLLSLQDRID 479
                                                                                                                                                                                                                                                                                       65 EDTTLEEAV----GLLRRVD 80
                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ephydroidea; Drc
NCBI_TaxID=7227;
Query Match
Best Local Simi
Matches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CG6509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9VKG8
```

```
SELD OR MK1369
                                                                                                                                                                                                                                              Methanopyrus
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9YHV2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9YHV2
                                                                                                                                        OBTVMO;
                                                                                                                          Q8TVM0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
                                                                                                 RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9YHV2
                                                                                                                                        QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΟŊ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dp
                                                         Q
                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
                                                                                                                                                                                                                                                                                                               2.
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                      16 ISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEAVGL 75
      Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, Ag00532; AAF531021; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=(KH-29;
Lin T.-N., Lin T.-J., Liou C.-M.;
"Aeromonas hydrophila strain CKH-29 prtSl gene complete cds.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF293977; AAG03073.1; -..
MEROPS; S01.274; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
18.1%; Score 84.5; DB 2; Length 453;
Best Local Similarity 30.0%; Pred. No. 0.65;
Matches 27; Conservative 14; Mismatches 30; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;
                                                                                                                                                                                                                                                                                 Query Match
18.2%; Score 85; DB 5; Length 1916;
Best Local Similarity 31.2%; Pred. No. 3.3;
Matches 20; Conservative 12; Mismatches 24; Indels
                                                                                                                                                                                                                                                          209863 MW; 32B2A61ABA6848F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BD55CE2B844E5148 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      453 AA.
                                                                                                 EMBL, AV069586; MAL39731.1; ---
HSSP, P31016; BBS9.
FIPBASS. F990003363; CG6509.
InterPro; IPR001478; PDZ.
InterPro; IPR001478; PDZ.
InterPro; IPR001452; SH3.
Ffam; PF00595; PDZ; 3.
SMART; SM00724; GMC; 1.
SMART; SM00228; PDZ; 4.
SMART; SM00326; SH3; 1.
PROSITE; PS50052; GANNYLATE_KINASE_2; 1.
PROSITE; PS50105; PDZ; 4.
SEQUENCE 1916 AA; 209863 MW; 32B2A61ABA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro: IPR001478; PDZ.
InterPro: IPR001340; Protease2C.
InterPro: IPR001364; Ser_protease_Try.
Pfam; PF00089; PDZ; 2.
Pfam; PF00089; Irypsin; 1.
PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50106; PD2; 2.
PROSITE; PS50140; TRYPSIN.DOM; 1.
Hydrolase; Protease; Secure protease.
SEQUENCE 453 AA; 47828 MW; BD55CE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2002 (TrEMBLrel. 20, HtrA-like serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aeromonas hydrophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=644;
                                                                                                                                                                                                                                                                                                                                                                                                                      1564 ISKL 1567
                                                                                                                                                                                                                                                                                                                                                                                            76 LRRV 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aeromonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9FD11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRTS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                     Dp
õ
```

GDALLEQISVIGGNLT------GIFIHRVTPGSAADQMALRPGTQIVMVDYEA 55

ò

```
căllus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae;
Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVTMLAFQGDALLEQISVIGGNLTGIFIHRVTPGSA--ADQMAL-RP-GTQIVMVDYEAS 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-AV19 / DSM 6324 / JCM 9639;
MEDLINE=21927647; PubMed=11930014;
Slesarev A.I., Mexhevaya K.V., Makarova K.S., Polushin N.N.,
Shcharbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
Malykh A.G., Koonin E.V., Kozyavkin S.A.;
"The complete genome of hyperthermophile Methanopyrus kandleri Av19
and monophyly of archaeal methanogens.";
EMBL; AE010430; AAM02582.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collins J.R., Rizzolo L.J.;
"Protein-binding domains of the tight junction protein, ZO-2, are highly conserved between avian and mammalian species."; Biochem. Biophys. Res. Commun. 252:617-622(1998).
-:- SIMILARITY: CONPAINS 1 SH3 DOMAIN.
EMBL; AF085184; AAC95469.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.3%; Score 81; DB 17; Length 334; 35.4%; Pred. No. 1.1; tive 10; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            334 AA; 35878 MW; 5940DBBD2133D92B CRC64;
                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Predicted enzyme related to selenophosphate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                             334 AA.
                                                                                                                 322 IRSFGELRAKIATMGADKQVALGLIR--DG 349
                                                                       81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                         56 ----SEPLFKAVLEDTTLEEAVGLLRRVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=RETINA;
MEDLINE=99057550; PubMed=9837755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 EPLFKAVLEDITLEEAVGL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tight junction protein.
                                                                                                                                                                                                                                                                                                                                                                                   Methanopyrus kandleri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=2320;
```

'n

```
Connolly K.S., Gunning K.M., Davis C.A., Kadner K., Subramanian S., Miguel T., Lewis K.D., Fridlyand J., Alcivare D., Benke J.A., Bondoc M., Bowen E., Chiang A., Critz P., Jaklevic M.A., Lindo K., Lindquist K., Miller C., Patel S., Piscia C., Riley B.E., Rojeski H., Sarmiento R., Yu C., Montenegro M., Aerts A., Chung A., Abrajano A., Rimmerly W., Martin C.H.; Ko C., Beall K., Woolley J.P., Stultz J.L., Kimmerly W., Martin C.H.; Squeencing of human chromosome 5."; Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | |: ||: ||: ||: ||: || || || || ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 QISVIGGNLT--GIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEA 72
          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Ricke D.O., Wagner R.P.;

"Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System.";

Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AC004227; AAC04379.1;

HSSP; Q12923; 3PPZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.0%; Score 79.5; DB 4; Length 579; 34.6%; Pred. No. 3.1; ive 12; Mismatches 28; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65197 MW; CAE221DE69CBF92D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50042; CNMP_BINDING_3; 1.
PROSITE; PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000595; cNMP_binding.
InterPro; IPR001478; PDZ.
InterPro; IPR000651; RasGEFN.
Pfam; PF00027; cNMP_binding; 1.
Pfam; PF00595; PDZ; 1.
Pfam; PF00618; RasGEFN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 34.0°,
Local 27; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | :|| : |:|| |
430 VEILRN-NTHLALTVKTN 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00100; CNMP; 1.
SMART; SM00228; PDZ; 1.
SMART; SM00229; RasGEFN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 VGLLRRVDGFCCLSVKVN 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KIA001LB (Fragment). KIA001LB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               579 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
SEQUENCE
                                                                                                                                                                             L 75
                                                                                                            76 L 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8TEA3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8TEA3
                                                                                                                                                                                                                                                                                                                                                      043386
                                                                                                                                                                                                                                                                                  RESULT 11
043386
                                                                                                                                                                                75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O8TEA3
ID O8
AC O8
DT 01
                                                                                                                                                                                                                                                                                                                                                                                      ACCOOS ON THE READ OF THE READ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δλ
                                           g
                                                                                                            Ω
                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 MLAF-QGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 ISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEAVGL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CDNA FLJ14386 fis, clone HEMBA1002417, moderately similar to TIGHT
Junction protein 20-1.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-EMBRYO, AND MAINLY HEAD;

ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,

Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,

Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Takeuchi K.,

Arita M., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;

"NEDO human cDNA sequencing project.";

Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

EMBL: AK027292: BAB55020.1;

InterPro: IPR001478; PDB_2.

InterPro: IPR001478; PDB_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.3%; Score 81; DB 13; Length 1163; 35.3%; Pred. No. 4.9; ive 16; Mismatches 20; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
17.1%; Score 80; DB 4; Length 548;
Best Local Similarity 34.4%; Pred. No. 2.6;
Matches 21; Conservative 9; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1163 AA; 130668 MW; 3639431A560B1D4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61005 MW; A1A18ECFDE2627AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              548 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS: PROJEST: ZONOCCLUDNS.
PRINTS: PROJEOD: ZONOCCLUDNS3.
PROSITE: PSSOODS: GUANYLATE_KINASE_2: 1.
PROSITE: PSSOODS: PDZ; 1.
PROSITE: PSSOODO: SH3; 1.
SEQUENCE 548 AA; 61005 MW; AlAIBECFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50052; GUANYLATE_KINASE_2; 1. PROSITE; PS50106; PDZ; 3. PROSITE; PS50002; SH3; 1.
HSSP; P31016; 1BE9.
InterPro; IPR000619, Guanylate_kin.
InterPro; IPR001478; PD2.
InterPro; IPR001452; SH3.
Pfam; PF00655; Guanylate_kin; 1.
Pfam; PF00655; PD2.
Pfam; PF000595; PD3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00625; Guanylate_kin; 1.
Pfam; PF00595; PDZ; 1.
                                                                                                                                                                                                                                      PRINTS; PRO1597; ZONOCCLUDNS.
PRINTS; PR01599; ZONOCCLUDNSZ.
PRINTS; PR01600; ZONOCCLUDNS3.
SMART; SM00072; Gukc; 1.
SMART; SM00228; PDZ; 3.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 17.3%
Best Local Similarity 35.3%
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    535 IVREDAVL 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 VL-EDTTL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SH3 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
096KB
AC 096KB
AC 096KB
DT 01-DE
DT 01-DE
DE CLUAN
DE CLUAN
OC BURATO
OC MAMMAD
RN FR TSQUE
RR TSQUE
RR TSQUE
RR A TSSQUE
RR EMBL;
DR RITERI
DR PRINTIP
DR PROSITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q
```

ä

```
Q8TEU6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  П
                       pp
                                                       QΥ
                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ă
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                              3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3
                                                                                                                             SEQUENCE FROM N.A.
Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (FBB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO74318; BABBS049.1;
SEQUENCE 1113 AA; 126109 MW; B12B7DFDDE8C502B CRC64;
                                                                                                                                                                                                                                                                                                                                           Kawasaki H., Chen E.J., Springett G.M., Graybiel A.M., Housman D.E.; "A new family of Rap guanine nucleotide exchange factors."; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases. "EMBL, AF117947; AAF22004.1; -.. HSSP; Q12959; 1PDR.
                                                                                                                                                                                                                                                                                                                          15 QISVIGGNLT--GIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEA 72
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
Washaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.0%; Score 79.5; DB 4; Length 1204; 34.6%; Pred. No. 7.5; 28; Indels 11.
                                                                                                                                                                                                                                              Local Similarity 34.6%; Score 79.5; DB 4; Length 1113; Local Similarity 34.6%; Pred. No. 6.8; Losservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
PDZ domain-containing guanine nucleotide exchange factor I.
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2003 FI. Colne HEP15081, highly similar to PDZ
domain-containing quanine nucleotide exchange factor I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137135 MW; 7AEADFE5CD00646B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1204 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50042; CNMP_BINDING_3; 1. PROSITE; PS50106; PDZ; 1. SEQUENCE 1204 AA; 137135 MW; 7AE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000651; RasGEFN.
InterPro; IPR001895; RasGRF_CDC25.
InterPro; IPR001159; RA_domain.
Pfam; PF00027; cNMP_binding; 1.
Pfam; PF00595; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000595; cNMP_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00595; PDZ; 1.
Pfam; PF00788; RA; 1.
Pfam; PF00617; RasGEF; 1.
Pfam; PF00618; RasGEF; 1.
SMART; SM00100; CNMP; 1.
SMART; SM00328; PDZ; 1.
SMART; SM0314; RA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                      | :|| : |:|| |
309 VEILRN-NTHLALTVKTN 325
                                                                                                                                                                                                                                                                                                                                                                                     73 VGLLRRVDGFCCLSVKVN 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SM00229; RasGEFN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001478; PDZ
                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity
27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                      NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Si
Matches 27;
                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09UHV4
                                                                                                                                                                                                                                                                                  Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               о9ин∨4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
543 QFSLNGGSEKGFGIFVEGVEPGSEAADSGLKRGDQIMEVNGQN------FENITFMKA 594
                      Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QISVIGGNLT -- GIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed-11524421;
Gao X. Satch T., Liao Y., Song C., Hu C.D., Kariya K., Kataoka T.;
"Identification and Characterization of RA-GEF-2, a Rap Guanhe
Nucleotide Exchange Factor That Serves as a Downstream Target of M-
                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
Kulperij H.B., de Rooij J., Rehmann H., van Triest M.,
Kulperij H.B., Bos J.L., Zwartkruis F.J.T.;
Wittinghofer A., Bos J.L., Zwartkruis F.J.T.;
"Characterization of the PDZ-GEFs, a family of guanine nucleotide exchange factors specific for Rapl and Rap2.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF478469; AAL79916.1; -.
SEQUENCE 1391 AA; 157495 MW; CCIB82FA932EB618 CRC64;
QISVIGGNLT - - GIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEA
                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Rapl guanine nucleotide-exchange factor PDZ-GEF2B.
Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                  PRT; 1391 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1509 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.0%; Score 79.5; 34.6%; Pred. No. 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem. 276:42219-4225(2001).
EMBL; AF394782; AAK83386.1;
Interpro: IPR000595; cNMP_binding.
Interpro: IPR001478; PDZ.
Interpro: IPR001651; RasGEFUD.
Interpro: IPR001895; RasGEFUD.
Interpro: IPR001895; RasGEFUD.
Interpro: IPR0001895; Ra. domain.
Pfam; PF00027; cNMP_binding; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rap guanine nucleotide exchange factor. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | :|| : |:|| |
595 VEILRN-NTHLALTVKTN 611
                                                                                                                             645 VEILRN-NTHLALTVKTN 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 VGLLRRVDGFCCLSVKVN 90
                                                                                73 VGLLRRVDGFCCLSVKVN 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00595;
PF00788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q96PC1;
                                                                                                                                                                                                                                                           Q8TEU6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q96PC1
                                                                                                                                                                                                                                     Q8TEU6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
Q96PC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ras.
  15
                                                                                                                                                                                              RESULT 14
```

. ب

THIS PAGE BLANK (USPTO)

Н

```
FT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human caspase recr
Human plakoglobin
Mouse ischaemic co
Human endometrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide
polypeptide,
caspase recr
plakoglobin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               predicted ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human caspase recr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     caspase recr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plakoglobin
                                                                                                                   January 22, 2003, 08:49:35; Search time 13.6425 Seconds (without alignments) 683.714 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1: /SIDSZ/gcgdata/geneseqp-embl/AA1980.DAT:*
2: /SIDSZ/gcgdata/geneseqp-embl/AA1981.DAT:*
3: /SIDSZ/gcgdata/geneseqy-embl/AA1981.DAT:*
4: /SIDSZ/gcgdata/geneseqy-embl/AA1982.DAT:*
5: /SIDSZ/gcgdata/geneseqy-embl/AA1983.DAT:*
6: /SIDSZ/gcgdata/geneseqy-embl/AA1984.DAT:*
6: /SIDSZ/gcgdata/geneseqy-embl/AA1986.DAT:*
7: /SIDSZ/gcgdata/geneseqy-embl/AA1986.DAT:*
8: /SIDSZ/gcgdata/geneseqy-embl/AA1980.DAT:*
9: /SIDSZ/gcgdata/geneseqy-embl/AA1980.DAT:*
10: /SIDSZ/gcgdata/geneseqy-embl/AA1980.DAT:*
11: /SIDSZ/gcgdata/geneseqy-embl/AA1980.DAT:*
12: /SIDSZ/gcgdata/geneseqy-embl/AA1980.DAT:*
13: /SIDSZ/gcgdata/geneseqy-embl/AA1980.DAT:*
14: /SIDSZ/gcgdata/geneseqy-embl/AA1980.DAT:*
15: /SIDSZ/gcgdata/geneseqy-embl/AA1992.DAT:*
16: /SIDSZ/gcgdata/geneseqy-embl/AA1993.DAT:*
17: /SIDSZ/gcgdata/geneseqy-embl/AA1993.DAT:*
18: /SIDSZ/gcgdata/geneseqy-embl/AA1993.DAT:*
19: /SIDSZ/gcgdata/geneseqy-embl/AA1993.DAT:*
10: /SIDSZ/gcgdata/geneseqy-embl/AA1993.DAT:*
11: /SIDSZ/gcgdata/geneseqy-embl/AA1993.DAT:*
12: /SIDSZ/gcgdata/geneseqy-embl/AA1993.DAT:*
13: /SIDSZ/gcgdata/geneseqy-embl/AA1993.DAT:*
                                                                                                                                                                                                                                                70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1000.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*/SIDS2/gcgdata/geneseqy/geneseqp-embl/AA2001.DAT:*/SIDS2/gcgdata/geneseqy/geneseqp-embl/AA2001.DAT:*/SIDS2/gcgdata/geneseqy/geneseqp-embl/AA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                         386
1 GDSFYIRVNLAMEGRAKGEL.....MKDTAAHGTIPNYSRAQQQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human
Human
Human
Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human
                                                                                                                                                                                                                                                                                                                                                                                             908470
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                    US-09-767-215-2_COPY_676_745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE07164
AAE07165
AAU01207
AAM38934
AAM38934
AAM93822
AAU01206
AAU73253
AAU347
ABB57253
AAU84308
                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Π
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A_Geneseq_101002:*
                                                                                                                                                                                                                                                                                                                                                                                                                                      length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10004
11139
11147
1147
350
746
1032
11032
1745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15:
116:
117:
118:
20:
                                                                                                                                                                                                                                                                                                                                                                                                                                      sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146
116
116
116
116
116
102.5
                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB & Maximum DB &
                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Махітит
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
9
```

Drosophila melanog Mouse tight juncti Human promach canc Human protein sequ Human protein sequ Novel human diagno Canine tight juncti Human tight juncti Human tight juncti Human tight juncti Canine tight juncti Human p-dlg protein Novel human diagno Propionibacterium Novel human diagno DLDL receptor bindi Amino acid sequenc Human pancreatic c Human pancreatic c Human pancreatic c Human pancreatic sy LDL receptor bindi Drosophila melanog Drosophila melanog Human DNA topoisom Mouse Doczalpha pr Drosophila melanog Human ORRY protein LDL receptor bindi Bacillus thuringie Bacillus thuringie Bacillus thuringie Bacillus thuringie	(CARD-14).  (CARD-14; chromosome 17; growth; cell death; cancer; therapy; erythematosus; neurological disorder; sease; inflammatory disorder; anemala; state syndrome; myocardial infarction; sease; allergic rhinitis; infection; immunosuppressive; nootropic; immunosuppressive; notropic; erial.  WMP-dependent protein kinase  EII phosphorylation site"  is II phosphorylation site"
ABB64619 AAM93968 AAAM93968 AAAM93968 AAB621366 AAB622366 AAB673253 ABB66089 AAB66089 AAM73250 AAM7320 AAM7320 AAM762030 AAM762030	rulenments  rulenm
88 255 255 255 255 255 255 255 255 255 2	y)  y)  it dom  it dom  it dom  it dom  NF-kB  kinso  kinso  croh  croh  croh  camp-  camp-  camp-  camp-  camp-  camp-  camp-
145 845 848 928 1037 1037 1037 1037 1037 104 104 107 107 107 107 107 107 107 107	first entry)  first entry)  recruitment domain  recruitment domain  recruitment domain  recruitment domain  recruitment conning  order; systemic lug  sease; parkinson's  disorder; myelodys  disorder; crohn's  disorder; crohn's  g disorder; crohn's  g disorder; crohn's  disorder; crohn's  disorder; crohn's  g disorder; crohn's  g disorder; crohn's  f disorder; crohn's  g disorder; crohn's  f disorder; crohn's  g disorder; crohn's  g disorder; crohn's  g disorder; crohn's  g disorder; crohn's  f disorder; croh
28228282828282828111111111111111111111	standard;  01 (firs pase recr spase recr actor kap e disorde 's diseas gical dis alling di ective; a ens.  Lo site 12 site 12 site 25
11.12.13.2.13.2.13.2.13.2.13.2.13.2.13.	(64 AAE07164; AAE07164; D6-NOV-20 luman cas luman; ca lucimmun ultoimmun ult
	RESULT AAAC AAAC AAAC AAAC AAAC AAAC AAAC AAA

```
/note= "cAMP- and cGMP-dependent protein kinase
phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Casein kinase II phosphorylation site"
926.929
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                     /note= "N-glycosylation. -
759..761
/note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                            .844
.e= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Casein kinase II phosphorylation site"
                                 .637
e= "Casein kinase II phosphorylation site"
                                                                                                                                            .727
e= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                       "Casein kinase II phosphorylation site"
                                                      .655
e= "Protein kinase C phosphorylation site"
                                                                                                                                                                           "Casein kinase II phosphorylation site"
                       "Casein kinase II phosphorylation site"
                                                                                      "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                            //note= "Casein kinase II phosphorylation
168..870
//note= "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                               .896
.e= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                .
863
e= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .949
.e= "Peroxisomal targetting signal"
                                                                                                                                                                                                                                                                                                 /note= "Peroxisomal targetting signal"
796..799
                                                                                                                                                                                                                                                                                                                                                                                                                                        ..872
.872 cell attachment sequence"
                                                                                                                                                                                                                                                                                                                                                                   'label= Guanylate_kinase_domain
                                                                                                                                                                                                                                                                                                                     "N-myristoylation site"
                                                                                                                    "N-glycosylation site"
                                                                                                            /label= SH3_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JAN-2001; 2001WO-US02087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-FEB-2000; 2000US-0181159.
                                                                                                                                                                        /note= "Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "P
944..947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "C
976..979
                                                                                                                                                       /note= "P
725..728
                                                                                                                                                                                                            ..740
                                                                                                                                                                                                                                                      760..763
/note= "c
                                                                            .677
                                                                                                                                                                                                                                                                                                                                                                                         note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                    /note=
674..67
                                                                                                                                   note=
                                                                                                                                                                                                    'note=
                                                                                        'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-497073/54.
N-PSDB; AAD13447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200159065-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Andified-site
             Modified-site
                                                                                                                        Modified-site
                                                                                                                                             Modified-site
                                                                                                                                                                 Modified-site
                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                         Modified-site
                                  Modified-site
                                                       Modified-site
                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bertin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                         Jomain
                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                    Domain
   .369
e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .452
e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .466
e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
465
e= "Protein Kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .472
e= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .504
e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                              .252
e= "Protein Kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                         .262
e- "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                             .283
e- "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                       300
- "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                             .309
e- "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .368
te= "Protein kinase C phosphorylation site"
                                                                                        .21..123
note= "Protein kinase C phosphorylation site"
[26..420
                                                                                                                                                        .c= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                         . 243
te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                               "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        site"
    60..62
/note= "Protein kinase C phosphorylation site"
91..93
                                  "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                          "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .365
e- "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                        _227
.e= "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .386
e= "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .381
e= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                   .256
.e- "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .406
e- "Leucine zipper pattern"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              587..592
/note= "N-myristoylation site"
589..592
                                              114.117
/note="N-glycosylation site"
117.122
/note="N-myristoylation site"
                                                                                                                                                "N-myristoylation site"
                                                                                                                                                                                         "N-myristoylation site"
                                                                                                                          /label= Coiled_Coil_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
.516
e= "N-myristoylation
                                                                                                                                                                                                                                                                               label- k-Box_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68..660
/label= PDZ_domain
                                                                                                                                                                                                                                                                                                                                                                                           /note= "C
290..293
                                                                                                                                                                      'note= "C
.61..166
                                                                                                                                                                                                                                                                     .325
                                                                                                                                                                                                                                      'note= "T
:21..224
                                                                                                                                                note-
                                                                                                                                                                                                                note=
                                                                                                                                                                                                                                                           note=
                                                                                                                                                                                                                                                                                                                                                                     note-
                                                                                                                                                                                                                                                                                                                                                                                                                 note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note=
                                      'note=
                                                                                                                                                                                            note=
                                                                                                                                                                                                                                                                                                                            note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
     Modified-site
                          Modified-site
                                                Modified-site
                                                                     Modified-site
                                                                                                                                    Modified-site
                                                                                                                                                         Modified-site
                                                                                                                                                                               Modified-site
                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                               Domain
                                                                                                                                                                                                                                                                     Domain
```

site"

/note= "N-myristoylation site" 1002..1004 /note= "Protein kinase C phosphorylation site" An isolated caspase recruitment domain polypeptide useful for

```
RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                              AAU01207
 ŏ
                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; caspase recruitment domain-14; CARD-14; chromosome 17; nuclear factor kappa B; NF-kB; cell growth; cell death; cancer; therapy; autoimmune disorder; systemic lupus erythematosus; neurological disorder; Alzheimer's disease; Parkinson's disease; inflammatory disorder; anaemia; haematological disorder; myelodysplastic syndrome; myocardial infarction; stroke; immune disorder; Crohn's disease; allergic rhinitis; infection:
                                                      The present sequence is human caspase recruitment domain-14 (CARD-14). The CARD-14 gene is located on chromosome 17. The CARD-14 is used for the detection of modulators that modulates the ability of CARD-14 to bind to Bol-10 and stimulates phosphorylation of Bol-10 or activation of nuclear factor-kappa B (NF-kB). The CARD-14 is useful for regulating growth and cell death and useful for the treatment of cancer. It is also useful for the treatment of cancer. It is also useful for the treatment of autoimmune disorders (e.g., systemic lupus erythematosus), neurological disorders e.g., Alzheimer's and Parkinson's disease, inflammatory disorders, haematological disorders (e.g., according to an anemia myelodysplastic syndromes), myocardial infarctions, strokes, immune disorders (e.g., Crohn's disease, allergic rhinitis), cell signalling disorders and certain viral and bacterial infections.
regulating growth and cell death and useful for the treatment of cancer
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                        1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHGTI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell signalling disorder; cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antibacterial.
                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                            Length 1004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human predicted caspase recruitment domain-14 (CARD-14).
                                                                                                                                                                                                                                         Score 386; DB 22;
Pred. No. 7.9e-43;
                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Encoded by TGG"
                                                                                                                                                                                                                                                                                                                                                                                                                            AAE07165 standard; Protein; 1139 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                  Claim 1; Fig 1A-1E; 109pp; English
                                                                                                                                                                                                                                         100.0%; Sci
100.0%; Pri
tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-JAN-2001; 2001WO-US02087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-FEB-2000; 2000US-0181159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                     Local Similarity 100. ies 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-497073/54.
                                                                                                                                                                                                                                                                                                                                                        111111111
736 PNYSRAQQQL 745
                                                                                                                                                                                                                  1004 AA;
                                                                                                                                                                                                                                                                                                                                         61 PNYSRAQQQL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAD13448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200159065-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bertin J;
                                                                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE07165;
                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                       Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                AAE07165
                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                               셤
```

```
ö
                                                                                                                                                             The present sequence is predicted human caspase recruitment domain-14 (CARD-14). The CARD-14 gene is located on chromosome 17. The CARD-14 is used for the detection of modulators that modulates the ability of CARD-14 to bind to Bol-10 and stimmlates phosphorylation of Bol-10 or activation of nuclear factor-kappa B (NF-kB). The CARD-14 is useful for regulating growth and cell death and useful for the treatment of autoimmune disorders (e.g., salso useful for the treatment of autoimmune disorders (e.g., and Parkinson's disease, inflammatory disorders e.g., Alzheimer's and Parkinson's disease, inflammatory disorders, haematological disorders (e.g., annemia, myelodysplastic syndromes), myocardial infarctions, strokes, immune disorders (e.g., Crohn's disease, allergic rhinitis), cell signalling disorders and certain viral and bacterial infections.
An isolated caspase recruitment domain polypeptide useful for regulating growth and cell death and useful for the treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHGTI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; caspase recruitment domain; CARD-11; Bcl-10; NF-kappaB; apoptosis; hyperproliferative disorder; autoimmune; neurological; inflammatory disorder; viral infection; stress-related response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "cAMP- and cGMP-dependent protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162..165
/note= "Casein kinase II phosphorylation site"
168..171
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22; Length 1139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (00..102
/note= "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human caspase recruitment domain, CARD-11 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 386; DB 22;
100.0%; Pred. No. 9.2e-43;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "Coiled coil domain"
                                                                                                                Disclosure; Fig 2A-2C; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "CARD domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU01207 standard; Protein; 1147 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175..183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130..431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1139 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 70; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PNYSRAQQQL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU01207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
```

```
/note= "cAMP- and cGMP-dependent protein kinase
phosphorylation site"
                                                                                                                                                                     /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"
                                                                                                                                                                                                                                                                                            /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "Protein kinase C phosphorylation site"
592..695
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     779.782
/note= "Casein kinase II phosphorylation site"
787..789
                                                                                                                                                                                                                                               ..479
te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                ...510
.e= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                         "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                ...581
te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "N-myristoylation site"
725.-728
7725.-728
761.-766
761.-766
                                                                         site"
                                                                                                     . 289
te= "Casein kinase II phosphorylation site"
                                                                                                                       ..292
te= "Protein Kinase C phosphorylation site"
                                                                                                                                                    "Casein kinase II phosphorylation site"
                                                                                                                                                                                                  "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                    "Casein kinase II phosphorylation site"
                  "Casein kinase II phosphorylation site"
                                   "Tyrosine kinase phosphorylation site"
"Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          .641
e= "Glycosaminoglycan attachment site"
                                                               . 245
:e- "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /Boce
/66..834
/note= "SH3 domain"
/76..779
/note= "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                 "N-myristoylation site'
                                                                                                                                                                                                                                                                                                                                                              "N-glycosylation site"
                                                                                                                                                                                                                           ...475
te= "N-glycosylation site"
                                                       "N-glycosylation site"
                                                                     /note= "Proc-
282.285
-+o= "Amidation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "MAGUK domain"
638..641
                                                                                                                                                                                                                                                                                                                                                                                                                                "PDZ domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "N
710..715
                                                                                                                                                                                                                                                                                                                                                                                                                                          535..1147
                   /note= "C
                                                                                                                                                                                                           ..474
                                                                                                                                                                                                                                                                                                                                                                                                                      .748
 /note= "T
182..185
                                            .244
                                                                                                                                    /note= "P
378..381
                                                                                                                                                             .432
                                                                                                                                                                                                                                                                                                                                                                        ..592
                                                                                                                                                                                                                                                                                                                                                                                          .637
                                                                                                                                                                                         459..461
                                                                                                                                                                                                   /note= "471..474
                                                                                                                                                                                                                                                                                                                558..560
                                                                                                                                                                                                                                                                                                                                                                                 /note=
634..63
                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note=
                                                                                                                                                     'note=
                                                                                                                                                                                                                                                                            'note=
                                                                                                                                                                                                                                                           'note=
                                                                                                                                                                                                                       note
                                                                                                                                                                                                                                                                                                                                             'note=
                                      'note=
                                                         'note=
                                                                                                                'note=
                                                                                                                                                                                                                                                                                                                                                                         587
                                                                                                                                                                                                                                                                                                                                                      584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aodified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                      Modified-site
                                                                                                                         Modified-site
                                                                                                                                           Modified-site
                                                                                                                                                             Modified-site
                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                   Modified-site
         Modified-site
                           Modified-site
                                              Modified-site
                                                                 Modified-site
                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jomain
                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
```

```
The present sequence represents novel human caspase recruitment domain, CARD-11. The polynucleotide encoding this sequence was commain, CARD-11. The polynucleotide encoding this sequence was isolated from a human T-cell CDNA library. Also described are conveil human sequences for CARD-9 and CARD-10 (AAU01205, AAU01206) and rat CARD-9 (AAU01204). CARD-10 and CARD-11 interact with Bol-10 which is thought to activate nuclear factor (NF) kappaB can apoptosis. The sequences of the invention can be used for treating a disorder associated with abnormal levels of apoptosis by modulating the expression or activity of CARD-10, or CARD-11.

They can be used for the treatment of hyperproliferative disorders (e.g. cancer), autoimmune disorders (e.g. systemic lupus erythematosus), neurological disorders (e.g. Alzheimer's disease), inflammatory disorders (e.g. Crohn's disease), and viral infection (e.g. HIV). The CARD polypeptide, polynucleotide and an antibody which selectively binds to CARD can be used in screening and detection assays (e.g. chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel caspase recruitment domain (CARD) proteins, CARD-9, CARD-10, CARD-11, useful as targets for therapy, as immunogens, and in screening
                                                                                                                    /note= "N-myristoylation site"
857.859
872.875
/note= "Protein kinase C phosphorylation site"
772.875
/note= "Casein kinase II phosphorylation site"
882.1147
897..900
                                                                                                                                                                                                                                          site"
                                                                                                                                                                                                                                                                                 7.65.929
/note= "Casein kinase II phosphorylation site"
935..937
                                                                                                                                                                                                                                                                                                                 /note= "Protein kinase C phosphorylation site"
1003..1006
                                                                                                                                                                                                                                                                                                                                                             note= "Casein kinase II phosphorylation site"
[010..1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Casein kinase II phosphorylation site"
                                                                     8477.850
/note= "Casein kinase II phosphorylation site"
853..858
/note= "Protein kinase C phosphorylation site"
                            "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                       note= "Tyrosine kinase phosphorylation site"
1050..1055
                                                                                                                                                                                                                                          "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                      .922
e= "N-myristoylation site"
                                        .828
e= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                     note= "N-myristoylation site"
088.1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Fig 14A-14C; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0507533.
2000US-0513904.
2000US-0685791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2000; 2000WO-US32716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0168780
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Ca
1120..1123
               816..819
                                                                                                                                                                                                                                             /note=
                                 /note=
                                                                                                                                                                                                                                                                           /note=
                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                      1088.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-367809/38.
N-PSDB; AAS05389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200140468-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-FEB-2000;
25-FEB-2000;
10-OCT-2000;
                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
               Modified-site
                                             Modified-site
                                                                           Modified-site
                                                                                                       Modified-site
                                                                                                                                     Modified-site
                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bertin J;
                                                                                                                                                                                                 Domain
```

Ŋ

```
Sequence
                                                                                                                                                                             61
                                                                                                                                                                                                       09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang
                                                                                                                                                                                                                                                            AAM38934
                                                                                                                                                                                                                                                                                       SS X SS
                                                                                                                                                g
                                                                                                                                                                            ò
                                                                                                                                                                                                    g
                                                                                                                        ò
                                                                                                                                                              2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated plakoglobin interacting polypeptide (I). (I) is useful as a medicament and in the manufacture of a medicament for treating plakoglobin related diseases, such as skin carcinoma or an acantholytic disease, and oscreen compounds that interfere with the interaction of the polypeptide with plakoglobin The plakoglobin related diseases include basal cell carcinoma, squamous cell carcinoma, extramammary Paget's disease, Naxos disease, heart diseases, skin blistering and acantholytic diseases such as subcorneal acantholysis, Grover's disease, Hailey-Hailey's disease or Darier's disease, and ectodermal dysplasia/skin fragility syndrome. AAU73245-
                The
mapping, tissue typing), predictive medicine (prognostic assays, monitoring clinical trials, and therapy (treatment and proph/laxis). The CARD polypeptide may be used to screen for drugs that bind to and/or modulate it. CARD sequences are potential targets for regulating inflammation. cancer. NF kappab signalling, stress related response and apoptosis in human disease. A host cell containing a polynucleotide encoding CARD can be used to create transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    cardiant;
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptide, useful for treating skin carcinoma or acantholytic disease such as Grover's and Darier's disease, comprises a protein interacting with human plakoglobin and involved in transduction of plakoglobin related signal to nucleus
                                                                                                                                                                                         1 GDSFYIRVNLAMEGRAKG-ELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHGT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; plakoglobin; cytostatic; osteopathic; dermatological; cardian plakoglobin related disease; skin carcinoma; acantholytic disease; basal cell carcinoma; Maxos disease; extramammary Paget's disease; heart disease; skin blistering; subcorneal acantholysis; Grover's disease; Hailey-Hailey's disease; Darier's disease; ectodermal dysplasia; skin fragility syndrome.
                                                                                                                                                              5
                                                                                                                                   Length 1147;
                                                                                                                                                                                                                                                                                                                                                                                                                        Human plakoglobin interacting protein PLA_2H12, SH3 domain.
                                                                                                                                                              Indels
                                                                                                                                   ; Score 146; DB 22;
; Pred. No. 1.9e-10;
12; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vanlandschoot A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; Figure 4; 98pp; English.
                                                                                                                                                                                                                                                                                                                                         AAU73249 standard; Protein; 82 AA
                                                                                                                                     37.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAY-2001; 2001WO-EP04872.
                                                                                                                                                46.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-MAY-2000; 2000EP-0201668
                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                  Query Match
Best Local Similarity 46.5 Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F, Bonne S,
                                                                                                                                                                                                                                                                       825 IPSYSRAQQLL 835
                                                                                                                                                                                                                                             IPNYSRAQQQL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-062246/08
                                                                                                         1147 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200185933-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                             12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                  AAU73249;
                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Van Roy
                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                           RESULT 4
                                                                                                                                                                                                                  g
                                                                                                                                                                                         ò
                                                                                                                                                                                                                                             ö
```

```
2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynuclectides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                                                             Gaps
                                                                                                                                                                                                        2 DSFYIRVNLAMEGRAKGE-LQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHGTI 60
                                                                                                                                                                                                                                                    EPFYIRANLTLPERADPHALCVKAQEILRLVDSAYKRRQEWFCTRVDPLTLRD-LDRGTV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peripheral nervous system, neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease, Huntington's disease, hademostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemctactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ren F, W
Zhang J;
                                                                                                                                                             5,
AAU73254 represent novel human plakoglobin interacting protein amino acid sequences and related sequences of the invention.
                                                                                                                 Length 82;
                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oian XB,
Yang Y,
                                                                                                                                                               29;
                                                                                                               Score 116; DB 23;
Pred. No. 7.8e-08;
1; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen R, Ma Y,
Xu C, Xue AJ,
R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; SEQ ID NO 2079; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            such as central nervous system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM38934 standard; Protein; 350 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human polypeptide SEQ ID NO 2079.
                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wehrman T, X
Goodrich R,
                                                                                                                 30.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-DEC-2000; 2000WO-US34263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0653450
2000US-0662191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Asundi V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0693036
2000US-0727344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-442253/47.
N-PSDB; AAI58090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang Z, W
Zhou P,
                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                      PNYSRAQQQL 70
                                                                                                                                                                                                                                                                                                                               ||| ||| ||| |
|PNYQRAQQLL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu C,
                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-OCT-2000;
                                                                                                          Query Match
Best Local Simi
Matches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-AUG-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM38934;
```

ñ

```
The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been scolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                ä
Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression. Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      830 Primers useful for synthesizing full length cDNA clones and their
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                               DSFYIRVNLAMEGRAKGE-LQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHGTI 60
                                                                                                                                                                                                                                                                                     Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kawai Y;
T, Koga
                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; SEQ ID NO 3879; 1380pp + sequence listing; English.
                                                                                                                                                                                                  Length 350;
                                                                                                                                                                                                                                  29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashi K, Ishii S,
K, Kojima S, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; full length cDNA; cDNA synthesis; oligo-capping.
                                                                                                                                                                                                  Score 116; DB 22;
Pred. No. 4.8e-07;
                                                                                                                                                                                                                                11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM93822 standard; Protein; 746 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human polypeptide, SEQ ID NO: 3879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nishikawa T, Isogai T,
tu A, Sugiyama T, Nagai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use in genetic manipulation -
                                                                                                                                                                                                   30.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-JUL-1999; 99JP-0194486.
11-JAN-2000; 2000JP-0118774.
02-MAY-2000; 2000JP-0183765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUL-2000; 2000EP-0114089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-524255/58.
                                                                                                                                                                                                                 Local Similarity
Les 28; Conserv
                                                                                                                                                                                                                                                                                                                                 61 PNYSRAQQQL 70
                                                                                                                                                                                                                                                                                                                                                              PNYORAQQLL 91
                                                                                                                                                                     350 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAK94778
                                                                                                                                      specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP1130094-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-SEP-2001.
                                                                                                                                                                        Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM93822;
                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ota T,
                                                                                                                                                                                                                                                                 ~
                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                              82
                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                              Q
```

```
Gaps
                                                                                   2 DSFYIRVNLAMEGRAKGE-LQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHGTI 60
specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                      Human; caspase recruitment domain; CARD-10; Bcl-10; NF-kappaB; apoptosis; hyperproliferative disorder; autoimmune; neurological; inflammatory disorder; viral infection; stress-related response.
                                                               2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 245
te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7112.115
/note= "Casein kinase II phosphorylation site"
113..118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                313..315
/note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                  "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78..80
/note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                            site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Tyrosine kinase phosphorylation site"
230..251
                                         Length 746;
                                                                                                                                                                                                                                                                                                                                                                                                                                           "Protein kinase C phosphorylation
                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Leucine zipper homology region"
                                                                                                                                                                                                                                                                    Human caspase recruitment domain, CARD-10 polypeptide.
                                         30.1%; Score 116; DB 22; 40.0%; Pred. No. 1.2e-06;
                                                                                                                                                                                                                                                                                                                                                                 15..20
/note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Tropomyosin domain"
412..415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Coiled coil domain"
                                                               11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Amidation site'
                                                                                                                                                                                                                                                                                                                                                                                                                       "CARD domain"
                                                                                                                                                                                                       AAU01206 standard; Protein; 1032 AA.
                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Pi
293..296
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        366..398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .207
                                                                                                                                                                                                                                                                                                                                                                                                              23..123
                                                                                                                                                                                                                                                                                                                                                                                                                                 ..70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                          478 PNYQRAQQLL 487
                                                    Similarity
                                                                                                                              61 PNYSRAQQQL 70
                      AA;
                      746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                            Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                             Mac.
Local Sim.
28;
                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                               12-SEP-2001
                                                                                                                                                                                                                          AAU01206;
                       Sequence
                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                Matches
                                                                                                                                                                                  RESULT 7
                                                                                                                                                                                                                                     SXS
                                                                                                       Dp
                                                                                                                              Ω
```

```
.513 .
e= "Casein kinase II phosphorylation site"
                                                                                                                                                 .552
.e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                 .693
:e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                        74. 756
7note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           .757
.e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .784 -
e= "Protein Kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .. 832
te= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..870
te= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..872
te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .441
.e= "Casein Kinase II phosphorylation site"
                                                                                                                                                                                                                                         .605
.e- "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                             .644
.e- "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                          "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                        .751
.e= "Casein kinase II phosphorylation site"
"Casein kinase II phosphorylation site"
                                                                            .481
ce= "Casein kinase II phosphorylation site"
                                                                                                                                           "Protein kinase C phosphorylation site"
                                                                                                                                                                   .560
e= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                       . 573
te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                       739
- "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                     "Glycosaminoglycan attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .1032
.e= "Guanylate kinase (GUK) domain"
                 "Leucine zipper homology
                                                                                                                                                                                                                                                                                              .661
.e= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ...766
... N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "N-myristoylation site"
                                                                                                        note= "N-myristoylation site"
                                                                                                                                                                                               "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                    ..715
te= "N-glycosylation site"
                                                                      "N-glycosylation site"
                                                                                                                                                                                                                                  "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           915..918
/note= "Amidation site"
                                        .
.1032
re= "MAGUK domain"
                                                                                                                                                                                                                                                                                                                                                   .04..772
'note= "SH3 domain"
                                                                                                                                                                              /note= "P
                                                                                                                                  .514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..814
         .447
                                                                                                                                                                                                                                                             ..641
                                                                                                                                                                                                                                                                                                                 581..684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note=
                                                                                                                                                                                                                                                      note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note=
                                                                                                                          note=
                                                                                                                                                              'note=
                                                                                                                                                                                                 note=
                                                                                                                                                                                                                                                                                                          note=
                                                                                                                                                                                                                                                                                                                                                                               note=
                                                                                                                                                                                                                                                                                                                                                                                                   note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note=
                                    'note=
                                                                                       note=
                                                                                                                                                                                                                   "note=
                                                                                                                                                                                                                                                                       'note=
                                                                                                                                                                                                                                                                                                                            note-
                                                                                                                                                                                                                                                                                                                                             'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note=
                                                                                                                                                                                                                                           503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      368
                         Modified-site
                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                           Modified-site
                                                                                               Modified-site
                                                                                                                 Modified-site
                                                                                                                                                   Modified-site
                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
         Region
                                           Domain
                                                                                                                                                                                                                                                                                                                                                     Domain
```

```
The present sequence represents novel human caspase recruitment domain, CARD-10. The polynucleotide encoding this sequence was isolated from a human skin CDAR library. Also described are novel human sequences for ARD-9 and CARD-11 interary. Also described are novel human sequences corrected and CARD-11 interact with Bcl-10 which is thought to activate nuclear factor (NF)-kappaB and apoptosis. The sequences of the invention can be used for treating a disorder associated with abnormal levels of apoptosis by modulating the expression or activity of CARD-9, CARD-10, or CARD-11. They can be used for the treatment of hyperproliferative disorders (e.g. cancer), autoimmune disorders (e.g. CARD-10, or CARD-11. They can be used for the treatment of Systemic lupus erythematosus), neurological disorders (e.g. and viral infection (e.g. HIV). The CARD pupperlide, polynucleciide and an antibody which selectively binds to CARD can be used in screening and detection assays (e.g. chromosomal mapping, tissue typing), correct for requisition and/or modulate it. CARD sequences are potential targets for requiating inflammation, cancer, NF kappaB corrected and apoptosis in human disease. A bost call containing a polynuclectide encoding CARD can be used to create transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel caspase recruitment domain (CARD) proteins, CARD-9, CARD-10, CARD-11, useful as targets for therapy, as immunogens, and in screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 DSFYIRVNLAMEGRAKGE-LQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHGTI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                /note= "N-myristoylation site"
1022..1024
/note= "Protein kinase C phosphorylation site"
/note= "Casein kinase II phosphorylation site"
/note= "Casein kinase II phosphorylation site"
                "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 30.1%; Score 116; DB 22; Best Local Similarity 40.0%; Pred. No. 1.8e-06; Matches 28; Conservative 11; Mismatches 29;
                /note= "Protein kinase C phospl
981..986
/note= "N-myristoylation site"
1021..1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 9; Fig 10A-10C; 145pp; English.
                                                                                                                                                                                                                                                                                         99US-0168780.
2000US-0507533.
2000US-0513904.
2000US-0685791.
                                                                                                                                                                                                                                                                                                                                                                             (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                        01-DEC-2000; 2000WO-US32716
947..949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-367809/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1032 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PNYSRAQQQL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAS05388
                                                                                                                                                                                        WO200140468-A2
Modified-site
                                Modified-site
                                                                  Modified-site
                                                                                                    Modified-site
                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                          18-FEB-2000;
25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                            10-OCT-2000;
                                                                                                                                                                                                                                                                                          03-DEC-1999;
                                                                                                                                                                                                                      07-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                Bertin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  764
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
```

5;

ထ

```
ABB57253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
AAU84308
                                                                                                                                                                                                                                                                                                                                                       genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated plakoglobin interacting polypeptide (i). (I) is useful as a medicament and in the manufacture of a medicament for treating plakoglobin related diseases, such as skin carcinoma or an acantholytic disease, and to screen compounds that interfere with the interaction of the polypeptide with plakoglobin related diseases include basal carcinoma, squamous cell carcinoma, extramammary Paget's disease, Naxos disease, heart diseases, skin blistering and acantholytic diseases such as subcorneal
                                                                                                                   Human; plakoglobin; cytostatic; osteopathic; dermatological; cardiant; plakoglobin related disease; skin carcinoma; acantholytic disease; basal cell carcinoma; squamous cell carcinoma; Naxos disease; extramammary Paget's disease; hart disease; skin blistering; subcorneal acantholysis; Grover's disease; Hailey-Hailey's disease; Darier's disease; ectodermal dysplasia; skin fragility syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 DSFYIRVNLAMEGRAKGE-LQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHGTI 60
                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide, useful for treating skin carcinoma or acantholytic disease such as Grover's and Darier's disease, comprises a protein interacting with human plakoglobin and involved in transduction of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acantholysis, Grover's disease, Hailey'Hailey's disease or Darier's disease, and ectodermal dysplasia/skin fradility syndrome. AAU73245-AAU73254 represent novel human plakoglobin interacting protein amino acid sequences and related sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.1%; Score 116; DB 23; Length 1032; 40.0%; Pred. No. 1.8e-06; tive 11; Mismatches 29; Indels 2
                                                                                                                                                                                                                                                                                                                               (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
                                                                                               Human plakoglobin interacting protein #3.
                                                                                                                                                                                                                                                                                                                                                      Vanlandschoot A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     plakoglobin related signal to nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; Protein; 1745 AA.
                        AAU73247 standard; Protein; 1032 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Figure 3; 98pp; English.
                                                                                                                                                                                                                                                                                02-MAY-2001; 2001WO-EP04872.
                                                                                                                                                                                                                                                                                                       09-MAY-2000; 2000EP-0201668
                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                       Bonne S,
                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-062246/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       764 PNYORAQQLL 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1032 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
es 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PNYSRAQQQL 70
                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAS98203
                                                                                                                                                                                                                                WO200185933-A2.
                                                                      12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                       Van Roy F,
                                                                                                                                                                                                                                                        15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB57253
                                                AAU73247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                          Ношо
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB57253
             AAU73247
                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (1) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (1). The method is useful for examining the ischaemic condition (e.g. compression centering the protein occlusive ischaemia or vasospastic ischaemia) by measuring the protein sequences in ABB57020 to ABB57314) or by determining the expression profile of a gene group comprising these genes. The expression profile of a gene group comprising these genes are used as an indicator when screening for ischaemic condition improving drugs or thrappeutics for ischaemic condition improving drugs or thrappeutics for ischaemic condition related sequence, which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
                                                          Mouse ischaemic condition related protein sequence SEQ ID NO:699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
                                                                                                                 Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ishii Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human endometrial cancer related protein, TJP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 102.5; DB 2 Pred. No. 0.00023; ); Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takahashi Y, Nagata T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 1740-1748; 2690pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU84308 standard; Protein; 1736 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.6%;
                                                                                                                                                                                                                                                                                                                                                                                                          18-MAY-2001; 2001WO-JP04192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-MAY-2000; 2000JP-0145977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Asai S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-034733/04.
N-PSDB; ABI99666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1745 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||| :||:|
574 IPNKNRAEQ 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 IPNYSRAQQ
                                                                                                                                                                                                                                                                                 WO200188188-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAY-2002
                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ishikawa K,
07-MAR-2002
                                                                                                                                                                                                                                                                                                                                            22-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU84308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
```

σ

```
60 IPNYSRAQQ 68
                                                                                                                                                                                                N-PSDB; ABL08722
            WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200185933-A2.
                                                                                                                                                                                                                                                     interactions -
                                      27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-NOV-2001
                                                                                                                                                          Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU73251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU73251
  Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                     The invention relates to diagnosing endometrial cancer in a subject suspected of having endometrial cancer comprising determining the expression of a set of nucleal acid molecules or expression products in an endometrial sample suspected of being cancerous, where the set of nucleic acid molecules comprises at least 2 nucleic acid molecules comprises an array of at least 2 of the 50 nucleic acids bound to a solid substrate. Also included is a solid-phase protein microarray comprising at least 2 antibodies or its antigen protein microarray comprising at least 2 antibodies or its antigen properties from the 50 fully defined sequences as given in the specification, fixed to a solid substrate. The methods and arrays are specification, fixed to a solid substrate. The methods and arrays are treatment regimes and identification of lead compounds useful for the treatment of endometrial cancer. The present sequence is one of 50 proteins differentially expressed between cancerous and non-cancerous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                            Diagnosing endometrial cancer comprises determining expression of nucleic acid molecules or expression products that are differentially expressed in normal and malignant endometrium \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   504 GDSFYIRTHFEYEKESPYGLSFNKGEVFRAVDTLYNGKLGSWLAIRIGKNHKE--VERGI 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 23; Length 1736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.5%; Score 98.5; DB 23; Length 36.2%; Pred. No. 0.0008; ive 9; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster polypeptide SEQ ID NO 20649.
Human; endometrial cancer; differential expression;
                                                                                                                                                                                                                                                                                                                 Claim 33; Page 225-231; 233pp; English.
                                                                                                                                                                    (BGHM ) BRIGHAM & WOMENS HOSPITAL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB64619 standard; Protein; 1445 AA.
            DNA microarray; protein microarray
                                                                                                               31-JUL-2001; 2001WO-US24104.
                                                                                                                                           31-JUL-2000; 2000US-221735P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 36.2
Matches 25, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster
                                                                                                                                                                                                                        WPI; 2002-179967/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1736 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||| :||:|
562 IPNKNRAEQ 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPNYSRAQQ 68
                                                                                                                                                                                                                                      N-PSDB; ABK35528,
                                                             WO200209573-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmaceutical
                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-2002
                                                                                     07-FEB-2002
                                                                                                                                                                                              Mutter GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB64619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB64619
δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

```
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
The sequence acta for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; plakoglobin; cytostatic; osteopathic; dermatological; cardiant; plakoglobin related disease; skin carcinoma; acantholytic disease; basal cell carcinoma; squamous cell carcinoma; Maxos disease; extramammary Paget's disease; hart disease; skin blistering; subcorneal acantholysis; Grover's disease; Hailey-Hailey's disease; Darier's disease; ectodermal dysplasia; skin fragility syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 20649; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.3%; Score 97.5; DB 22 ilarity 31.9%; Pred. No. 0.00086; Conservative 13; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse tight junction domain 20-1, SH3 domain.
                                                                                                                                                                                                                                                                     Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU73251 standard; Protein; 89 AA.
                                                                                                                                                                                                                                                                     Li PWD,
23-MAR-2001; 2001WO-US09231.
                                                                        23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                 Adams M,
                                                                                                                                                                                                                                                                                                                                      WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
es 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1445 AA;
                                                                                                                                                                                    (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                556 IPNKSRAEE 564
```

```
(HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ota T, IS
Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB93753;
                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                        Query Match
                              Ota T,
                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                      AAB93753
                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                          Q
 ò
                                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                      The invention relates to an isolated plakoglobin interacting polypeptide (I). (I) is useful as a medicament and in the manufacture of a medicament for treating plakoglobin related diseases, such as skin carcinoma or an acantholytic disease, and to screen compounds that interfere with the interaction of the polypeptide with plakoglobin related diseases include basal carcinoma, squamous cell carcinoma, extramammary Paget's disease, Naxos disease, heart diseases, skin blistering and acantholytic diseases such as subcorneal acantholysis, Grover's disease, Hailey's disease or Darier's disease, and ectodermal dysplasia/Skin fragility syndrome. AAU73245-AAU7324 represent novel human plakoglobin interacting protein amino acid sequences and related sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                    New polypeptide, useful for treating skin carcinoma or acantholytic diseases such as Grover's and Darier's disease, comprises a protein interacting with human plakoglobin and involved in transduction of plakoglobin related signal to nucleus
                                                                                                                                                                                                                                                                                                                                                                                    2 DSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGTI 60
                                                                                                                                                                                                                                                                                                                                                   ٠,
ش
                                                                                                                                                                                                                                                                                                                                DB 23; Length 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     marker; screening; micro-metastasis;
                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human stomach cancer expressed polypeptide SEQ ID NO 4.
                                                                                                                                                                                                                                                                                                                               25.0%; Score 96.5; DB 23; 36.8%; Pred. No. 3.7e-05; ive 9; Mismatches 31;
                                        (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
                                                              Vanlandschoot A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM93968 standard; Protein; 548 AA
                                                                                                                                                       Example 4; Figure 4; 98pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9905-015959
9905-0159590.
200005-0118776.
200005-0183322.
200007-0183767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000WO-JP05063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99JP-0248036
02-MAY-2001; 2001WO-EP04872
                     09-MAY-2000; 2000EP-0201668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 36.8
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peritoneal dissemination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     stomach cancer;
                                                              Bonne S,
                                                                                 WPI; 2002-062246/08
                                                                                                                                                                                                                                                                                                            89 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                          || :||:|
PNKNRAEQ 66
                                                                                                                                                                                                                                                                                                                                                                                                                PNYSRAQQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200109317-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JAN-2000;
17-FEB-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUL-1999;
27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-FEB-2001
                                                              ъ,
                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM93968
                                                                                                                                                                                                                                                                                                                                 Query Match
                                                              Van Roy
                                                                                                                                                                                                                                                                                                                                                                                                                                   59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ношо
                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM93968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
The invention relates to stomach cancer-expressed genes (AAI93442-AAI991317) and the encoded proteins (AAM93967-AAM94039). The GAAI934A2-AAI99317) and the encoded proteins for screening for the early stages of the disease. The proteins and peptides can be used as targets for screening for compounds to treat the disease. They can also be used for predicting micro-metastases. The gene can predict peritoneal dissamination.
Saito K, Yamamoto J;
Otsuki T, Aburatani H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection
                                                                                                                                                                                       New Stomach cancer-associated genes, useful as markers in blood tests for screening for the early stages of the disease ^{\rm -}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 GDSFYIRTHFELEPSPPSGLGFTRGDVFHVLDTLHPGPGQSHARGGHWLAVRMGRDLREQ 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; primer; detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHA---HRVNSYTMKD--TA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saito K,
, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 96.5; DB 22;
Pred. No. 0.00035;
7; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashi K, S
A, Nagai K,
hikawa T, Hayashi K, S
Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human protein sequence SEQ ID NO:13422
                                                                                                                                                                                                                                                                             Claim 1; Page 67-69; 242pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sogai T, Nishikawa T,
Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB93753 standard; Protein; 548
  Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.0%;
38.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUL-1999; 99JP-0248036.
27-AdG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 38.4 nes 28; Conservative
                            Ishii S, Sugiyama T, W
Kodama T, Midorikawa Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164 ERGIIPNOSRAEO 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-318749/34.
                                                                                                            WPI; 2001-570287/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 AHGTIPNYSRAQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     548 AA;
  Isogai T,
                                                                                                                                            N-PSDB; AAI93843
```

```
The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises a fleast 15 nucleotides; or (b) a combination of an onligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the olynucleotide which comprises a 1'-end sequence of polynucleotide which comprises at 15 nucleotides and the combination of the specification. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and the full-length cDNAs. The primers are also useful for the particularly full-length cDNAs. The primers are also useful for the chetchion and/or diagnosis of the abnormality of the full-length cDNAs. The primers are also useful for the full-length cDNAs are primers allow obtaining of the full-length cDNAs are primers allow obtaining of the full-length cDNAs represent human amino acid sequences; and AAH13628 and AAH13633 to AAH13632 represent human amino acid sequences; and AAH13632 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; kinase; enzyme; PKIN-13 protein; immune system disorder; anaemia; acquired immune deficiency syndrome; thymic hypoplasia; Crohn's disease; asthma; neurological disorder; epilepsy; Charoct-Marie-Tooth disease; AIDS; seizures; cell proliferative disorder; cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma; developmental disorder; Down's syndrome; gene therapy; protein therapy; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHA---HRVNSYTMKD--TA 55
  and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 96.5; DB 22;
Pred. No. 0.00035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33;
                                                      Claim 8; SEQ ID 13422; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "GLGF domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "GLGF domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20..101
/~~te= "PDZ domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "PDZ domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "PDZ domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE21718 standard; Protein; 928 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.0%;
38.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 25.0°
Best Local Similarity 38.4°
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204..280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= |
388..46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
391..47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10..99
/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 ERGIIPNOSRAEQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human PKIN-13 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 AHGTIPNYSRAQQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               548 AA;
                      full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE21718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
AAE21718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
```

```
The present invention relates to human kinases (PKIN) and polynucleotides encoding such proteins. PKIN sequences of the invention are useful for diagnosing, treating or preventing disorders associated with aberrant expression of PKIN, particularly immune system disorders (e.g. acquired immune deficiency syndrome (AIDS), thymic hypoplasia, Crohn's disease, anaemia, asthma), neurological disorders (e.g. epilepsy, Charcor-Marieroch disease or seizures), call proliferative disorders (e.g. cancers such as adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma, myene therapy and developmental disorders (e.g. Down's syndrome). They are also used in gene therapy and protein therapy. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human kinases, useful for diagnosing, treating or preventing immune system disorders (e.g. Crohn's disease), neurological disorders (e.g. epilepsy), or cell proliferative disorders (e.g. cancers such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gandhi AR;
Tribouley CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    484 GDSFYIRTHFELEPSPPSGLGFTRGDVFHVLDTLHPGPGQSHARGGHWLAVRMGRDLREQ 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHA---HRVNSYTMKD--TA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nguyen DB, Walia NK, Hafalia AJA, Yao MG, Gandhi AF, Ding L, Patterson C, Yue H, Baughn MR, Tribouley Elliott VS, Lu Y, Ison CH, Au-Young J, Tang YT; Burrill JD, Marcus GA, Zingler KA, Lu DAM, Lal PG; Warren BA, Kearney L, Policky JL, Thangavelu K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 96.5; DB 23;
Pred. No. 0.00068;
                                                                                           /note= "Leucine zipper domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 68; Page 174-176; 218pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: January 22, 2003, 08:52:21
Job time : 15.6425 secs
429..439
/note= "PDZ domain"
733..754
                                                                                                                                                                                                                                                                                                                                                                      20000S-231357P.
2000US-232654P.
2000US-234902P.
2000US-236499P.
2000US-238389P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.0%;
38.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                 31-AUG-2001; 2001WO-US27219
                                                                                                                                                                                                                                                                                                                                                   2000US-229873P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-240542P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leukemia or lymphoma)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-329769/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 AHGTIPNYSRAQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   928 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAD34310
                                                                                                                                                         WO200218557-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                    22-SEP-2000;
29-SEP-2000;
06-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gururajan R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                             08-SEP-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                   31-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thornton M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Azimzai Y,
Ramkumar J,
                                                                                                                                                                                                                   07-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bandman O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burford N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
   Domain
                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
FFFFFFF ANALAS DAX BARBARA BAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
```

;;

THIS PAGE BLANK (USPTO)

```
Sequence 21, Application US/09562737
Fatent No. 6428967
GENERAL INFORMATION:
APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708
CURRENT APPLICATION NUMBER: 2000-05-01
KUNBER OF SEQ ID NOS: 132
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
LENGTH: 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-562-737-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 2
US-09-562-737-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21, Appl
Sequence 27, Appl
Sequence 4, Appli
Sequence 7, Appli
Sequence 2, Appli
Sequence 22, Appli
Sequence 24, Appli
Sequence 26, Appli
Sequence 27, Appli
Sequence 27, Appli
Sequence 27, Appli
Sequence 27, Appli
Sequence 4, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 28, Appl
Sequence 21, Appl
Sequence 27, Appl
Sequence 8, Appli
Sequence 9, Appli
                                                                                                                                                                                                                                                                                                                                                         (without alignments)
429.229 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                          January 22, 2003, 08:52:30; Search time 4.79839 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-767-215-2_COPY_676_745
386
1 GDSFYIRVNLAMEGRAKGEL.....MKDTAAHGTIPNYSRAQQQL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-023-731-4
US-09-023-731-1
US-09-562-737-24
US-08-662-737-24
US-08-040-751-3
US-08-962-190-2
US-08-962-190-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-562-737-29
US-09-113-750A-3
US-08-652-255-22
US-09-834-497A-22
US-09-503-444A-22
US-08-300-584-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-562-737-28
US-09-562-737-27
US-08-448-170-8
US-08-100-1803-9
US-08-100-1803-9
US-08-170-4
US-08-174-038-4
US-08-779-046-4
US-08-881-340-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-476-123-4
US-08-944-483-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                       protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   566
724
1422
11174
11174
11174
1174
361
361
361
361
361
510
510
538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \tilde{\kappa} \circ 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

5083

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB
Maximum DB
                                                                                                                                                                                                       OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
                                                                                                                                                                                                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
```

```
4
                       Sequence 48,
Sequence 11,
Sequence 15,
Sequence 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 FYIRVNLAMEGRAKG-----ELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAH 57
            Sequence 2
Sequence 1
Sequence 1
                                                                            Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                             Sequence
                                                                                                                                                Sequence Sequence S
                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic ; OTHER INFORMATION: Sequence US-09-562-737-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                        Sequence 28, Application US/09562737
Patent No. 6428967
GENERAL INFORMATION:
APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/09/562,737
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
US-08-404-445-3

US-09-562-737-22

US-08-469-260A-170

US-09-171-461-48

US-09-178-252-11

US-08-349-867-23

US-08-349-867-27

US-08-399-476-27

US-08-239-476-27

US-08-598-305A-27

US-08-598-305A-35

US-08-598-305A-35

US-08-598-305A-35

US-08-598-305A-38

US-08-598-305A-35

US-08-598-305A-35

US-08-598-305A-35

US-08-598-305A-35

US-08-598-305A-35

US-08-598-305A-35

US-08-598-305A-38

US-08-598-305A-38
                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 63.5; D
; Pred. No. 6.3;
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          16.5%;
                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              23; Conservative
  323
724
6094
6094
11148
11148
11148
11148
11148
11148
11148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 GTIPNYSRAQQQ 69
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
```

```
APPLICANT: Payne, Jewel
APPLICANT: Cummings, David A.
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Narva, Kenneth E.
APPLICANT: Stelman, Steve
TITLE OF INVENTION: No. 615589el Bacillus thuringiensis Isolate Denoted
TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTM-FQGCGCWHAHRVNSYTMKDTAAH-G 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1227;
                                                                                                                     SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 58; DB 1
Pred. No. 59;
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUDRESSEE: Jay M. Sanders
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERRUCE/DOCKET NUMBER: M/S 102D.C1
TELECOMMUNICATION INFORMATION:
TELEPRAN: (904) 372-5800
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/069,902
FILING DATE: 01-JUNE-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/759,247
FILING DATE: 13-SEPT-1991
CLASSIFICATION: 424
                                                                                                                                                                               APPLICATION NUMBER: US/08/448,170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/08961803
Patent No. 6150589
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.0%; Sco
29.9%; Pre
tive 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                  IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1227 amino acids
                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION: B.t.
TITLE OF INVENTION: Bnc
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: peptide US-08-448-170-8
                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1132 TAACNSR 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Florida
Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 TIPNYSR 65
                                     32606
                                                                                                  COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                            SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-961-803-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ōλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Stelman, Steve TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted TITLE OF INVENTION: B.t. PSI58C2, Active Against Lepidopteran Pests, and Genes TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
                                                                                                                                                                                 3,
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 FYIRVNLAME-----GRAKGELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHG 58
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                       4 FYIRVNLAME-----GRAKGELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description of Artificial Sequence: Synthetic Sequence
                                                  Description of Artificial Sequence: Synthetic Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 15.2%; Score 58.5; DB 4; Length 724; Best Local Similarity 31.4%; Pred. No. 27; Matches 22; Conservative 7; Mismatches 32; Indels
                                                                                                                                        Score 62.5; DB 4; Length 724;
Pred. No. 8.4;
9; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Herz, Joachim
APPLICANT: Herz, Joachim
TITLE OF INVENTION: LDL Receptor Signaling Pathways
TITLE REFERENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/09/562,737
CURRENT FILIG DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 27
LENGTH: 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27, Application US/09562737 Patent No. 6428967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/08448170 Patent No. 5723758 GENERAL INFORMATION:
APPLICANT: Payne, Jewel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cummings, David A. APPLICANT: Cannon, Raymond J.C. APPLICANT: Narva, Kenneth E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence
                    ORGANISM: Artificial Sequence
                                                                                                                                            Query Match
Best Local Similarity 31.0%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 487 FIPSKRRVERR 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     487 RIPSKRRVER 496
                                                                                                                                                                                                                                                                                                       59 TIPNYSRAQQQ 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 TIPNYSRAQQ 68
                                                          ) OTHER INFORMATION:
) OTHER INFORMATION:
US-09-562-737-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE:
; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-562-737-27
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
US-09-562-737-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-448-170-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                           õ
                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
```

ä

```
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/100,709 FILING DATE: 29-JUL-1993 ATTORNEY/AGENT INFORMATION: NAME: EGOLf. Chilstopher REGISTRATION NUMBER: 27633
          APPLICATION NUMBER: US/08/100,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
BEDIUM TYPE: Floppy disk
CMBUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08176865; Patent No. 5616319; GENERAL INFORMATION:
                                                                    ATORNEY/AGENT INFORMATION:
NAME: EGOLf, Christopher
REGISTRATION NUMBER: 2763
REFERENCE/DOCKET NUMBER: 7205
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 72
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                        15.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1229 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 15.0%
Best Local Similarity 29.9%
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-100-709-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 29-JUL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pennsylvania
                                                                                                                                                                                                                                                                                                               amino acid
                                  FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1134 TAACNSR 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 TIPNYSR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19103
                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
US-08-176-865-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Donovan, William P.
APPLICANT: Donovan, Vuping
APPLICANT: Tan, Yuping
APPLICANT: Jany, Christine S.
APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ъ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1074 GRGYILKVTAYKEGYGEGCVTIH--EIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQG 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTM-FQGCGCWHAHRVNSYTMKDTAAH-G 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.0%; Score 58; DB 4; Length 122
29.9%; Pred. No. 59;
tive 12; Mismatches 31; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                     CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/069,902
FILING DATE: 01-JUNE-1993
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/759,247
FILING DATE: 13-SEPT-1991
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/448,170
FILING DATE: 23-MAY-1995
CLASSIFICATION NUMBER: WS 102DCD1
FILING DATE: 33-MAY-1995
CLASSIFICATION NUMBER: WS 102DCD1
FILING DATE: 33-MAY-1995
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
THOTHER SECTION INFORMATION: TELEPHONE: (352) 375-8100
THOTH: LANGE OF TELEPHONE: (352) 375-8100
                                                                 FILING DATE: 31-0CT-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08100709
Patent No. 5322687
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 29.9%
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1132 TAACNSR 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 TIPNYSR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U
ZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-961-803-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
US-08-100-709-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuping
APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
APPLICANT: GONZALEZ Jr., Jose M.
ATITLE OF INVENTION: BACILLUS THURINGIENSIS CIYET4 AND CIVET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
                                                                                                                                      4; Gaps
                                                                                                      1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTM-FQGCGCWHAHRVNSYTMKDTAAH-G 58
     Length 1229;
                                                       31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF ANY OF SEQUENCES: 5
NUMBER OF SEQUENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,865
FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
Score 58; DB 1;
Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
```

э;

```
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                  Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                   U.S.A.
                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1134 TAACNSR 1140
                 1134 TAACNSR 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 TIPNYSR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                   19103
                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
US-08-881-340-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-779-046-4
                                                                         RESULT 9
US-08-779-046-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δλ
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Tan, Yuping
APPLICANT: Jany, Christine S.
APPLICANT: GONZALEZ Tr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CIYET4 AND CIYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3,
                                                                                             ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ::|| || :| || :| || 1076 GRGYILRVTAYYEGYGEGCVTIH--EIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQG 1133
                                                                                                                                                        1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTM-FQGCGCWHAHRVNSYTMKDTAAH-G 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                             4; Gaps
                                                                                                                                1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTM-FQGCGCWHAHRVNSYTMKDTAAH-G 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 1229;
59;
                                                       DB 1; Length 1229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31; Indels
                                                                                             31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S. ADDRESSEE: Nadel STREET: 1601 Market Street, 36th Floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.0%; Scor.
29.9%; Pred. No. 55,
...a 12; Mismatches
                                                                                           12; Mismatches
                                                     Score 58; DB
Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRELL APPLICATION NUMBER: US/08/474,038
FILING DATE: 07-JUN-1995
CLASSIPECATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,865
FILING DATE: 30-DEC-1993
APPLICATION NUMBER: US 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Egolf, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMUNICATION INFORMATION:
TELECHONE: 215-757-1590
INFORMATION FOR SEQ 1D NO: 4:
                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08474038 Patent No. 5679343 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Donovan, William P.
                                                       15.0%;
29.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 29.99
Matches 20; Conservative
                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-474-038-4
protein
                                                       Query Match
Best Local Similarity
Matches 20; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                               1134 TAACNSR 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 TIPNYSR 65
                                                                                                                                                                                                           59 TIPNYSR 65
 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
     ; MOLECULE TO
US-08-176-865-4
                                                                                                                                                                                                                                                                                                                          US-08-474-038-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                      qq
                                                                                                                                                                                                             õ
```

```
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuping
APPLICANT: Jany, Christine S.
APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THORINGIENSIS CLYET4 AND CLYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTM-FQGCGCWHAHRVNSYTMKDTAAH-G 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuping
APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CIYET4 AND CIYET5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                             ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S. ADDRESSEE: Nadel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Mismatches
                                                                                                                                                                                                                                                                                                          ADDRESSEE: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 58;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/779,046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILTING DATE: 06-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA: 08/100,709
FILING DATE: 29-JUL-1993
ATTONNEY/AGENT INFORMATION: NAME: EGOLf, Christopher REGISTRATION NUMBER: 27633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08881340
Patent No. 5942658
GENERAL INFORMATION:
APPLICANT: Donovan, William P.
Sequence 4, Application US/08779046 Patent No. 5854053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 7:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 29.9%;
Matches 20; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1229 amino acids
```

Wed

```
5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 RSQGDLTSSQHEIVHFTDVFIAGSGPISCTYARHIIDNTSTTK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1. Application US/09023731
Patent No. 6291648
GENERAL INFORMATION:
APPLICANT: Kawamura, Yukio; Morita,
APPLICANT: Kawamura, Yukio; Morita,
TITLE OF INVENTION: ANTITUMOR PROTEIN AND
TITLE OF INVENTION: GENE ENCODING SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 RAKGELQVHCNEVLHVTDTMFQGCG --- CWHAHRV -- NSYTMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 57.5; Di
Pred. No. 1.8;
FILING DATE: 13-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 29275/1997
FILING DATE: 13-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: KENNETH H. SONNENFELD
REGISTATION NUMBER: 3,285
REFERENCE/DOCKET NUMBER: 3479-4000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 758-4800
TELEX: 421792
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: MORGAN & FINNEGAN, L.L.P. STREET: 345 PARK AVENUE CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORFEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MTCROSOFT WORD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,731
FILING DATE: 13-FEB-199
PRIOR APPLICATION DATA: PS-1997
ATTORNEY AGENT INFORMATION:
AMAE: KENNETH H. SONNENFELD
REGISTRATION NUMBER: 33,285
REFERENCE/DOCKET NUMBER: 3479-4000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1758-4800
TELECOMMUNICATION 1758-4800
TELECOMMUNICATION 1758-4800
TELECOMMUNICATION 1758-4800
TELECOMMUNICATION 1758-4800
TELECOMMUNICATION 1758-4800
TELECOMMUNICATION 2500 DNO: 1:
                                                                                                                                                                             3479-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3479-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.9%;
32.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 14.99
Best Local Similarity 32.69
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: peptide US-09-023-731-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-09-023-731-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
US-09-023-731-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGIH:
                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
         TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ::|| || || || 1076 GRGYILRVTAYKEGYGEGVTIH--EIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQG 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTM-FQGCGCWHAHRVNSYTMKDTAAH-G 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.0%; Score 58; DB 2; Length 1229; 29.9%; Pred. No. 59; tive 12; Mismatches 31; Indels
                                                                            ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
                                                                                                                                                                                                                                                         COMPUTER RELABLE FORM:
MEDIUM TYPE: FIDPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,340
FILING DATE: 24-JUN-1997
CLASSIFICATION 1424
PRIOR APPLICATION NUMBER: 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INPORMATION:
NAME: EGOLf, Christopher
REGISTRATION NUMBER: 27633
REGISTRATION NUMBER: 27633
REGISTRATION NUMBER: 27633
RECISTRATION SEQ ID NO: 4:
TELEPHONE: 215-757-1590
INPORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-023-731-4
Sequence 4, Application US/09023731
Sequence 4, Application US/09023731
Setuent No. 6291648
GENERAL INFORMATION:
APPLICANT: Kawamura, Yukio; Morita,
APPLICANT: Akihir: Izumo, Koji.; Saka, Tomohide.
TITLE OF INVENTION: ANTITUMOR PROTEIN AND
TITLE OF INVENTION: GENE ENCODING SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                               STREET: 1601 Market Street, 36th Floor CITY: Philadelphia STATE: Pennsylvania COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: MORGAN & FINNEGAN, L.L.P. STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/023,731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD 97
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 29.9%
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-881-340-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY I
                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
    TITLE OF INVENTION: TO NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1229 amir
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1134 TAACNSR 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 TIPNYSR 65
                                                                                                                                                                                                                       19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
```

g ò

Wed Jan 22 10:56:42 2003

```
3;
                                     2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||: :| || || : :| || 431 FYIKALFDYDKTKLCGFLSQALSMHFGDVLHVINASDE--EWWQAQRVHSDS--ETDRIG 486
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 FYIRV-----NLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE NUMBER OF SEQUENCES: 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-562-737-24
                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 724;
 DB 4; Length 566;
                                     15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28; Indels
                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INFORMION: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/09/562,737
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 24
LENGTH: 724
                                                                                               16 RSQGDLTSSQHEIVHFTDVFIAGSGPISCTYARHIIDNTSTTK 58
                                                                          15 RAKGELQVHCNEVLHVTDTMFQGCG---CWHAHRV--NSYTMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.9%; Score 57.5; DB 4; 28.2%; Pred. No. 36; Live 14; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: ABBOTT LABORATORIES D377/AP6D 100 ABBOTT PARK ROAD
                                     9; Mismatches
14.9%; Score 57.5; 1
32.6%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAMI J. PILOT-MATIAS
GEORGE J. DAWSON
GEORGE G. SCHLAUDER
SURESH M. DESAI
THOMAS P. LEARY
ANTHONY SCOTT MUERHOFF
JAMES C. ERKER
SHERI L. BUIJK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 82, Application US/08469260A Patent No. 6451578
                                                                                                                                                                                                      Sequence 24, Application US/09562737
Patent No. 6428967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISA K. MUSHAHWAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 28.29
Matches 20; Conservative
                                      14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABBOTT PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        487 FIPSKRRSERR 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 TIPNYSRAQQQ 69
                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
STREET: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-08-469-260A-82
                                                                                                                                                                   RESULT 13
US-09-562-737-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT
   Query Match
                                     Matches
                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

```
GENERAL INFORMATION:
APPLICANT: Payne, Jewel M
APPLICANT: Payne, Jewel M
APPLICANT: Sick, August J
TITLE OF INVENTION: No. 5407825el Bacillus thuringiensis isolates
TITLE OF INVENTION: active against Lepidopteran Pests and Genes Encoding No.
TITLE OF INVENTION: Lepidopteran-active Toxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 YVQHIWHVPDRTMFPELXCNHLXRMPCYRSNHRVGHWKGPNRSSIQK 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 HCNEVLHVTD-TMFQGCGCWHAHRVNSYTMKDTAAHGTIPNYSRAQQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.25
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 56.5; DB 4;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: DAVID R. SALIWANCHIK
2421 N.W. 41st STREET, SUITE A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                              NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REPERENCE/DOCKET NUBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MA39.C1.D3
                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,260A
                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/040,751
FILING DATE: 19930329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-040-751-3; Sequence 3, Application US/08040751; Patent No. 5407825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: SALIWANCHIK, DAVID R.
REFERENCE/DOCKET NUMBER: MA
TELECOMMUNICATION INFORMATION:
TELECHONE: 904-375-8100
                                                                                                                                                                                                                                                                 TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 82:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.6%;
                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1422 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1174 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: DAVID R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 15; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAINESVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: AMINO ACID STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19
CLASSIFICATION:
                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32606
                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-469-260A-82
  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ωÿ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
```

Search completed: January 22, 2003, 08:57:39 Job time : 6.79839 secs

э Э THIS PAGE BLANK (USPTO)

```
Sequence 82, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 1641, Appl
Sequence 1641, Appl
Sequence 1641, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 6, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Appli
Sequence 1, Appli
Sequence 38, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Appli
Sequence 5, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 98, Appl
Sequence 4, Appli
                                                                                                                                                              (without alignments) 500.428 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                        January 22, 2003, 08:49:35; Search time 2.82258 Seconds
                                                                                                                                                                                                                               US-09-767-215-2_COPY_676_745
386
1 GDSFYIRVNLAMEGRAKGEL......MKDTAAHGTIPNYSRAQQQL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_UBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_UBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_UBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-742-684-4
US-09-764-877-1641
US-09-925-302-696
US-10-076-840-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0 US-09-911-969-4
0 US-09-911-969-1
0 US-09-866-562-38
US-08-424-550B-82
0 US-09-919-497-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-919-497-98
US-09-785-548-4
                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-965-313-4
US-09-732-234-6
US-09-784-859-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-767-215-2
US-09-767-215-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-032-159A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-976-059-14
US-09-976-059-15
                                                                                                                                                                                                                                                                                                                                                                                                   122226 seqs, 20178551 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10
10
10
10
10
10
10
10
10
10
10
10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1000.0

23.7.6

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0

20.0.0
                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB
Maximum DB
                                                                                           OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Result
```

```
Sequence 104, App
Sequence 213, App
Sequence 215, App
Sequence 215, App
Sequence 21, Appl
Sequence 21, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 21, Appl
Sequence 118, Appl
Sequence 128, Appl
Sequence 128, Appl
Sequence 136, Appl
Sequence 136, Appl
Sequence 255, Appl
Sequence 277, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHGTI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1004;
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09767215
Patent No. US20020081636A1
GENERAL INC. US20020081636A1
GENERAL INC. US20020081636A1
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN VAND USES THEREOF
FILE REFERENCE: 07334-142001
CURRENT APPLICATION NUMBER: 05/09/767,215
CURRENT FILING DATE: 2001-01-22
PRIOR PAPLICATION NUMBER: 60/181,159
PRIOR FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE FastSEQ for Windows Version 4.0
       0 US-09-808-602-104

0 US-09-808-602-104

0 US-10-108-605-253

0 US-10-108-605-253

0 US-09-764-864-1139

1 US-09-764-864-1139

1 US-09-802-660-1

0 US-09-802-660-1
                                                                                                                                                                                                                US-09-764-869-1183
US-10-016-447-7
US-09-764-864-1428
US-09-912-020-355
US-09-912-020-355
US-09-923-302-612
US-09-874-138-7
US-09-874-138-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 386; DB 10;
Pred. No. 3.5e-41;
Mismatches 0;
                                                                                                                                                                                                       US-10-001-857-178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Sc
100.0%; Pr
tive 0;
10000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70; Conservative
                                                                                                        11148
11155
11156
11163
11186
1551
75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PNYSRAQQQL 70
LENGTH: 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
US-09-767-215-5
                                                                                                                                                                                                                                                                                                                                                                                         US-09-767-215-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-767-215-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            736
 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

Sequence 5, Application US/09767215
Patent No. US20020081636A1
GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

 $\alpha$ 

```
TYPE: PRT
                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                 QΥ
                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GDSFYIRVNLAMEGRAKG-ELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHGT 59
                                                                                                                                                                                                                                                                                                                                                 1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHGTI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence B. Application US/10032159A

patent No. US20020164703A1

GENERAL INFORMATION:
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Reed, John C.
APPLICANT: Reed, John C.
APPLICANT: Godzik, Adam
TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,
TITLE OF INVENTION: ENCODING UNCLEIC ACIDS, AND METHODS OF USE
FILE REFERENCE: P-LJ 5100
CURRENT APPLICATION NUMBER: US/10/032,159A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 60/257,457
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastsEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 98, Application US/09919497
Patent No. US20020106662A1
GENERAL INFORMATION
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER FILE REFERENCE: B0801/7225
CURRENT FILLNG DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US/09/919,497
PRIOR APPLICATION NUMBER: US 60/221,735
                                                                                                                                                                                                                                                                    Length 1138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.6%; Score 145; DB 9; Length 1247; 46.5%; Pred. No. 2.5e-10;
                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                              Ouery Match
100.0%; Score 386; DB 10;
Best Local Similarity 100.0%; Pred. No. 4.1e-41;
Matches 70; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Mismatches
                 CURRENT APPLICATION NUMBER: US/09/767,215
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 60/181,159
PRIOR FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
FILE REFERENCE: 07334-142001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 46.5
Matches 33; Conservative
                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-767-215-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111111111
785 PNYSRAQQQL 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 IPNYSRACOOL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PNYSRAQQQL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
US-10-032-159A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: ,1247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-919-497-98
                                                                                                                                                                LENGTH: 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-032-159A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQ
                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                          셤
```

```
.;
?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                           1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                  Length 1736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kawamura, Yukio; Morita,
Akihiro; Izumo, Koji.; Saka, Tomohide.
TITLE OF INVENTION: ANTITUMOR PROTEIN AND
GENE ENCODING SAME
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 DSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCW 41
                                                                                                                                                    Score 98.5; DB 10
Pred. No. 0.00032;
9; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/911,969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 63;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09911969
Patent No. US20020137896Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09785548 Patent No. US20020155577A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.3%;
32.5%;
              NUMBER OF SEQ ID NOS: 100
SOFWRARE: Patentin version 3.0
SEQ ID NO 98
LENCTH: 1736
                                                                                                                                                     Query Match 25.5%;
Best Local Similarity 36.2%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
PRIOR FILING DATE: 2000-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : ORGANISM: Homo sapiens US-09-785-548-4
                                                                                                  ; ORGANISM: Homo sapiens
US-09-919-497-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                      ||| :||:|
562 IPNKNRAEQ 570
                                                                                                                                                                                                                                                                                                60 IPNYSRAQO 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-911-969-4
                                                                                                                                                                                                                                                                                                                                                                                                     US-09-785-548-4
```

?

```
Gaps
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     805 FYI--NLKLKERLNEDFDHFC-----SCYQYQDGCIVWHQY-INCFTLQDLLQH 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
                                                                                                                                                                                     5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 FYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQ---GCGCWHAHRVNSYTMKDTAAH
                                                                                                                                          DB 10; Length 566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 14.8%; Score 57; DB 10; Length 1050; Best Local Similarity 28.1%; Pred. No. 35; Matches 16; Conservative 10; Mismatches 17; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                Sequence 38, Application US/09866562
Patent No. US20020009758A1
GENERAL INFORMATION:
APPLICANT: Harlocker, Susan L.
APPLICANT: Wang, Tongtong
APPLICANT: Riee, Jennifer
APPLICANT: Switzer, Anne
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER.
FILE REFERENCE: 210121:502
                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                   16 RSQGDLTSSQHEIVHFTDVFIAGSGPISCTYARHIIDNTSTTK 58
                                                                                                                                                                                   15;
                                                                                                                                                                                                                               15 RAKGELQVHCNEVLHVTDTMFQGCG---CWHAHRV--NSYTMK
                                                                                                                       14.9%; Scor.
32.6%; Pred. No. 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: ABBOTT LABORATORIES D377/AP6D STREET: 100 ABBOTT PARK ROAD CITY: ABBOTT PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/866,562
CURRENT FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 96
SEQ ID NO 38
                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: JAMES C. ERKER
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAHWAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 82, Application US/08424550B Patent No. US20020119447A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
           TYPE: amino acid
                                                                                                                                                                                     14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 60064-3500
                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-424-550B-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1050
                                                                                                                                                                                                                                                                                                                                        RESULT 8
US-09-866-562-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-866-562-38
                                                                         ;
US-09-911-969-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQ
                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                        Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kawamura, Yukio; Morita,
Akihiro; Izumo, Koji.; Saka, Tomohide.
TITLE OF INVENTION: ANTITUMOR PROTEIN AND
GENE ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 RSQGDLTSSQHEIVHFTDVFIAGSGPISCTYARHIIDNTSTTK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 RAKGELQVHCNEVLHVTDTMFQGCG---CWHAHRV--NSYTMK 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10;
PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/023,731
FILING DATE: 13-FEB-1998
APPLICATION NUMBER: JP 29275/1997
FILING DATE: 13-FEB-1997
ATORNEY/AGENT INFORMATION:

NAME: KENNETH H. SONNENFELD
REGISTATION NUMBER: 33,285
REFERENCE/DOCKET NUMBER: 3479-4000
TELEFAN: (212) 751-6849
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: MICROSOFT WORD 97
CURRENT APPLICATION NUMBER: US/09/911,969
FILING DATE: 24-Jul-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 29275/1997
FILING DATE: 13-FEB-1998
APPLICATION NUMBER: JP 29275/1997
FILING DATE: 13-FEB-1997
ATTORNEY AGENT INFORMATION:
REGISTRATION NUMBER: 33,285
REGISTRATION NUMBER: 33,389
REGISTRATION NUMBER: 33,389
TELECOMMUNICATION INFORMATION:
TELECHENDER: (212) 758-4800
TELECTAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 14.9%; Score 57.5; D Best Local Similarity 32.6%; Pred. No. 0.94 Matches 14; Conservative 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear ; MOLECULE TYPE: peptide ; SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-09-911-969-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09911969
Patent No. US20020137896A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
US-09-911-969-1
```

ò g .∵

```
RESULT 12
US-09-976-059-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-09-742-684-4
                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 FYIRVNLAME-----GRAKGELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-919-497-59

Sequence 59, Application US/09919497

Sequence 59, Application US/09919497

Sequence 59, Application US/09919497

SERBEAL INFORMATION:

APPLICANT: Mutter, George L.

TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER

FILE REFERENCE: B00801/7225

CURRENT APPLICATION NUMBER: US/09/919,497

CURRENT APPLICATION NUMBER: US 60/221,735

PRIOR APPLICATION NUMBER: US 60/221,735

PRIOR FILING DATE: 2000-07-31

NUMBER OF SEQ ID NOS: 100

SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 YVQHIWHVPDRTMFPELXCNHLXRMPCYRSNHRVGHWKGPNRSSIQK 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27; Indels
                                                      SOFTWARENT STILLING NOTION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550B
FILING DATE:
CLASSIFICATION: 435435
ATTONREY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 35.27.PC.01
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 HCNEVLHVTD-TMFQGCGCWHAHRVNSYTMKDTAAHGTIPNYSRAQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ilarity 31.9%; Score 56.5; 1
Conservative 4; Mismatcher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 54.5;
Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application US/09976059 Patent No. US20020164747A1
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 708-938-2022
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 1422 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Farnet, Chris
APPLICANT: Zazopoulos, Emmanuel
APPLICANT: Staffa, Alfredo
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 14.1%;
1 Similarity 29.6%;
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-08-424-550B-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRGANISM: Homo sapiens
US-09-919-497-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 530 FIPSKRRVERR 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 21; Conserva
                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 15; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIPNYSRAQQQ 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-09-976-059-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 59
LENGTH: 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    οp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
```

```
3
                                                                                                                                                                                                                                                                                                                                               3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Mathews, Lawrence S.
Vale, Wylie W.
Tsuchida, Kunihiro
TITLE OF INVENTION: CECPTOR(S) OF THE ACTIVIN/TGF-BETA SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                           3789 GAEVYRMYTSGSTGRPKGVVTTHQNLVDLATDT-----CWGPTPRVLFHAPHAFDASSY 3842
                                                                                                                                                                                                                                                                                                                                               Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                              1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCW------HAHRVNSY 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Zazopoulos, Emmanuel
APPLICANT: Staffa, Alfredo
TITLE OF INVENTION: Genes and Proteins for Biosynthesis of Ramoplanin
FILE REFERENCE: 3019-PCT
CURRENT APPLICATION NUMBER: US/09/976,059
CURRENT FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.0
SEQ ID NO 15
TITLE OF INVENTION: Genes and Proteins for Biosynthesis of Ramoplanin FILE REFERENCE: 3019-PCT CURRENT APPLICATION NUMBER: US/09/976,059 CURRENT FILING DATE: 2001-10-15 NUMBER OF SEQ ID NOS: 34 SOFTWARE: PatentIn version 3.0 SEQ ID NO 14 LENGTH: 4999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 4999;
                                                                                                                                                                                                                                                                                                 Length 4999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ...νπελλΕΕ: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
STATE: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 53.5; DB 9;
Pred. No. 6.2e+02;
2; Mismatches 23;
                                                                                                                                                                                                                                                                                              Score 54.5; DB 9;
Pred. No. 4.6e+02;
3; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MADDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 15, Application US/09976059; Patent No. US20020164747A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09742684 Patent No. US20010039036Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 30.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 30.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT; ORGANISM: Actinoplanes sp. US-09-976-059-15
                                                                                                                                                                                                                               ; ORGANISM: Actinoplanes sp. US-09-976-059-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Farnet, Chris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: CA
```

```
51 -- MKDTAAHGTIPNYSR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                73 LFLVDTGVSTCWPGWSR 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SITE
LOCATION: (208)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-09-925-302-696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 VNS 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KNA 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 409
                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (4)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (1)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (10)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          i,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1641, Application US/09764877

Sequence 1641, Application US/09764877

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REPERENCE: FC005

CURRENT APPLICATION NUMBER: US/09/764,877

CURRENT FILING DATE: 2001-01-17

Prior application data removed - refer to PALM or file wrapper

NUMBER OF SEQ ID NOS: 4031

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10;
                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/476,123
FILING DATE: CUNKNOWN>
APPLICATION NUMBER: 08 08/300,584
FILING DATE: 02-SEP-1994
APPLICATION NUMBER: US 07/880,220
FILING DATE: 08-MAY-1991
APPLICATION NUMBER: US 07/713,229
FILING DATE: 09-CT-1991
APPLICATION NUMBER: US 07/773,229
APPLICATION NUMBER: US 07/773,229
APPLICATION NUMBER: US 07/773,229
APTORNEY_AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 52.5; DE
Pred. No. 55;
4; Mismatches
                 APPLICATION NUMBER: US/09/742,684 FILING DATE: 19-Dec-2000 CLASSIFICATION: <unknown>
                                                                                                                                                                                                                                                                                                                                      NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9927
TELECOMMUNICATION:
TELEPHONE: 619-546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECLLE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-742-684-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       276 KGNL-VSWNELCHITETMARGLAYLH 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 KGELQVHCNEVLHVTDTMFQGCGCWH 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 510 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 4:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 13.6%;
Best Local Similarity 46.2%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-09-764-877-1641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1641
LENGTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
```

```
4
                                                                                                                                                                                                                                                                                        3;
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE LOCATION: (20)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE LOCATION: (43)
                                                                                                                  ; LOCATION: (43); ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-877-1641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-302-696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (111) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                          5 YIRVNLAMEGRAKGELQVHCN-----EVLH--VTDTMFQGCG----CWHAHR 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 696, Application US/09925302

Patent No. US2002004941A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

FILE PEFERENCE: PA104

CURRENT APPLICATION NUMBER: US/09/925,302

CURRENT APPLICATION NUMBER: PCT/US00/05918

PRIOR PELING DATE: 2000-03-08

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 896

SEQ ID NO 696

SEQ ID NO 696
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 26.0%; Pred. No. 12;
Matches 20; Conservative 8; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 409;
                                                                                                                                                                                                                                                                                                                                        4 FYIRVNLAMEGR --- AKGELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYT ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.5%; Score 52; DB 10;
illarity 27.0%; Pred. No. 49;
Conservative 10; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: January 22, 2003, 08:52:54
Job time : 3.82258 secs
```

THIS PAGE BLANK (USPTO)

```
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
```

protein - protein search, using sw model ĕ

January 22, 2003, 08:49:35 ; Search time 5.3629 Seconds (without alignments) 1254.807 Million cell updates/sec Run on:

US-09-767-215-2\_COPY\_676\_745 386 1 GDSFYIRVNLAMEGRAKGEL......MKDTAAHGTIPNYSRAQQQL 70 Perfect score:

Sequence:

283224 segs, 96134422 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

283224 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 sed Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	0	tight junction pro	(104 prote	jun		rotein -	hypothetical prote	thimet oligopeptid	3-hydroxy-3-methyl	transforming prote	transcription requ	probable retroelem	bacterio-opsin act	hypothetical prote	hypothetical prote	⊐	DNA polymerase III	microtubule-associ	hypothetical prote	hypothetical prote	D14R protein - var	hypothetical prote	_	hypothetical prote	⊂	probable sulfate a	early E2A DNA-bind	centrosome-associa
SUMMARIES	ID	T22166	A46431	146236	154378	JE0366	A47747	T13703	T00346	HYRTTH	D70185	C36365	AI3184	H84495	F84176	B83505	T23215	AI2238	G82100	A55665	E82386	T26727	A72175	T32811	JW0092	T15771	T36152	G81256	ERADA7	T13802
	н рв	!																		9										S
	Length	103,	174	77	111	116	173	136	128	99	43	50	29	41	86	22	41	54	116	989	10	16	37	77	105	86	34	38	51	109
æ	Query	7.	ė.	26.2	δ.	'n.	ď.	δ.		16.5	ď.	15.4		•	υ.	υ.	5		ď.	15.0	4	4	4	٠	4	4	4	•	₹.	14.5
	Score	105.5	102.5	101	100	100	98.5	97.5	78.5	63.5	09	59.5	59.5	59.5	59.5	59	59	58.5	58.5	58	57	57	57	57	57	56.5	26	56	26	26
	Result No.	П	7	æ	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

C;Accession: A46431 C;Accession: A46431 R;Itoh, M.; Nagafuchi, A.; Yonemura, S.; Kitani-Yasuda, T.; Tsukita, S.; Tsukita, S. J. Cell Biol. 121, 491-502, 1993 A;Title: The 220-kD protein colocalizing with cadherins in non-epithelial cells is id

A; Reference number: A46431; MUID:93252986; PMID:8486731

A; Accession: A46431 A; Status: preliminary

C;Špecies: Mus musculus (house mouse) C;Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999

tight junction-associated protein ZO-1 - mouse

A.Molecule fype: nucleic acid A.Residues: 1-1745 <1TO> A.Cross-references: GB:101440; NID:g303709; PIDN:BAA03274.1; PID:d1003784; PID:g30371 A.Experimental source: F9 cells A.Note: Sequence extracted from NCBI backbone (NCBIN:131200, NCBIP:131201) C.Superfamily: guanylate kinase homology; GLGF domain homology

C28A5.1 protein (c	hyoscyamine (68)-d	membrane glycoprot	SAR DNA-binding pr	hypothetical prote	hypothetical prote	Vif protein - Maed	spore coat protein	polyprotein - deng	5-methyltetrahydro	nonstructural prot	genome polyprotein	genome polyprotein	polyprotein - deng	titin - rabbit (fr	hypothetical prote
S43579	A40005	HLBECM	T06379	T10665	T35547	JQ1163	F69604	PQ0507	D83404	A25817	GNWVDP	GNWVJA	JS0219	S20901	T23867
N	1	Н	7	7	7	~	7	7	7	7	٦	Н	7	7	7
1223	344	368	550	855	1678	231	513	614	766	882	3388	3391	3391	6805	238
14.5	14.4	14.4	14.4	14.4	14.4	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.1
		D.	S	'n	'n.	55	55	55	52	55	55	55	55	55	54.5
26	55.5	55.	55.	52	55										54

## ALIGNMENTS

```
A;Gene: CESP:F44D12.1
A;Map position: 4
A;Introns: 46/2; 105/3; 187/3; 283/1; 365/3; 444/2; 501/2; 605/1; 688/1; 922/2; 980/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                        3
                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-1034 <WIL>
A; Cross-references: EMBL: 268298; PIDN: CAA92607.1; GSPDB: GN00022; CESP: F44D12.1
hypothetical protein F44D12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
                                                                                                                                                                                                                                                                                                                                                                                                              Length 1034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                          27.3%; Score 105.5; DB 2;
35.2%; Pred. No. 9.1e-05;
tive 12; Mismatches 31;
                                                                                                                submitted to the EMBL Data Library, December 1995
Aferference number: 219525
Aferesion: T22166
Aferesion: T22166
Afertus: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                    A; Experimental source: clone F44D12 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 27.3%
Best Local Similarity 35.2%,
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 IPNYSRAQQQL 70
                                                                       C; Accession: T22166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
A46431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

3

qq ò

```
C; Accession: A47747

K; Willott, E.; Balda, M.S.; Fanning, A.S.; Jameson, B.; Van Itallie, C.; Anderson, J. Proc. Natl. Acad. Sci. U.S.A. 90, 7834-7838, 1993

A; Title: The tight junction protein ZO-1 is homologous to the Drosophila discs-large A; Reference number: A47747; MUID:93361541; PMID:8395056
                                                                                                                                                                                                                                                                                                                                                                                                                                                    are highly cons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB:AF085184; NID:93820579; PIDN:AAC95469.1; PID:93820580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 02-Jun_1994 #sequence_revision 02-Jun-1994 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                             tight junction protein, 20-2 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               604 GDSFFIRSHFECEKETPQSLAFTRGEVFRVVDTLYDGKLGNWLAVRIGNELEK----GL 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
                                                                                GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-1736 <WIL>
A;Cross-references: GB:L14837; NID:g292937; PIDN:AAA02891.1; PID:g292938
                                                                                                                                                                                                                                                                                                                                                                              C;Accession: JE0366
R;Collins, J.R.; Rizzolo, L.J.
Blochem. Biophys. Res. Commun. 252, 617-622, 1998
A;Title: Protein-binding domains of the tight junction protein, ZO-2, A;Reference number: JE0366; MuID:99057550; PMID:9837755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: guanylate kinase homology; GLGF domain homology
C;Keywords: alternative splicing; membrane protein; phosphoprotein
F;15-94/Domain: GLGF domain homology <GLG1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.5%; Score 98.5; DB 2;
llarity 36.2%; Pred. No. 0.0012;
Conservative 9; Mismatches 32;
Pred. No. 0.00048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.9%; Score 100; DB 2; 37.7%; Pred. No. 0.0005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;181-248/Domain: GLGF domain homology <GLG2>F;416-486/Domain: GLGF domain homology <GLG3>F;633-782/Domain: guanylate kinase homology <GKI>
             39.1%; Pred. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tight junction protein 20-1 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 37.79
Matches 26; Conservative
                      Local Similarity 39.1%
nes 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1163 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPNRSRAEQ 636
                                                                                                                                                                                                 ||| |||:|
659 IPNKSRAEQ 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 IPNYSRAQQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 IPNYSRAQO
                                                                                                                                                                          60 IPNYSRAQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                        Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              628
                                                                                       Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
                                                                                                                                                                                                                                                                                    RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ρp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                       ò
                                                                                                                                g
                                                                                                                                                                             δ
                                                                                                                                                                                                                 Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                  рĭ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       two novel genes and reduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                      5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Homo sapiens (man)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C; Accession: 154378
E; Duclos, F; Rodius, F; Wrogemann, K; Mandel, J.
Hum. Mol. Genet. 3, 909-914, 1994
A; Title: The Friedrich ataxia region: characterization of two novel genes an A; Reference number: 154378; MUID:95038744; PMID:7951235
A; Rocession: 154378
A; Rollecule Type: mRNA
A; Rollecule Type: mRNA
A; Residues: 1-1116 <RES
A; Cross-references: GB:L27476; NID:9498012; PIDN:AAA61300.1; PID:9498013
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 GDSFFIRSHFECEKETPQSLAFSRGEVFRVVDTLYDGKLGHWLAVRIGNELEK----GL 243
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
                                                                                                                                                        Gaps
                                                                                                                                                                                                 1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                           Length 1745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: X104
C;Superfamily: guanylate kinase homology; GLGF domain homology
F;37-116/Domain: GLGF domain homology <GLG1>
F;731-879/Domain: guanylate kinase homology <GKI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 26.2%; Score 101; DB 2; Length 77
Best Local Similarity 39.1%; Pred. No. 0.00024;
Matches 27; Conservative 7; Mismatches 29; Indels
                                                                                                                                                        31; Indels
                                                                                                              5
                                                                                                           Score 102.5; DB 2
Pred. No. 0.00038;
9; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                          F;27-106/Domain: GLGF domain homology <GLG1>
F;428-498/Domain: GLGF domain homology <GLG3>
F;645-794/Domain: guanylate kinase homology <GKI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.9%;
                                                                                                           Query Match 26.6%;
Best Local Similarity 37.7%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene X104 protein - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 IPNKSRAEQ 252
                                                                                                                                                                                                                                                                                                                                 IPNKNRAEQ 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 IPNYSRAQQ 68
                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                      IPNYSRAQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
```

d ò g

3

Wed

protein

```
A;Accession: D70185
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-431 < KLES>
A;Cross-references: GB:AE001169; GB:AE000783; NID:92688611; PIDN:AAC67032.1; PID:9268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      including the amino end of the mature protein, were \boldsymbol{c} in testes, brain, and pituitary predominantly in a so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Note: sequence extracted from NCBI backbone (NCBIN:142522, NCBIN:142524, NCBIP:1425 A.Note: rhis report is a correction to A36165 A.Note: this report is a correction to A36165 A.Note: his report is a correction to A36165 A.Note: n. Dando, P.M.; Brown, M.A.; Barrett, A.J. Biochem. J. 309, 203-207, 1995 A.Title: Rat thingt oligopeptidase: large-scale expression in Escherichia coli and ch A; Reference number: $55999; MUID:95344370; PMID:7619057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Description: hydrolyzes peptide bonds on the carboxyl side of hydrophobic residues C; Superfamily: thimet oligopeptidase C; Keywords: hydrolase; metalloproteinase; oligopeptidase; zinc F; 2-687/Product: thimet oligopeptidase #status predicted <MAT> F; 473,477,480/Binding site: zinc (His) #status predicted <F; 474/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Note: this is an engineered sequence expressed in Escherichia coli
R;Pierotti, A.; Dong, K.W.; Glucksman, M.J.; Orlowski, M.; Roberts, J.L.
Biochemistry 29, 10323-10329, 1990
A;Title: Wolecular cloning and primary structure of rat testes metalloendopeptidase
A;Reference number: A36165, WUID:91084500; PMID:2261476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "3. hydroxy-3-methylglutaryl-CoA reductase (mvaA) homolog - Lyme disease spirochete C; Species: Borrella burgdorferi (Lyme disease spirochete)
C; Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
C; Accession: D70185
B; Fraser, C. M.; Casjens, S.; Huang, W. M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, A; Authors: Smith, H.O.; Venter, J.C.
A; Pittle: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A; Reference number: A70100; MUID:98065943; PMID:9403685
C; Species: Rattus norvegicus (Norway rat)
C; Date: 30-Sep-1992 #sequence_revision 17-Nov-1995 #text_change 07-May-1999
C; Accession: 388760, 454152; S55999; A36165
R; McKie, N.; Dando, P.M.; Rawlings, N.D.; Barrett, A.J.
Biochem. J. 295, 57-60, 1993
A; Title: Thinget oligopeptidase: similarity to 'soluble angiotensin II-binding A; Reference number: S38760; MUID:94029935; PMID:8216239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 DSFYIRVNL----AMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAA 56
                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-687 <MCK.
R; Pierotti, A.; Dong, K.W.; Glucksman, M.J.; Orlowski, M.; Roberts, J.L.
Biochemistry 33, 622, 1994
A; Reference number: A44152; MUID:94114549; PMID:8286394
A; Contents: corrections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 16.5%; Score 63.5; Di
Best Local Similarity 30.0%; Pred. No. 9.5;
Matches 18; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 320-350;578-597,'F',599-687 <PIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: significant sequence differences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Molecule type: mRNA
A Cross-references: GB:M61142
A Note: parts of this sequence,
C:Comment: This enzyme is found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-9 <MC2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A36165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: A54152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cispecies: Homo sapination (Figure 1) (Figur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thimet oligopeptidase (EC 3.4.24.15) - rat
N;Alternate names: endo-oligopeptidase A; endopeptidase 24.15; Pz-peptidase; soluble med
                                                                                                                                                                                                                                                                                                                                         C; Accession: T13703
R; Takahisa, M; Togashi, S.; Suzuki, T.; Kobayashi, M.; Murayama, A.; Kondo, K.; Miyake, Genes Dev. 10, 1783-1795, 1996
A; Title: The Drosophila tamou gene, a component of the activating pathway of extramacrod A; Reference number: 217700; MUID:96312452; PMID:8698238
A; Accession: T13703
A; Molecule type: mRNA
A; Residues: 1-1367 cTAKA
A; Residues: 1-1367 cTAKA
A; Residues: 1-1367 cTAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:D83477; NID:g1498136; PIDN:BAA11923.1; PID:g1498137 C;Genetics:
                                                                                                                                                                                                                                                     Species: Drosophila melanogaster
:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
:Accession: T13703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         498 GDSFHIKTHFHCDNPSKGEMAFKAGDVFRVIDTLHNGVVGSWQVLKIGRGHQE--MQRGV 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGC-GCWHAHRVNSYTMKDTAAHGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ٠.
ش
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 20.3%; Score 78.5; DB 2; Local Similarity 34.9%; Pred. No. 0.25; hes 22; Conservative 10; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.0012;
                                                                                                                                                                                                                     tamA protein - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 97.5; D
; Pred. No. 0.00
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein KIAA0583 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: FlyBase: FBgn0003177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 25.3%;
Best Local Similarity 31.9%;
Matches 22; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPNKSRAEE 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 IPNYSRAQQ 68
        IPNKNRAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene: tamon (tam)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1013 IPS 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 IPN 62
        295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

Wh Vu B.

3,

Wed Jan 22 10:56:43

```
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cidate: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
CiAccession: H84495
Riini, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, Nature 402, 761-768, 1999
A;Tille: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID: 20083487; PMID: 10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dacterio-opsin activator-like protein [imported] - Halobacterium sp. NRC-1 C;Species: O2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 R;My W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasi E,My W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pon, M.; Shukla, H.D.; Lasi E,My W.V.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jung, K.H.; Alam, M.; Freitas, T. M.; Falam, M.; Freitas, T. M.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M. A;Reference number: A84160; MUID:20504483; PMID:11016950 A;Accession: F84176 A;Accession: F84176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GB: AE004437; NID: 910579808; PIDN: AAG18778.1; GSPDB: GN00138
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: GB: AE002093; NID: 94263646; PIDN: AAD15368.1; GSPDB: GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 LMAQGNFKKPKCTHCNRIGHTVDKCYK-------VHGYPPGHPRANQQ 342
1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMF----QGC---GCWHAHRVNSYTMKD 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 LAMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHGTIPNYSRAQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                               236 GLGIVVLPVFMVQESLASGDLEEVVPGYSHAGADL 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 59.5; DB Pred. No. 17; 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 59.5;
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.4%;
25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-411 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Accession: H84495
A, Status: preliminary
A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225 IRAFGTI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 TAAHGTI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: At2g11140
A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                              49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
                                                                                                                                                                                                                                         RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
                                 g
                                                                                          Qγ
                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                        transforming protein homolog MRAS3 - Rhizomucor racemosus
C;Species: Rhizomucor racemosus
R;Casale, W.L.; McConnell, D.G.; Wang, S.Y.; Lee, Y.J.; Linz, J.E.
Mol. Cell. Biol. 10, 6654-6654. 1990
A;Title: Expression of a gene family in the dimorphic fungus Mucor racemosus which exhib
A;Reference number: A36365; MUID:91061774; PMID:1701021
A;Recession: C36365
A;Recession: C36365
A;Recession: C36365
A;Recession: G8:M55177
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Reywords: GFP binding; nucleotide binding; P-loop
F;11-126/Domain: translation elongation factor Tu homology
F;11-126/Megion: GTP-binding motif
F;123-126/Region: GTP-binding NKXD motif
F;133-125/Region: GTP-binding SkK/L motif
F;133-125/Region: GTP-binding skK/L motif
F;23,24,42,123,124,126,125,Hinding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transcription regulator, LysR family Atu5206 [imported] - Agrobacterium tumefaciens (str
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C;Accession: A13184
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ster, E.W.
A.Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                         ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE008687; PIDN:AAL45895.1; PID:g17743640; GSPDB:GN00188 A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48
                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37;
                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 15.4%; Score 59.5; DB 2; Length 206; Best Local Similarity 37.0%; Pred. No. 8.2; Matches 17; Conservative 6; Mismatches 12; Indejs 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 299;
                                                               Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 MEGRAK----GELQVHCNEVLHVTDTM---FQGCGCWHAHRVNS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 DSFY----IRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Genome: plasmid
C;Superfamily: conserved hypothetical protein HI1364
                                                               Match 15.5%; Score 60; DB 2; Local Similarity 38.5%; Pred. No. 16; les 10; Conservative 7; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 15.4%; Score 59.5; Di
Best Local Similarity 25.3%; Pred. No. 12;
Matches 24; Conservative 10; Mismatches
                                                                                                                                                                                                                    10 LAMEGRAKGELQVHCNEVLHVTDTMF 35
         A; Experimental source: strain B31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-299 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: AI3184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: Atu5206
                                                               Query Match
                                                                                                 Best Loca
Matches
                                                                                                                                                                                                                                         366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ř
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                         qq
                                                                                                                                                                                     á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
```

ä

Ebhardt, H.; Lowe, T.M.;

ë

Gaps

```
B83505
hypothetical protein PA1118 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: B83505
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Vuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathch, Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: B83505
A;Status: pre-liminary
A;Molecule type: DNA
A;Residues: 1-227 <STO>
A;Cross-references: GB:AE004542; GB:AE004091; NID:99947034; PIDN:AAG04507.1; GSPDB:GN001
C;Genetics:
A;Gene: PA1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 15.3%; Score 59; DB 2; Length 227; Best Local Similarity 28.8%; Pred. No. 10; Matches 17; Conservative 7; Mismatches 33; Indels
```

Search completed: January 22, 2003, 08:54:42 Job time : 8.3629 secs

Qy Db

4 FYIRVNLAMEGRAKGELQVH--CNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHGTI 60

THIS PAGE BLANK (USPTO)

```
5.1.3
Compugen Ltd.
version :
GenCore
Copyright (c) 1993
```

- protein search, using sw model OM protein

January 22, 2003, 08:49:35 ; Search time 2.72849 Seconds (without alignments) 1064.082 Million cell updates/sec Run on:

US-09-767-215-2\_COPY\_676\_745 Title: Perfect score:

1 GDSFYIRVNLAMEGRAKGEL...........MKDTAAHGTIPNYSRAQQQL 70 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 Total number of hits satisfying chosen parameters:

112892 segs, 41476328 residues

Searched:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

;		æ			SUMMARIES	
ult No.	Score	Query	Length	DB	ID	Description
1	386	100.0	1004	٦	CARE_HUMAN	Q9bx16 homo sapien
7	283.5		666	٦	CARE_MOUSE	O mus m
m	146		1147	Н	CARB_HUMAN	Q9bx17 homo sapien
4	116	30.1	1032	٦	CARA_HUMAN	7 пото
5	106		1021	-	CARA_MOUSE	mus m
9	105		905	Н	ZO3_MOUSE	mus
7	102.5		1745	Н	ZO1_MOUSE	P39447 mus musculu
œ	101		1174	Н	ZOZ_CANFA	Q95168 canis famil
0	100		1190	Н	ZOZ_HUMAN	Q9udy2 homo sapien
10	66		1167	Н	ZO2_MOUSE	mus n
11	98.5		1736	٦	ZO1_HUMAN	Q07157 homo sapien
12	96.5		933	Н	ZO3_HUMAN	homod
13	94.5		868	-	ZO3_CANFA	canis
14	63.5		989	Н	MEPD_RAT	
15	62.5		664	Н	EMAP_LYTVA	Q9y1c1 lytechinus
16	62.5		724	7	DLG4_MOUSE	
17	9		431	Н	HMDH_BORBU	O51628 borrelia bu
18	59.5		202	Н	RAS3_RHIRA	
19	59		415	٦	BCAT_CAEEL	m
20	58.5		1159	Н	DP3A_VIBCH	P52022 vibrio chol
71	28	•	989	-	EMAP_STRPU	~
22	28		1227	7	C1BE_BACTU	bacillus
23	58		1229	-	C1BB_BACTU	bacillus
24	58		1231	П	C1BD_BACTZ	Q9zaz5 bacillus th
22	57		1050	-	BU1B_HUMAN	O60566 homo sapien
56	26	14.5	517	7	DNB2_ADE07	P04497 human adeno
27	26	14.5	1174	-	C1EB_BACTA	Q03745 bacillus th
28	55.5	14.4	344	Н	HY6H_HYONI	7
29	55.5	14.4	368	7	VGH3_HCMVA	0
30	55	14.2	513	-	COTA_BACSU	~
31	52	•	531	7	NXF3_HUMAN	Q9h4d5 homo sapien
32	52	٠	166	7	METE_PSEAE	1703
33	22	14.2	1683	-	POLG_DEN2T	P27914 dengue viru

P12823 d genome po P07564 d genome po P14340 d genome po P04980 escherichia Q91681 salmonella P78352 homo sapien P22990 d genome po P22991 d genome po P22991 d genome po P27270 tomato yell P45813 mycobacteri OS8498 pyrococcus	343000000000000000000000000000000000000
POLG_DENZP POLG_DENZJ POLG_DENZN REP_ECOLI REP_ECOLI REP_SALTY DLG4_HUMAN POLG_DENZ YV1_TYLCM RS13_MYCBO TY 762_PYRHO TY 762_PYRHO TY 502_PYRHO TY 502_PYRHO	
	4
3388 3391 3391 674 674 767 3391 115 115 123 243	)
113.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	
000 000 000 000 000 000 000 000 000 00	
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	

## ALIGNMENTS

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -:- SUBCELLULAR LOCATION: Cytoplasmic.
-:- TISSUE SPECIFICITY: Expressed in placenta. Also detected in HeLa SI cells, but not in the other cancer cell lines tested.
-:- SIMILARITY: CONTAINS I CARD DOMAIN.
-:- SIMILARITY: CONTAINS I PDZ/DHR DOMAIN.
-:- SIMILARITY: CONTAINS I GANNYLAFE KINASE-LIKE DOMAIN.
-:- CAUTION: SUPPosed to contain a SH3 domain which is not detected by PROSITE, Pfam or SMART.
                                                O9BXIG; O9BVB5;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 14 (CARD-containing MAGUK protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=21255663; PubMed=11356195;
Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.;
"Carmal, a CARD-containing binding partner of Bc110, induces Bc110
phospporylation and NE-kappaB activation.";
FEBS Lett. 496:121-127(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.; FEBS Lett. 505:198-198(2001).
                                                                                                                                                                                                                                                      [1]
MEDLINE=21192234; PubMed=11278692;
MEDLINE=21192234; PubMed=11278692;
MEDLING=21192234; PubMed=11278692;
METLIN J., Wang L., Guo Y., Jacobson M.D., Poyet J.-L.,
Srinivasula S.M., Merriam S., DiStefano P.S., Alnemri E.S.;
"CARD11 and CARD14 are novel caspase recruitment domain
(CARD)/membrane-associated guanylate kinase (MAGUK) family members
that interact with BCIIO and activate NF-kappaB.";
J. Biol. Chem. 276:11877-11882(2001).
                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                     1004 AA
                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [4]
SEQUENCE OF 1-740 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Cervix, and Colon;
                                     STANDARD;
                                                                                                                                                            CARD14 OR CARMA2.
                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                             2) (Carma 2)
                                     CARE_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERRATUM.
                  CARE_HUMAN
RESULT 1
```

```
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O9BXL7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARB_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A PACA CONTRACT OF THE PROPERTY OF THE PROPERT
qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 14 (Bcl10-interacting MAGUK protein
                                                                                                                                                                                                                                                                                                                                                                                                                                 GUANYLATE KINASE.
DYEASEPLFKAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYKRLLQDLEAK -> SRARPLLSPGLLMGTVAAGGVTQAD
FTSPRRCRSTLGWASALSWADVKRSAHL (IN REF. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           676 GDSFYIRVNLAMEGRAKGELOVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHGTI 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Bimpl, a MAGUK family member linking protein kinase C activation to Bcll0-mediated NF-kappa B induction."; J. Biol. Chem. 276:30589-30597(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDSFYIRVNLAMEGRAKGELOVHCNEVLHVTDTMFOGCGCWHAHRVNSYTMKDTAAHGTI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Benito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: Activates NF-kappaB via Bcl10 and IKK.
-:- SUBUNIT: CARD14 and Bcl10 bind to each other by CARD-CARD interaction (By similarity).
-:- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-:- SIMILARITY: CONTAINS 1 CARD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-21381892; PubMed-11387339;
MCAllister-Lucas L.M., Inohara N., Lucas P.C., Ruland J., Ber
Li Q., Chen S., Chen F.F., Yamaoka S., Verma I.M., Mak T.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7469BBB56BE06073 CRC64;
                                                                                                                                                                                                                                                                                                                                                                     CARD. (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 386; DB 1;
Pred. No. 4.2e-40;
0; Mismatches 0;
                                                                                                                                                                                                                                                          PROSITE; PS50209; CARD; 1.
PROSITE; PS50209; GANULATE_KINASE_1; FALSE_NEG.PROSITE; PS50052; GUANULATE_KINASE_2; 1.
PROSITE; PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH01326
                                                                                                      EMBL; AY032927; AAK54453.1; -.
EMBL; BC018142.2; AAH8142.1; -.
EMBL; BC001336; AAH01326.1; ALT_INIT.
INTERPRO; IPR000619; Guanylate_Kin.
INTERPRO; IPR001478; PDZ.
SMART; SM00072; GUKC; 1.
SMART; SM0028; PDZ; 1.
                                                                                    EMBL; AF322642; AAG53403.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 82-743 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1004 AA; 113299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 100.0
Watches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11111111
736 PNYSRAQQQL 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PNYSRAQQQL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;

 (Bimp2).
 CARD14 OR BIMP2.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Breast;
                                                                                                                                                                                                                                                                                                                                                 Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARE_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Li Q., Che
Nunez G.;
                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q99KF0;
                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
-!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
-!- SIMILARITY: CONTAINS 1 GUANYLATE KINASE-LIKE DOMAIN.
-!- CAUTION: Supposed to contain a SH3 domain which is not detected by PROSITE, Pfam or SMART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHGTI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=21255663: PubMed=11356195; Gaide O., Hartinon F., Micheau O., Bonnet D., Thome M., Tschopp J.; Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.; Carmal, a CARD-containing binding partner of Bcll0, induces Bcll0 phosphorylation and NF-kappaB activation."; FEBS Lett. 496:121-127(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21192234; PubMed=11278692; MEDLINE=21192234; PubMed=11278692; M. Warg L., Guo Y., Jacobson M.D., Poyet J.-L., Srinivasula S.M., Merriam S., Distefano P.S., Alnemri E.S.; "CARDII and CARDI4 are novel caspase recruitment domain CARDI4 are ssociated quanylate kinase (MAGUK) family members that interact with Bcll0 and activate NF-kappaB."; J. Biol. Chem. 276:11877-11882(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      743 QAQQQLLA -> HLLEDHRS (IN REF. 2)
113496 MW; D18350DA12430255 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 11 (CARD-containing MAGUK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARD. (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 283.5; DB Pred. No. 2.3e-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GUANYLATE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1147 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFam; PF00595; PDZ; 1.
PROSTTE; PS50209; CARD; 1.
PROSTTE; PS00866; GUAN'LATE_KINASE_1;
PROSTTE; PS50052; GUAN'LATE_KINASE_2;
PROSITE; PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDZ.
                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF363457; AAK60137.1; -. EMBL; BC004692; AAH04692.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.48;
75.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107
411
655
986
743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                732 PNYSQAQQQL 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    999 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PNYSRAQQQL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3) (Carma 1).
CARD11 OR CARMA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARB_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local 9
```

```
SEQUENCE FROM N.A.
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
                                                                             Interaction.

-1. SUBCELLUIAR LOCATION: Cytoplasmic.
-1. SUBCELLUIAR LOCATION: Cytoplasmic.
-1. TISSUE SPECIFICITY: Detected in adult peripheral blood leukocytes, thymus, spleen and liver. Also found in promyelocytic leukemia HL-60 cells, chronic myelogenous leukemia K562 cells, Burkitt's lymphoma Raji cells and colorectal adenocarcinoma SW480 cells. Not detected in HeLa S3, Molt-4, A549 and G431 cells.
-1. SIMILARITY: CONTAINS 1 CARD DOMAIN.
-1. SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
-1. SIMILARITY: CONTAINS 1 GANVIDHE KINASE-LIKE DOMAIN.
-1. CAUTION: Supposed to contain a SH3 domain which is not detected by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARA_HUMAN STANDARD; PRT; 1032 AA.
09BMT7; Q9UGRE; Q9Y3H0;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 10 (CARD-containing MAGUK protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GDSFYIRVNLAMEGRAKG-ELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHGT 59
                       Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J., FEBS Lett. 505:198-198(2001).
-!- FUNCTION: Activates NF-KappaB via Bcll0 and IKK. Stimulates the phosphorylation of Bcll0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human),
Sukaryota i Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                         Length 1147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 103 CARD.
123 442 COILED COIL (POTENTIAL).
673 748 PDZ.
966 1131 GUNYLATE KINASE.
808 808 P -> L (IN REF. 2).
1147 AA; 132641 MW; 913A4B015D2B36CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50209; CARD; 1.
PROSITE; PS50209; CARD; 1.
PROSITE; PS500856; GUANYLATE_KINASE_1; FALSE_NEG.
PROSITE; PS50106; GUANYLATE_KINASE_2; FALSE_NEG.
PROSITE; PS50106; PD2; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.8%; Score 146; DB 1; 46.5%; Pred. No. 3.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                      Genew; HGNC:16393; CARDII.'
InterPro; IPR0000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
SMART; SM00228; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                             EMBL; AF322641; AAG53402.1; -.
                                                                                                                                                                                                                     PROSITE, Pfam or SMART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 46.5
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||:|||||| |
825 IPSYSRAQQLL 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 IPNYSRAQQQL 70

 (Carma 3).
 CARD10 OR CARMA3.

                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
          ERRATUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARA_HUMAN
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
RAM Wang L. COOK Y. Nanng W.-J., Ke X. Poyet J.-L., Manji G.A.,
RAM Wang L. COOK Y. Nanng W.-J., Ke X. Poyet J.-L., Manji G.A.,
RAM Wang L. COOK Y. Nanng W.-J., Ke X. Poyet J.-L., Manji G.A.,
RAM Wang L. COOK Y. Nanng W.-J., Ke X. Poyet J.-L., Manji G.A.,
RAM WANG L. COOK Y. Nanng W.-J., Ke X. Poyet J.-L., Manji G.A.,
RAM WANG L. CALLOR Space Fearly Mander that Interacts with Boilio and activates
R. J. BIOL Chem. 276:12465-124662001).
RAM Gaide O. Martinon F. Micheau O., Bonnet D., Thome M., Tschopp J.;
RAM Gaide O., Martinon F. Micheau O., Bonnet D., Thome M., Tschopp J.;
RERATUM.
RERRATUM.
RERRATUM.
RERRATUM.
REMANTH.
RERRATUM.
REMANTH.
RERRATUM.
RAM WASHING F. WANG-11366195; Buskiewich R., Beare D. M.,
RAM WANG C. WASHINON F. W. Colle C. C., Collier R. E., Connor R.,
RAM BENGINES. C. Binkey S. E., Bitdgeam A. M. Buck D., Micheau G.,
RAM BENGINES. C. Binkey S. E., Bitdgeam A. M. Buck D.,
RAM BENGINES. C. Binkey S. E., Bitdgeam A. M. Buck D.,
RAM BENGINES. C. Binkey S. E., Bitdgeam A. M. Buck D.,
RAM BENGINES. C. Binkey S. E., Bitdgeam A. M. Buck D.,
RAM BENGINES. C. Binkey S. E., Bitdgeam A. M. Buck D.,
RAM BENGINES. C. Binkey S. E., Bitdgeam A. M. Buck D.,
RAM BENGINES. C. Binkey S. E., Bitdgeam A. M. Buck D.,
RAM BENGINES. C. Binkey S. E., Riddgeam A. M. Buck D.,
RAM BENGINES. C. Binkey S. E., Riddgeam A. M. Buck D.,
RAM BENGINES. C. Binkey S. E., Riddgeam A. M. Buck D.,
RAM BENGINES. C. Binkey S. E., Riddgeam A. M., Buck D.,
RAM BENGINES. C. Binkey S. E., Riddgeam A. M., Buck D.,
RAM BENGINES. C. Binkey S. E., Riddgeam A. M., Buck D.,
RAM BENGINES. C. Binkey S. E., Riddgeam A. M., Buck D.,
RAM BENGINES. C. Binkey S. E., Riddgeam A. M., Buck D.,
RAM BENGINES. C. Binkey S. E., Riddgeam A. M., Buck D.,
RAM BENGINES. C. Binkey S. E., Riddgeam A. M., Buck D.,
RAM BENGINES. C. Binkey S. E., Riddgeam A. M., Buck D.,
RAM BENGINES. C. Binkey S. E., Riddgeam A. M., Buck D.,
RAM BENGINES. C. Binkey S. E., Riddgeam A. M., Buck D.,
RAM BENGINES. C. Binkey S. E., Riddgeam A. M., Buck D.,
RAM BENGINES. C. Binkey S. E., R
```

```
coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZO3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sest Local
                                                                                                                                                                                                                                                                                        Coiled
                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
203_MOUSE
1D 203_MOUSE
203_MOUSE
DT 16-0C
DT 16-0C
DT 15-JU
DE TIGHT
OS MANS M
OS M
OS 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         755
Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ōλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qγ
                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 10 (Bcl10-interacting MAGUK protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interaction. They both participate in a complex with MALT1, where MALT1 binds to Bcllo.
-!- TISSUE SPECIFICITY: Highly expressed in kidney, heart followed by brain, lung, liver, skeletal muscle and testis.
-!- SIMILARITY: CONTAINS 1 CARD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                   CAUTION: Supposed to contain a SH3, a PDZ and a guanylate kinase-
like domain. But none of these 3 domains are detected by PROSITE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 DSFYIRVNLAMEGRAKGE-LQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHGTI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
MEDLINE=21391892; PubMed=11387339;
MCAllister-Lucas L.M., Inohara N., Lucas P.C., Ruland J., Benito A., Li Q., Chen S., Chen F.F., Yamaoka S., Verma I.M., Mak T.W., Nunez G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Binpl, a MAGUK family member linking protein kinase c activation to Bcl10-mediated NF-kappa B induction.", biol. Chem. 276:30589-30597(2001).
-!- FUNCTION: Activates NF-kappaB via Bcl10 and IKK.
-!- FUNCTION: Activates NF-kappaB via Bcl10 and IKK.
                                                            Pfam or SMART.
CAUTION: Ref.4 sequence differs from that shown due to various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                                                                          Length 1032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q -> R (IN REF. 4),
K -> KQ (IN REF. 4; CAB63075).
R -> L (IN REF. 4),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             > L (IN REF. 4).
8377319AB82A0949 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARD.
COILED COIL (POTENTIAL).
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.1%; Score 116; DB 1;
40.0%; Pred. No. 1.6e-06;
tive 11; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1021 AA.
SIMILARITY: CONTAINS 1 CARD DOMAIN.
                                                                                                                                                                                                                                                                                                     EMBL, AY028896; AAK26165.1; -.
EMBL, AX032928; AAK54454.1; -.
EMBL; AL049851; CAB63075.1; ALT_SEQ.
EMBL, AL049851; CAB63076.1; ALT_SEQ.
EMBL, AL022315; CAB42832.1; ALT_SEQ.
PROSITE; PS50209; CARD; 1.
                                                                                                       gene identification problems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115946 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1115
456
574
289
917
932
                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 11
138 45
567 57
289 26
917 91
932 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PNYSRAQQQL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;

    (Bimpl).
    CARD10 OR BIMPl.

                                                                                                                                                                                                                                                                                                                                                                                                                                      coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARA_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
CARA_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,
,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- CAUTION: Supposed to contain a SH3, a PDZ and a guanylate kinase-
like domain. But none of these 3 domains are detected by PROSITE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 DSFYIRVNLAMEGRAKGE-LQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHGTI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
15-UN-2002 (Rel. 41, Last annotation update)
Tight junction protein ZO-3 (Zonula occludens 3 protein) (Zona occludens 3 protein) (Tight junction protein 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.5%; Score 106; DB 1; Length 1021; 37.1%; Pred. No. 2.7e-05; Live 12; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 POLY-SER.
114413 MW; 4811A09BDB8F792C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         CARD. COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     905 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P31016; 1BFE.
MGD; MGI:1351650; Tjp3.
InterPro; IPR000619; Guanylate_kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=BALB/c;
MEDLINE=20069797; Pubmed=10601346;
                                                                                                                                                                                                                                                                                                                                                 EMBL; AF363456; AAK60136.1; -. PROSITE; PS50209; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF157006; AAF24175.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                         115
450
565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                558 56
1021 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||| ||||||
|PNYQRAQQLL 764
                                 like domain. Bu
Pfam or SMART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PNYSRAQQQL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
```

Wed Jan 22 10:56:43 2003

```
1430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                        1242 124
1424 143
1745 AA;
                                                                                                                                                                                                                                                                                                                                       Sest Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                     ||| :||:|
574 IPNKNRAEQ 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                         60 IPNYSRAQQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZOZ_CANFA
Q95168;
                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZOZ_CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
  ò
                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                         Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                     3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: CONTAINS 1 GUANYLATE KINASE-LIKE DOMAIN.
SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                        26
                                                                                                                                                                                                                       1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAA----
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Itoh M., Nagafuchi A., Yonemura S., Yasuda-Kitani T., Tsukita S., Tsukita S.; "The 220-kD protein colocalizing with cadherins in non-epithelial
                                                                                                                                                                                27.2%; Score 105; DB 1; Length 905; 37.2%; Pred. No. 3.2e-05; ive 8; Mismatches 29; Indels 12;
                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
1fight junction protein ZO-1 (Zonula occludens 1 protein) (Zona cocludens 1 protein) (Tight junction protein 1).
                                                                                                                                         SH3.
GUANYLATE KINASE.
(; B787BA1592661FEE CRC64;
        InterPro; IPR001452; SH3.
Pfam; PF00595; PD2; 3.
Pfam; PF00625; Guanylate_kin; 1.
SMART; SM0072; GuKc; 1.
SMART; SM00328; PD2; 3.
SMART; SM0326; SH3; 1.
PROSITE; PS50055; GUANYLATE_KINASE_1; FALSE_NEG.
PROSITE; PS50002; GUANYLATE_KINASE_2; 1.
PROSITE; PS50002; SH3; FALSE_NEG.
                                                                                                       Tight junction; SH3 domain; Repeat; Membrane.
DOMAIN 11 93 PD2 1.
PD2 2.
DOMAIN 368 434 PDZ 3.
                                                                                                                                                                                                                                                                                                                             PRT; 1745 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93252986; PubMed=8486731;
                                                                                                               93 PD
264 PD
434 PD
540 SH
754 GU
                                                                                                                                                                                                                                                                      | ||| |||:|
522 DLREQERGVIPNQSRAEQ 539
                                                                                                                                                                                                                                                          57 -----HGTIPNYSRAQQ 68
                                                                                                                                                                                Ouery Match 27.29
Best Local Similarity 37.2
Matches 29; Conservative
InterPro; IPR001478; PDZ
                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                  368 4
467 5
654 7
905 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                            ZO1_MOUSE
                                                                                                                                                               SEQUENCE
                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                        염
                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                             염
```

```
;
;
modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  516 GDSFYIRTHFEYEKESPYGL,SFNKGEVFRVVDTLYNGKLGSWLAIRIGKNHKE--VERGI 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94179414; PubMed-8132716;
Jesaitis L.A., Goodenough D.A.;
"Molecular characterization and tissue distribution of ZO-2, a tight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96421547; PubMed=8824195;
Beatch M., Jesaitis L.A., Gallin W., Goodenough D.A., Stevenson B.I. The tight junction protein Zo-2 contains three PDZ (PSD-95/Discs-Large/ZO-1) domains and an alternatively spliced region.";
J. Biol. Chem. 271:25723-25726(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Čhordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ٠.
ښ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tight junction protein ZO-2 (Zonula occludens 2 protein) (Zona cocludens 2 protein) (Tight junction protein 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 102.5; DB 1; Length 1745; Pred. No. 0.00013; 9; Mismatches 31; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C3DA2C0A9F411F66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00856; GUANYLATE_KINASE_1; FALSE_NEG PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GUANYLATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeat; Membrane.
PDZ 1.
PDZ 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1174 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY - PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-PRO
                                                                                                                                     PIR; A46431; A46431.
HSSP; P31016; 1BE9.
MGD: 98759; Typ1.
InterPro: IPR000619; Guanylate_kin.
InterPro: IPR001478; PDZ.
InterPro: IPR001452; SH3.
InterPro: IPR001906; ZU5.
Pfam; PP00018; SH3; 1.
Pfam; PP00018; SH3; 1.
Pfam; PP00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194710 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.68;
37.78;
                                                                                                                 EMBL; D14340; BAA03274.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tight junction; SH3 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00791; 2U5; 1.
SMART; SW00072; GUKC; 1.
SMART; SW00228; PD2; 3.
SMART; SW00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50106; PDZ; 3
PROSITE; PS50002; SH3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
```

```
SEQUENCE FROM N.A. (ISOFORM A1).
  3
                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                     PRODUCED BY ALTERNATIVE SELECTION.
-!- SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: CONTAINS 1 GH3 NAVATE KINASE-LIKE DOMAIN.
-!- SIMILARITY: BELONGS TO THE MANALET SMILLS OF CELL JUNCTION PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cuno. Suppressor procein: , , , , Cell Biol. 124:94-961(1994).
-!- FUNCTION: PLAYS A ROLE IN TIGHT JUNCTIONS AND ADHERENS JUNCTIONS.
-!- SUBGNIT: INTERACTS WITH OCCLUDIN.
-!- SUBCELLULAR LOCATION: PERTPHERAL MEMBRANE. CYTOPLASMIC SIDE.
-!- ALTERNATIVE PRODUCTS: Z ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat; Membrane; Alternative splicing. PDZ 1. PDZ 2. PDZ 3.
  junction protein homologous to ZO-1 and the Drosophila discs-large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202_HUMAN STANDARD; PRT; 1190 AA. O9UDVD; 099839; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 1fight junction protein ZO-2 (Zonula occludens 2 protein) (Zona occludens 2 protein) (Tight junction protein ZO-2 (Zonula occludens 2 protein) (Tight junction protein ZO-2 (Zonula occludens 2 protein) (Tight junction protein ZO-2 (Zonula occludens 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MW; 45AB836BBDDB1226 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 101; DB 1; Le
Pred. No. 0.00013;
7; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00856; GUANYLATE_KINASE_1; FALSE_NEG. PROSITE; PS50052; GUANYLATE_KINASE_2; 1. PROSITE; PS50106; PDZ; 3. PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GUANYLATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 0.00 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
InterPro; IPR001452; SH3.
Ffam: PF00018; SH3; 1.
Pfam: PF00555; PDZ; 3.
Pfam: PF00625; Guanylate_kin; 1.
SWART; SW00072; GuK; 1.
SWART; SW00228; PDZ; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-GLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    493 574
588 653
680 860
1146 1149
1174 AA; 132085 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.2%;
39.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L27152; AAC37332.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tight junction; SH3 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 39.1 ies 27; Conservative
                          tumor suppressor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P31016; 1BE9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||| |||:|
643 IPNKSRAEQ 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 IPNYSRAQQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
    NA THE TERM NA THE PRESENTATION OF THE TERM NA THE TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).

C. -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; A1 (SHOWN HERE), C1, A2 AND C2;

ARE PRODUCED BY ALTERNATIVE SPLICING AND ALTERNATIVE INITIATION.

C. -!- TISSUE SPECIFICITY: THIS PROTEIN IS FOUND IN EPITHELIAL CELL
JUNCTIONS. ISOFORM A1 IS ABUNDANT IN THE HEART AND BRAIN WHEREAS

C. ISOFORM C1 IS EXPRESSED AT HIGH LEWEL IN THE KIDNEY, PANCREAS,
HEART AND PLACENTA. IN BRAIN AND SKELETAL MUSCLE, ONLY ISOFORM A1

IS DETECTABLE. ISOFORM C1 IS FOUND IN NORMAL AS WELL AS IN MOST

ON NORMAL TISSUE.

IN NORMAL TISSUE.

-!- SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.

-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

-!- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.

-!- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION 1086

ONWARD DUE TO A FRAMESHIFT.
                                                                   Duclos F., Rodius F., Wrogemann K., Mandel J.L., Koenig M.; "The Friedreich ataxia region: characterization of two novel genes and reduction of the critical region to 300 kb."; Hum. Mol. Genet. 3:909-914(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlenski A., Ketels K.V., Korovaitseva G.I., Talamonti M.S., Oyasu R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scarpelli D.G.; "Organization and expression of the human zo-2 gene (tjp-2) in normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlenski A., Ketels K.V., Engeriser J.L., Talamonti M.S., Tsao M.-S., Koutnikova H., Oyasu R., Scarpelli D.G.; "Zo-2 gene alternative promoters in normal and neoplastic human pancreatic duct cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Aortic smooth muscle;
Adams L.D., Werny I., Schwartz S.M.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PLAYS A ROLE IN TIGHT JUNCTIONS AND ADHERENS JUNCTIONS.
-!- SUBBUNIT: INTERACYS WITH OCCUDIN.
-!- SUBGELLULAR LOCATION: PERIPHERAL MEMBRANE, CYTOPLASMIC SIDE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99287578; PubMed=10360833; Chlenski A., Ketels K.V., Tsao M.-S., Talamonti M.S., Anderson M.R., Oyasu R., Scarpelli D.G.; "Tight junction protein Zo-2 is differentially expressed in normal pancreatic ducts compared to human pancreatic adenocarcinoma."; Int. J. Cancer 82:137-144(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-104 FROM N.A. (ISOFORMS A1 AND C1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARTIAL SEQUENCE FROM N.A. (ISOFORMS A1 AND C1).
                                                                                                                                                                                                                                                                                               FROM N.A. (ISOFORMS A1; C1; A2 AND C2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochim. Biophys. Acta 1493:319-324(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, L27476; AAA61300.1; ALT_FRAME.
EMBL, AF177533; AAD20387.2; -.
EMBL, AF043195; AAD20387.2; JOINED.
EMBL, AF043196; AAD20387.2; JOINED.
EMBL, AF043197; AAD20387.2; JOINED.
EMBL, AF17518; AAD20387.2; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Pancreas;
MEDLINE=99426875; PubMed=10495427;
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20472048; PubMed=11018256;
FISSUE=Brain;
MEDLINE-95038744; PubMed=7951235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Int. J. Cancer 83:349-358(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1047-1167 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neoplastic tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Pancreas;
                                                                                                                                                                                                                                                                                                                                                 TISSUE=Pancreas;
                                                                                                                                                                                                                                                                                                    SEQUENCE
```

```
JOINED.
JOINED.
JOINED.
                                                                                                                                                                    JOINED.
                                                                                                                                                                                           JOINED.
JOINED.
JOINED.
JOINED.
JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                        JOINED.
JOINED.
JOINED.
JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                                                                           JOINED.
JOINED.
                     JOINED.
JOINED.
JOINED.
JOINED.
JOINED.
JOINED.
                                                             JOINED.
                                                                                                      JOINED.
                                                                                                                 JOINED.
                                                                                                                                                    JOINED.
                                                                                                                                                                                                                                                                                                                  JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                        Genew; HGNC:11828; TJP2.
InterPro; IPR000161; Guanylate_kin.
InterPro; IPR001478; PDZ.
InterPro; IPR001452; SH3.
                                                                                     JOINED.
                                                                                                                                                                                                                                                                                                                                                          AAD56219.2; JOINED AAD56219.2; JOINED
                                                                                                                                                                                                                                                                                                              JOINED
                                                                                                                                                                                                                                                                                                                                                                      AAD56219.2; JOINED AAD56219.2; JOINED
                                                                          JOINED
                                                                                                                                                               JOINED
                                                                                                                                                                                                                                                                                                                                               AAD56219.2;
                                                                                                                                                                                                                                                                                                  AAD56219.2;
                                                                                                                                                                                                                                                                                                                                                                                             U84581; AAB41794.1;
                                                                                                                                                                                                                            AAD56218.
                                                                                                                                                                                                                                                                                                                  AAD56219.
                                                                                                                                                                                                                                                                                            AAD56219.
                                                                                                                                                                                                                                                                                                              AAD56219.
                                                                                                                                                                                                                                                                                                                                          AAD56219.
                                                                                                                                                                                                                                                               AAD56218.
                                                                                                                                                                                                                                                                     AAD56218.
                                                                                                                                                                                                                                                                                      AAD56219.
                                                                                                                                                                                                                                                                                                                              AAD56219.
                                                                                                                                                                                                                 AAD56218.
                                                                                                                                                                                                                                         AAD56218.
                                                                                                                                                                                                                                                    AAD56218
                                                                                                                                                                                                                                                         AAD56218.
                                                                                                                                                                                                                                                                                 AAD56218.
                                                                                                                                                                                                                                                                                                       AAD56219.
                                                                                                                                                                                                AAD56218
                                                   AAD20387
                                                                    AAD20387
                           AF177524;
AF177525;
                                                                                                                                                                                                                                                                                                                                                                 AF177528;
                       AF177523;
                                                             AF177530;
                                                                   AF177531;
                                                                                                                                                                                                 AF043196;
                                                                                                                                                                                                                                                                                                  AF043197;
                                                                                     AF043196;
                                                                                          AF043197;
                                                                                                                                              AF177526;
                                                                                                                                                                                                                                                                                                                                                                                                 P31016;
          EMBL)
                                                                                                                                                                                                                                                                                                                                    EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                      EMBL;
EMBL;
EMBL;
                                                                                                                 EMBL)
                                                                                                                                                                                                                                                               EMBL;
EMBL;
                                                                                                                                                                                                                                                                                           EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                       EMBL;
EMBL;
                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                   EMBL;
EMBL;
                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                  EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
                                                                        PROSITE; PS00856; GUANYLATE_KINASE_1; FALSE_NEG.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PDZ; 3.
PROSITE; PS50002; SH3; 1.
Tight junction; SH3 domain; Repeat; Membrane; Alternative splicing; Allernative initiation.
TIGHT JUNCTION PROTEIN ZO-2, ISOFORMS
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-C57BL/6 X CBA;
MBDLINE-99150392; PubMed=10026224;
Itoh M., Morita K., Tsukita S.;
"Characterization of 20-2 as a MAGUK family member associated with
tight as well as adherens junctions with a binding affinity to
                                                                                                                                                               A1/A2.
TIGHT JUNCTION PROTEIN 20-2, ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein) (Zona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 100; DB 1; Length 1190;
Pred. No. 0.00018;
7; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                        MISSING (IN ISOFORM A2/C2).

N -> T (IN REF 1).
P -> S (IN REF 1).
FFN -> SFT (IN REF 1).
K -> N (IN REF 1).
C -> H (IN REF 1).
P -> S (IN REF 1).
RALQ -> GGGL (IN REF 1).
S -> N (IN REF 5).
GSYG -> RSYG (IN REF 5).
GSYG -> RSYG (IN REF 5).
EYR -> INS (IN REF 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tight junction protein ZO-2 (Zonula occludens 2
occludens 2 protein) (Tight junction protein 2).
TJP2 OR ZO2.
                                                                                                                                                                                       C1/C2.
FOR ISOFORMS C1/C2
PDZ 1.
                                                                                                                                                                                                                                                                 GUANYLATE KINASE.
POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1167 AA
                                                                                                                                                                                                                          PDZ 2.
PDZ 3.
SH3.
Pfam; PF00018; SH3; 1.
Pfam; PF00595; PDZ; 3.
Pfam; PF00625; Guanylate_kin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                    24
385
599
669
1110
7110
802
803
812
813
813
813
813
813
813
813
81113
81113
81113
81113
81113
81113
                                   SMART; SM00072; GUKC; I
SMART; SM00228; PDZ; 3
SMART; SM00326; SH3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         659 IPNKSRAEQ 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 IPNYSRAQQ 68
                                                                                                                                                                           24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZO2_MOUSE
                                                                                                                                                                                                              DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
VARSPLIC
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                    INIT_MET
                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local
                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
202_MOUSE
TD 202_M
AC 0920U
DT 16-0C
DT 16-0C
DT 15-JU
DE Tight
DE CCIU
GN 18-0C
CCIU
GN CCIU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Н
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
```

5;

œ

```
MEDLINE=93361541; PubMed=8395056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
             SO THE FEFFE FEFFE BRAND BRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQ
                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tight junction protein 20-1 (Zonula occludens 1 protein) (Zona occludens 1 protein) (Tight junction protein 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131614 MW; F15DA3EBC3F9434F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF0018; SH3; 1.
Pfam; PF0018; SH3; 1.
Pfam; PF00595; PDZ; 3.
Fram; PF00525; Guanylate_kin; 1.
SMART; SM00022; PDZ; 3.
SWART; SM00226; SH3; 1.
SWART; SM00226; SH3; 1.
PROSITE; PS00856; GUANYLATE_KINASE_1; FALSE_NEG.
PROSITE; PS00065; GUANYLATE_KINASE_2; 1.
PROSITE; PS50005; SH3; 1.
Tight junction; SH3 domain; Repeat; Membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 99; DB 1;
Pred. No. 0.00023;
7; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SH3.
GUANYLATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last Sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1736 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-GLU
                                                                                                                                                                                                                                                                                                                                                                HSSP; P31016; 1BE9.
MGD; MGI:1341872; Tjp2.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; Pbz.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDZ 1.
PDZ 2.
PDZ 3.
                                                                                                                                                                                                                                                                                                                                              EMBL; AF113005; AAD19964.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.6%;
39.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 39.1:
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1167 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||| |||:|
639 IPNKSRAEQ 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 IPNYSRAQQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TJP1 OR ZO1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZO1_HUMAN
Q07157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
201_HUMAN
1D 201_H
AC 20715
DT 01-0C
DT 01-0C
DT 15-JU
DE Tight
DE OCCLU
GN HOMO
OC MARMAN
OC MARMAN
OC NOBL
RN [1]
RR [1]
RR [1]
             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ,
,
                          -: SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.
-: SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-: SIMILARITY: CONTAINS 1 GUANYLATE KINASE-LIKE DOMAIN.
-: SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tight junction; SH3 domain; Alternative splicing; Repeat; Membrane; Phosphorylation.
Willott E., Balda M.S., Fanning A.S., Jameson B., van Itallie C.,
Anderson J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 98.5; DB 1; Length 1736; Pred. No. 0.00042; 3; Mismatches 32; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISSING (IN SHORT ISOFORM). W; 508D01B7A0814FFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00856; GUANYLATE_KINASE_1; FALSE_NEG-
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SH3.
GUANYLATE KINASE.
POLY-PRO.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDZ 1.
PDZ 2.
PDZ 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000906; 2US.
Pfam; PF00595; PDZ; 3.
Pfam; PF00625; Guanylate_Kin; 1.
Pfam; PF00701; 2US; 1.
SMART; SM00072; GuKc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.5%;
36.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L14837; AAA02891.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

Query Match

Best Local Similarity 30....

Best Local Similarity 50....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P31016; 1BFE.
Genew; HGNC:11827; TJP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001452; SH3
                                                                                                                                                                                                                                                                                                                                                                   PTM: PHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50106; PDZ;
PROSITE; PS50002; SH3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    572
782
1236
1420
989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00228; PDZ; 3.
SMART; SM00326; SH3; 1.
SMART; SM00218; ZU5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A47747; A47747.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 910 98
1736 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 601009;
```

2.

33; Indels

```
28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                     ZO3_CANFA
                                                                                                                                                                                                                                                                                                           HIDD THE PROPERTY OF THE PROPE
                                              δλ
                                                                                         Dp
                                                                                                                                        ŏ
                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
Burkhart-Schultz K., Brower A., Gordon L., Diasa J., Ranirez M.,
Stilwagen S., Phan H., Velasco N., Do L., Regala W., Terry A.,
A Avila J., Liu S., Attix C., Andreise T., Trankheim M.,
A Amico-Keller G., Coefield J., Duarte S., Lucas S., Bruce R.,
A Thomas P., Quan G., Kronmiller B., Arellano A., Sanders C., Ow D.,
A Nolan M., Trong S., Kobayashi A., Olsen A.S., Carrano A.V.;
Sequence analysis of a 3.5 Mb contig in human 19p13.3 containing a
r serine protease gene cluster.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY).
--- SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.
--- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
--- SIMILARITY: CONTAINS 1 GANNYLAFE KINASE-LIKE DOMAIN.
--- SIMILARITY: CONTAINS 1 GANNYLAFE KINASE-LIKE DOMAIN.
--- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
17-JUN-2002 (Rel. 41, Last annotation protein) (Zona cocludens 3 protein) (Zona TUP3 OR ZO3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GUANYLATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P31016; 1BRE.
Genew; HGNC:11829; TJP3.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PD2.
InterPro; IPR001478; PD2.
InterPro; IPR001452; SH3.
InterPro; IPR00555; Guanylate_kin; 1.
SMART; SM00255; Guanylate_kin; 1.
SMART; SM00226; PD2; 3.
SMART; SM00226; PD2; 3.
SMART; SS00055; GUANYLATE_KINASE_1; FALSE_NEG.
PROSITE; PS500505; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PD2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tight junction; SH3 domain; Repeat; Membrane.
DOMAIN 11 93 PDZ 1.
DOMAIN 394 460 PDZ 2.
DOMAIN 489 563 SH3.
                                                                                                                                                                                       933 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AC005954; AAC72274.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102800 MW;
                                                                                                                                                                                       STANDARD;
                                              ||| :||:|
562 IPNKNRAEQ 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    933 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                   68
                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                   60 IPNYSRAQO
                                                                                                                                                                                       ZO3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                       ò
                                                             g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb.ch).
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.
-- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-- SIMILARITY: CONTAINS 1 GUANYLATE KINASE-LIKE DOMAIN.
-- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROFEINS.
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haskins J., Gu L., Wittchen E.S., Hibbard J., Stevenson B.R.,
"ZO-3, a novel member of the MAGUK protein family found at the tight
junction, interacts with ZO-1 and occludin.";
J. Cell Biol. 141:199-208(1998).
-!- SUBUNIT: INTERACTS WITH OCCLUDIN, CLAUDINS AND ZO-1.
  Gaps
                                              1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHA---HRVNSYTMKD--TA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCG-----CWHAHRVNSYTMKD 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tight junction protein ZO-3 (Zonula occludens 3 protein) (Zona occludens 3 protein) (Tight junction protein 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 898;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GUANYLATE KINASE.
8091D6132DB9F15D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 94.5; DB 1;
Pred. No. 0.00064;
7; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00856; GUANYLATE_KINASE_1; FALSE_NEG. PROSITE; PS550052; GUANYLATE_KINASE_2; 1. PROSITE; PS50106; PDZ; 3. PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat; Membrane
                                                                                                                                                                                                                                                                                                                           898 AA
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-98198478; PubMed-9531559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF023617; AAC39177.1; -. HSSP; P31016; 1BFE. InterPro; IPR000619; Guanylate_kin. InterPro; IPR001478; PDZ. InterPro; IPR001478; SH3. Ffam; PF00555; PDZ; 3. Pfam; PF00655; Guanylate_kin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDZ 1.
PDZ 2.
PDZ 3.
                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         750 G
98414 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.5%;
36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tight junction; SH3 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00072; Gukc; 1.
SMART; SM00228; PDZ; 3.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                           Canis familiaris (Dog)
                                                                                                                                               68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 898 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                               56 AHGTIPNYSRAQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                        ZO3_CANFA
O62683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 96.5; DB 1;
Pred. No. 0.00038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.0%;
38.4%;
```

Wed Jan 22 10:56:43 2003

78183 MW; F50E6290E0B6EA12 CRC64;

686 AA;

```
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
REPEAT
                                                                                                                                                                                                                                                                        EMAP_LYTVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                                                                                                                                                                                   RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                    EMAP
                                                                                                                                                                                                                                                                                                                  DDT TABLE TABLE TO DE SET TABLE TO DE SET TABLE 
SO
                                                                                                                                      ŏ
                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McKie N., Dando P.M., Rawlings N.D., Barrett A.J.; "Thimet oligopeptidase: similarity to 'soluble angiotensin II-binding protein' and some corrections to the published amino acid sequence of
    464 GDSFYIRTHFELEASPPSGLGFTRGDVFHVLDTLCPGPGPSGARGTHWLAVRMGRDLREQ 523
                                                                                                                                                                                                                                                                     01-MAR-1992 (Rel. 21, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
Thimet oligopeptidase (E. 3.4.Ld.15) (Endo-oligopeptidase A)
(Endopeptidase 24.15) (PZ-peptidase) (Soluble metallo-endopeptidase).
                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Testis;
MEDLINE=91084500; PubMed=2261476;
Pierotti A., Dong K.-W., Glucksman M.J., Orlowski M., Roberts J.L.;
"Molecular cloning and primary structure of rat testes
metalloendopeptidase EC 3.4.24.15.";
Biochemistry 29:10323-10329(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEGRADATION.
CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE OF THE PHE-|-ALA BOND
IN SUBSTRATES CONTAINING -PHE-|-ALA-ALA-PHE- AND SIMILAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the rat testis enzyme.":
Biochem. J. 295:75-60(1993).
-!- FUNCTION: INVOLVED IN THE METABOLISM OF NEUROPEPTIDES UNDER 20
AMINO ACID RESIDUES LONG. INVOLVED IN CYTOPLASMIC PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- SUBCELLULAR LOCATION: Cytoplasmic.
-:- TISSUE SPECIFICITY: IS EXPRESSED ABUNDANTLY IN THE TESTIS.
IT IS ALSO FOUND IN THE LIVER, LUNG AND KIDNEY.
-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZINC (CATALYTIC) (BY S
BY SIMILARITY.
ZINC (CATALYTIC) (BY S
ZINC (CATALYTIC) (BY S
                                                                                                                                                                                                                             686 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01432; Peptidase_M3; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001567; Peptidase_M3.
InterPro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Metalloprotease; Hydrolase; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-94029935; PubMed-8216239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- COFACTOR: BINDS 1 ZINC ION.
-!- SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M61142; AAA41586.1; -.
                                                                                                                                                                                                                                STANDARD;
                                                                                                              --ERGIIPNOSRAEQ 536
                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A36165; HYRTTH.
PIR; S38760; S38760.
MEROPS; M03.001; -.
                                                                  54 TAAHGTIPNYSRAQO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INIT_MET
METAL
ACT_SITE
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REVISIONS
                                                                                                                                                                                                                                MEPD_RAT P24155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METAL
                                                                                                                 524
                                                                                                                                                                                RESULT 14
                                                                                                                                                                                                        MEPD_RAT
                                                                                                                                                                                                                                  ga
                                                                    ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                              ñ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENTE FROM N.A.

MEDLINE-2070548: Pubbled=10603080;
Suprenant K.A., Tuxhorn J.A., Daggett M.A.F., Ahrens D.P.,
Suprenant K.A., Tuxhorn J.A., VanWinkle C.E., Livingston B.T.;
Hostetler A., Palange J.M., VanWinkle C.E., Livingston B.T.;
"Conservation of the WD-repeat, microtubule-binding protein, EMAP, in sea urchins, humans, and the nematode C. elegans.";
Dev. Genes Evol. 210:2-10(2000).
-!- FUNCTION: May modify the assembly dynamics of microtubules, such that microtubules are slightly longer, but more dynamic.
-!- SIMILARITY: CONTAINS 9 WD REPEATS (TRP-ASP DOMAINS).
-!- SIMILARITY: BELONGS TO THE EMAP FAMILY OF WD-REPEAT PROTEINS.
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            Lytechinus variegatus (Sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
                                                 Gaps
                                                                                           2 DSFYIRVNL----AMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 664;
    Length 686;
                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
77 KDa echinoderm microtubule-associated protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6F5E000E66707E78 CRC64;
                                            21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.2%; Score 62.5; DB 1; 30.1%; Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
    DB 1;
  16.5%; Score 63.5; DI 30.0%; Pred. No. 3.4;
                                                                                                                                                                                                                                                     664 AA
                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfan; PF00400; WD40; 7.
Pfan; PF00400; WD40; 7.
Probom; PD000018; WD40; 1.
SMART; SM00320; WD40; 7.
SMOSTIE; PS00678; WD_REPEATS_1; FALSE_NEG.
PROSITE; PS50082; WD_REPEATS_2; 4.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.7.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Microtubules; Repeat; WD repeat
                                              14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AF136234; AAD44709.1; -. InterPro; IPR005108; HELP. InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                               .6-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73423 MW;
                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      664 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 22; Conserv
Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=7654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172
218
2265
3307
3390
473
519
                                                                                                                                                                                                                                                     EMAP_LYTVA
Q9Y1C1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lytechinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
REPEAT
```

- pp ò
- 42 -HAHRVNSYTMKD 53 | | | : |:| 423 QHTQRWNKF-MED 434

oy D

Search completed: January 22, 2003, 08:53:37 Job time : 4.72849 secs

THIS PAGE BLANK (USPTO)

Q9V191 drosophila Q9V192 drosophila Q9Sv19 drosophila Q9Sv20 drosophila Q9Sv20 drosophila Q9Sv20 arabidopsis Q9sqn0 arabidopsis Q94Mx3 barbatia ca Q94M17 pseudomonas Q9527 mus musculu Q9Qpl5 drosophila Q9C0x1 drosophila Q9C0x1 drosophila Q9vq1 drosophila Q9vq1 drosophila Q9vq1 drosophila Q9vq1 drosophila

Q8yri3 anabaena sp Q91xv2 rattus norv Q9epx1 mus musculu

09f7t9 streptomyce 09s0r8 streptomyce

095m07 bos taurus QBvw07 homo sapien 060260 homo sapien 091wj1 mus musculu QBv520 monkeypox v Q91xv1 rattus norv

homo sapien drosophila

```
1 GDSFYIRVNLAMEGRAKG-ELQVHCNEVLHVTDTMFQGGGGWHAHRVNSYTMKDTAAHGT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Bustrychai, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohara O., Nagase T., Kikuno R., Okumura K.; "The nucleotide sequence of a long cDNA clone isolated from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.6%; Score 145; DB 4; Length 1171;
46.5%; Pred. No. 1.2e-10;
tive 12; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1171 AA; 134966 MW; FAS67ABBC8A703FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     spleen.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AK074049; BAB84875.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1171 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                  QBWW07
Q60260
Q91XV1
Q9VH92
Q9VH91
Q9VH91
Q9VH91
Q9VG0
Q91XN1
Q9FL5
Q9FL7
Q9FL
Q8TDM6
Q95V19
Q95M07
                                                                                                                                                                               5
116
117
117
116
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLJ00120 protein (Fragment) FLJ00120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
 ||:|||||| |
849 IPSYSRAQQLL 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 IPNYSRAQQQL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=SPLEEN;
 59.5
59.5
                                                                                                                                                                                                                                                                                                                                                                                  58.5
58.5
58.5
58.5
58
57.5
57.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8TES3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8TES3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
Q9NF04
 δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9nf04 caenorhabdi
Q9bk12 hydra atten
Q20398 caenorhabdi
Q92199 mus musculu
Q97758 canis famil
P70625 rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P70625 rattus norv
Q9yhv2 gallus gall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        096004 drosophila
094880 drosophila
09484 drosophila
09684 homo sapien
09684 drosophila
09483 homo sapien
09443 homo sapien
08443 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homo sapien
homo sapien
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8tes3 homo sapien
Q9nf04 caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homo sapien
                                                                                                                                           (without alignments)
1321.544 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                        January 22, 2003, 08:49:36; Search time 10.914 Seconds
                                                                                                                                                                                                                                  1 GDSFYIRVNLAMEGRAKGEL...........MKDTAAHGTIPNYSRAQQQL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                 671580
             GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                           671580 segs, 206047115 residues
                                                                                                                                                                                     US-09-767-215-2_COPY_676_745
386
                                                                                        - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8TES3
Q9NF04
Q9BKL2
Q20398
Q921G9
Q97758
P70625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q960N4
Q94880
Q9VHK4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q96KB4
Q9VKG8
Q9UE73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9Y4E3
Q8TDM7
                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_organelle:*
sp_phage:*
sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 su
                                                                                                                                                                                                                                                                                                                                                                                                   seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
111
13
5
5
5
5
5
5
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPTREMBL_21:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
200.33
20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10:
111:
12:
13:
14:
16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145
126.5
105.16
100.5
100.5
100.97.5
97.5
97.5
96.5
96.5
78.5
                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                 Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB
Maximum DB
                                                                                        OM protein
                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
Ю
```

5

```
Guanylate_kin
                                                             InterPro; IPR001452; SH3.
InterPro; IPR001906; ZU5.
Pfam; PF00625; Guanylate_kin; 1.
Pfam; PF00755; PDZ; 3.
Pfam; PF00791; ZU5; 1.
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 41...
Local 30; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | :|| |||:|
RGVLPNKSRAEQ 831
                   InterPro; IPR000619;
InterPro; IPR001478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 HGTIPNYSRAQO 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
es 25; Conserv
HSSP; P29476; 10AV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F44D12.1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F44D12.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              020398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
Q20398
  Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ά
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               490 GDNFYIRSHFSREKRDKASPLELSINEGDIFHYTDTLFGGTVGLWQARRYSSSENKGEP 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GDSFYIRVNLAMEGRAKG---ELQVHCNEVLHVTDTMFQG-CGCWHAHRV-NSYTMKDTA 55
                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fei K., Yan L., Zhang J., Sarras M.P. Jr.,
"Molecular and biological characterization of a zonula occludens-1
honologue in Hydra vulgaris, named HZO-1.",
Dev. Genes Evol. 210:611-616(2000).
EMBL, AF230482; AAK28322.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydra attenuata (Hydra) (Hydra vulgaris).
Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
Hydridae; Hydra.
NCBI_TaxID=6087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5; Length 1257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 32.8%; Score 126.5; DB 5; Length Best Local Similarity 42.5%; Pred. No. 4.3e-08; Matches 31; Conservative 11; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PD2; 3.
SEQUENCE 1257 AA; 139392 MW; 617E729417136819 CRC64;
                                                                                                                                                                                                                                                                                                            Sulston J.E.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1695 AA
  PRT; 1257 AA
                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             noser distriction of the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=21025567;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     investigating biology ". Science 282:2012-2018(1998). EMBL, AL132879; CAB60860.2; HSSP; Q12923; 3PDZ.
                                         01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00595; PDZ; 3.
Pfam; PF00791; ZU5; 1.
SMART; SM00722; GUKC; 1.
SMART; SM00228; PDZ; 3.
SMART; SM00218; ZU5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
  PRELIMINARY;
                                                                       01-OCT-2000 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                                                                                                                                       Y105E8C.B.
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | ||| : |:|
550 VKGVIPNQATAEQ 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 AHGTIPNYSRAQQ 68
                                                                                                                   Y105E8C.b protein.
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9BKL2
Q9BKL2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9BKL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
5
                                                                                                                                                                                                                                                                            4 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                       1 GDSFYIRVNLAMEGRAK-GELQVHCNEVLHVTDTMFQG-CGCWHAHRV--NSYTMKDTAA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
                                                                                                                                                                                                                                                                                                                                                   8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            investigating biology.";
Science 282:2012-2018(1998).
EMBL: 262998; CAA92607.1;
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR00019; Guarylate_kin.
SMART; SM00072; Gukc; 1.
SMART; SM00028; PDZ. 3.
PROSITE; PS550052; GUANYLATE_KINASE_2; 1.
SPROSITE; PS50106; PDZ, 3.
SEQUENCE 1034 AA; 116053 MW; 7E29646264FCD5BC CRC64;
                                                                                                                                                                                                                          Length 1695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                         190878 MW; AE0E7D09007316F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coles L.; Submitted (DEC-1995) to the {\tt EMBL/GenBank/DDBJ} databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                       30.1%; Score 116; DB 5; L 41.7%; Pred. No. 1.7e-06; vative 11; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.3%; Score 105.5; DB 5
35.2%; Pred. No. 2.5e-05;
tive 12; Mismatches 31
SMART; SM00072; GuKc; 1.
SMART; SM00072; GuKc; 1.
SMART; SM00228; PD2; 3.
SMART; SM00218; 2U5; 1.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50062; SH3; 1.
SEQUENCE 1695 AA; 190878 MW; AEOE7D0900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 IPNYSRAQQQL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δλ
```

```
InterPro; IPR001478; PDZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 IPNYSRAQQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P70625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
P70625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOTA THE REAL PARTS OF THE PART
   DR KEE DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BREED: COCKER SPANIEL;
MEDLINE=99196918; PubMed=10094817;
Gonzalez-Mariscal L., Islas S., Contreras R.G., Garcia-Villegas M.R.,
Betanzos A., Diaz-Quinonez A., Martin-Orozco N.,
Ortiz-Navarrete V., Cereijio M., Valdes J.;
"Molecular characterization of the tight junction protein ZO-1 in MDCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAA---- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 27.2%; Score 105; DB 11; Length 904; Best Local Similarity 37.2%; Pred. No. 2.4e-05; Matches 29; Conservative 8; Mismatches 29; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012518; AAH12518.1; -.
MGD; MG1:1351650; Tjp3.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99169 MW; A4D9C58AEEC485CC CRC64;
                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                         904 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1769'AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00625; Guanylate_kin; 1.
Pfam; PF00595; PDZ; 3.
PRINTS; PR01597; ZONOCCLUDNS.
PRNTMTS; PR01600; ZONOCCLUDNS3.
PROSITE: PS50106; PDZ; 3.
SEQUENCE 904 AA; 99169 MW; A4D9C58AEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Exp. Cell Res. 248:97-109(1999).
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
EMBL: U55935; AAD11529-1; --
HSSP; P31016; 1BE9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                 Similar to tight junction protein 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000619; Guanylate_kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 ----HGTIPNYSRAQQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
   |||: : | :
811 IPSSTTVYQAI 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZO-1 MDCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201-MDCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         097758
                                                                                                                          RESULT 5
Q921G9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
```

```
MEDLINE=2007A749; PubMed=10559001;
Adams L.D., Lemire J.M., Schwartz S.M.;
Asystematic analysis of 40 random genes in cultured vascular smooth muscle subtypes reveals a heterogeneity of gene expression and identifies the tight junction gene zonula occludens 2 as a marker of epithelioid 'pup' smooth muscle cells and a participant in carotid neolntimal formation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 102.5; DB 6; Length 1769;
Pred. No. 0.00012;
9; Mismatches 31; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 1769 AA; 197606 MW; 181E9F36CEBC96EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P70625; P97625;
01-FEB-1997 (TrEMBLrel. 02, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      813 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50052; GUANYLATE_KINASE_2; 1. PROSITE; PS50106; PD2; 1.
                                                                                                                                                                                                                                                                                         PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PDZ; 3.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zonula occludens 2 protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                       Pfam; PF00625; Guanylate_kin; 1. Pfam; PF00625; BD2; 3. Pfam; PF00018 SH3; 1. Pfam; PF00791; ZU5; 1. PRINTS; PR01597; ZONOCCLUDNS. PRINTS; PR01598; ZONOCCLUDNS. PRINTS; PR01600; ZONOCCLUDNS3.
                                                                                                                                                                                                                                                                                                                                                                                                                                26.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 26.69
Best Local Similarity 37.79
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
InterPro; IPR001452; SH3
InterPro; IPR000906; ZU5
                                                                                                                                                                                                 SMART; SM00072; GUKC; I
SMART; SM00228; PDZ; 3.
SMART; SM00326; SH3; I.
SMART; SM00218; ZU5; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
STRAIN=WISTAR-KYOTO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||| :||:|
573 IPNKNRAEQ 581
```

5;

```
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              094880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        094880
                              Q960N4
        RESULT 9
Q960N4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   094880
                                         ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 GDSFFIRSHFECEKETPQSLAFTRGEVFRVVDTLYDGKLGHWLAVRIGNELEK----GL 285
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
                                                                                              1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
                                                                                                                                                                                                                                                                                                                                                                                       Collins J.R., Rizzolo L.J.;
"Protein binding domains of the tight junction protein, ZO-2, are highly conserved between avian and mammalian species.";
Biochem. Biophys. Res. Commun. 252:617-622(1998).
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
EMBL; AF085184; AAC95469.1;
                                                                        ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
25.9%; Score 100; DB 13; Length 1163;
Best Local Similarity 37.7%; Pred. No. 0.00016;
Matches 26; Conservative 9; Mismatches 28; Indels 6.
                                                Score 100; DB 11; Length 813;
Pred. No. 0.0001;
7; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1163 AA; 130668 MW; 3639431A560B1D4E CRC64;
                              30EA78F19DE9C852 CRC64;
                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PD2; 3.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPRO00619; Guanylate_kin.
InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99057550; PubMed-9837755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001452; SH3.
Pfam; PF00625; Guanylate_Kin; 1.
Pfam; PF00555; PDZ; 3.
Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS: PRO1597; ZONOCCLUDNS.
PRINTS: PRO1599; ZONOCCLUDNS2.
PRINTS: PRO1600; ZONOCCLUDNS3.
                       1
90776 MW;
                                                 Query Match 25.9%;
Best Local Similarity 39.1%;
Matches 27; Conservative
                                                                                                                                                                                                                                   01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-JUN-2002 (TrEMBLrel. 21, Tight junction protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR01599; ZONOCCLUI
PRINTS; PR01600; ZONOCCLUI
SMART; SM00072; Gukc, 1.
SMART; SM00328; PDZ; 3.
SMART; SM00326; SH3; 1.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
                              813 AA;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P31016; 1BE9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||| |||:|
628 IPNRSRAEQ 636
                                                                                                                                                    ||| |||:|
286 IPNKSRAEQ 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 IPNYSRAQQ 68
                                                                                                                                        60 IPNYSRAQQ 68
                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                  TISSUE-RETINA;
           SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SH3 domain
                     NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                09YHV2
                                                                                                                                                                                            RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                   g
                                                                                                                                        ò
                                                                                                                                                            g
KW
FT
SO
                                                                                               οy
```

```
.;
;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stapleton M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Charvez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (Aug-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AYO51965; AAK93389.1; P.R. FlyBase; FB9n0003177; pyd.

R ItyBase; FB9n0003177; pyd.

R InterPro; IPR0010478; PDZ.

Pfam; PF00555; Guanylate_kin. 1.

R Pfam; PF00555; Guanylate_kin; 1.
                                                                                                                                                                LD4310.p..
PYD OR CG9763.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Prerygota; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Pteryota: Neoptera; Endopteryota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CANTON-S;
MEDLINE=96312452; PubMed=8698238;
MEDLINE=96312452; PubMed=8698238;
Kondo K., Miyake T., Ueda R.;
Kondo K., Miyake T., Ueda R.;
"The Drosophila tamou gene, a component of the activating pathway of extramacrochaetae expression, encodes a protein homologous to mammalian cell-cell junction-associated protein ZO-1.";
Genes Dev. 10:1783-1795(1996).
ENBL; D83477; BAA11923.1; -.
HSSP; Q12923; 3PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107338 MW; 5FA3A7D7D0922C2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.3%; Score 97.5; DB 5;
31.9%; Pred. No. 0.00028;
iive 13; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1367 AA
                                                              Created)
                                                          01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 31.9%
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYD OR TAMOU OR CG9763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                974 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           727 IPNKSRAEE 735
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 IPNYSRAQQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BERKELEY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1997
01-FEB-1997
```

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q96KB4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ор
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESTAINBERKELEY;

RA Addams M. D., Celniker S. E., Holt R. A., Evans C. A., Gocayne J. D.,

RADLINE-20196006; PubMed-10731132;

RA Admans M. D., Celniker S. E., Holt R. A., Evans C. A., Gocayne J. D.,

RA Admans M. D., Celniker S. E., Holt R. A., Evans C. A., Gocayne J. D.,

RA Amanatides P. G., Scherer S. E., Holt R. A., Evans G., Chen L. X.,

RA George R. A., Lewis S. E., Richards S., Ashburner M., Henderson S. N.,

RA George R. A., Lewis S. E., Richards S., Ashburner M., Henderson S. N.,

RA Brandon R. C., Rogers Y. -H. C., Helt G., Nelson C. R., Miklos G. L. G.,

RA Abril J. F., Agbayani A., An H. -J., Andrews Pfannkoch C., Baldwin D.,

RA Ballew R. M., Basu A., Baxter E. G., Helt G., Nelson C. R., Miklos G. L. G.,

RA Ballew R. M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E. M.,

RA Ballew R. M., Basu A., Bautler H., Cadieu E., Center A., Chandra I.,

RA Burtis K. C., Busam D. A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis K. C., Busam D. A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis K. Doup L. E. Downes M., Dugan-Rocha S., Dunkov B. C., Dunn P.,

RA Dodson K., Doup L. E., Downes M., Dugan-Rocha S., Dunkov B. C., Dunn P.,

RA Durbin K. J. Evangelista C. C., Ferrac C., Ferriera S., Fleischmann W.,

RA Burtis N. L., Harvey D., Heiman T. J., Wei M. -H., Ibegwam C.,

Alali M., Kalush F., Karpen G. H., Ke Z., Kennison J. A., Ketchum K. A.,

Jalali M., Kalush F., Karpen G. H., Ke Z., Kennison D.,

Alali M., Maltsh F., Karpen G. H., Ke Z., Kennison D.,

Alali M., Maltsh F., Karpen G. H., Ke Z., Kennison D.,

Alali M., Maltsh R., Martyph B., Mirphy L., Mizny D. M., Nelson D.K.,

RA Harklov G., Maltshian G. S., Pollarty J., Pull Y., Reese M. G.,

RA Ralazzolo M., Pittuman G. S., Pan S., Pollard J., Pull Y., Smith T.,

She Palazzolo M., Pittuman G. S., Pan S., Pollard J., Pull Y., Smith T.,

She She Ralazzolo W., Salden-Klamos I., Simpson M., Skupski M.P., Smith T.,
                                                                                                                                                                                                                                                                        3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera: Endopterygota: Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                 1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
                                                                                                                                                                                                                                Query Match 25.3%; Score 97.5; DB 5; Length 1367; Best Local Similarity 31.9%; Pred. No. 0.00042; Matches 22; Conservative 13; Mismatches 31; Indels 3;
                                                                                                                                                                                                148347 MW; 571C4566C6B6BBF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1445 AA.
           Interpro; IPR000619; Guanylate_kin.
Interpro; IPR001478; PDZ.
Interpro; IPR001452; SH3.
Pfam; PF00652; Guanylate_kin; 1.
Pfam; PF00555; PDZ, 2.
SWART; SW00072; GuKc; 1.
SWART; SW00228; PDZ, 3.
SWART; SW00328; PDZ, 3.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PDZ, 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21,
FlyBase; FBgn0003177; pyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                 1367 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       ||| |||:
556 IPNKSRAEE 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                60 IPNYSRAQQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYD protein.
PYD OR CG9763.
                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9VHK4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                            ô
```

```
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.
M. Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zhong X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
A. Gibbs R.A., Myers E.W., Rubin G.M., Venter J.G.,
The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
R. Embl. AE003680; AAF5400.1; -.
R. Fibbase; FSP1000137; pyd.
R. Fibbase; PSP0000137; pyd.
R. InterPro; IPR001478; pbz.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              498 GDSFHIKTHFHCDNPSKGEMAFKAGDVFRVIDTLHNGVVGSWQVLKIGRGHQE--MQRGV 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISQUENCE FROM N.A.

TISQUENCE FROM N.A.

TISQUENCE TO, AND MINLY HEAD;

TISQUENCE T., OLT T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

A Isogai T., OLT T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

A Aritam T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,

A Aritam W., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,

A Aritam A., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,

Nabo human cDNA sequencing project.";

L Submitted (MAY 2001) to the EMBL/GenBank/DDBJ databases.

E EMBL; AK027292; BAB55020.1;

InterPro; IPR001493; PDZ.

R InterPro; IPR001478; PDZ.

R InterPro; IPR001478; PDZ.

R Pfam: PF00525; Guanylate_kin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CDNA FLJ14386 fis, clone HEMBA1002417, moderately similar to TIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PSS0052; GUANYLATE_KINASE_2; 1.
PROSITE; PSS0106; PDZ; 6.
SEQUENCE 1445 AA; 156723 MW; A5675FB66676A40E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.3%; Score 97.5; DB 5; 31.9%; Pred. No. 0.00045; iive 13; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR01597; ZONOCCLUDNS.
PRRINTS; PR01600; ZONOCCLUDNS3.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00625; Guanylate_kin; 1. Pfam; PF00595; PD2; 2. Pfam; PF00791; ZU5; 1. SMART; SM0072; GuKc; 1. SMART; SM00228; PD2; 3. SMART; SM0028; SH3; 1. SMART; SM00218; ZU5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 31.9%
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001452; SH3
InterPro; IPR000906; ZU5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unction protein ZO-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||| |||::
556 IPNKSRAEE 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 IPNYSRAQQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
```

7

us-09-767-215-2\_copy\_676\_745.rspt

```
Q9UE73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
Q9UE73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δy
   RX ATAIN-BERKELEY;
RA Admans M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Admans M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA George R.A., Lewis S.E., E. Holt R.A., Evans C.A., Galle R.F.,
Randans M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Baxter E.G., Helf G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Mabayani A., An H.-J., Andrews-Feankoch C., Baldwin D.,
Ballew R.M., Basu M., Baxendale J., Bayraktaroglu L., Beaaley E.M.,
Raberson K.Y., Benos P.V., Berman B.P., Bandari D., Boltakavy S.,
RA Borkova D., Botchan M.R., Bulter H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Bulter H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Bulter H., Cadieu E., Center A., Chandra I.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferritera S., Fleischman W.,
RA Burtis K.J., Evangelista C.C., Ferraz C., Ferritera S., Fleischman W.,
RA Harris M.L., Harvy D., Halman T.J., Herrandez J.R., Gaser K.,
Alosin D., Mouston K.A., Howland T.J., Wei M.-H., Ibegvam C.,
RA Harris N.L., Houston K.A., Howland T.J., Wei M.-H., Ibegvam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A.,
Roully G., Maltshian N.V., Mobarry C., Morris J., Moshrefi A.,
Ralon D.R., Nelson D.R., Nixon K., Musskern D.R., Pacleb J.M.,
Ralon D.R., Nelson K.A., Howland S., Pan S., Pollard J., Barzolo M. R., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Raloner S.M., Moy M., Murphy B., Strond G., Yang K., Siden-Kimmes S.M., Woodage T., Simpson M., Strong R., Smith T.,
Raloner S.M., Woodage T., Stangen M., Strong S., Zhao G., Zhen G., Shen E.,
Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zho Q., Zhon, S., Zhan M., Zhong F.W., Rulls M., Zhong R.M., Wolley R.C., Wu D., Yang S., Zhon S., Zhong S., Zhan S., Scheeler F., Schen S., R., Tector C., Turner R., Venter E., Shen R., Schen S., Schen S., R., Schen
                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota, Neoptera, Endopterygota, Diptera, Brachycera; Muscomorpha,
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                        1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHA---HRVNSYTMKD--TA 55
                                                                                            5
                                                  Score 96.5; DB 4; Length 548;
Pred. No. 0.00019;
7; Mismatches 33; Indels 5
PROSITE; PS50002; SH3; 1.
SEQUENCE 548 Aa; 61005 MW; Alal@ECFDE2627AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CG6509 protein (LD32687p).
                                                                                                                                                                                                                                                                                                                                       PRT; 1916 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 287:2185-2195(2000).
                                                         25.0%;
38.4%;
                                                Query Match
Best Local Similarity 38.4<sup>†</sup>
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                             164 ERGIIPNOSRAEQ 176
                                                                                                                                                                                                        56 AHGTIPNYSRAQQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BERKELEY
                                                                                                                                                                                                                                                                                                 RESULT 13
Q9VKG8
                                                                                                                                                                                                                                                                                                                                           ολ
                                                                                                                                                                   셤
```

```
4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakamura H., Sudo T., Tsuiki H., Miyake H., Morisaki T., Sasaki J., Masuko N., Kochi M., Ushio Y., Saya H.; "Identification of a novel human homolog of the Drosophila dlg, P-dlg, specifically expressed in the gland tissues and interacting with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GDSFYIRVNLAMEGRA-KGELQVHCNEVLHVTDTMFQGC-GCWHAHRVNSYTMKDTAAH- 57
STRAIN-BERKELEY;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR030532; AAR53102.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1916;
                                                                                                                                                                                                                                                                                                                                                                                                                    24.6%; Score 95; DB 5; Length 191r
34.2%; Pred. No. 0.0014;
                                                                                                                                                                                                                                                                                                                                          SMART; SM00326; SH3; 1.
PROSTIE; PSS0032; GUNXLATE_KINASE_2; 1.
PROSTIE: PSS0106; PDZ; 4.
SEQUENCE 1916 AA: 209863 WW; 32B2A61ABA6848F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2002 (TrEMBLrel. 13, Last annotation update)
Discs large protein P-dlg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fram; PF00625; Guanyltte_Kin; 1.
Fram; PF00018; PD2; 2.
Fram; PF00018; SH3; 1.
SMART; SM00072; Gukc; 1.
SMART; SM00228; PD2; 2.
SMART; SM0025; Gukc; 1.
FROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PD2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         p55.";
FEBS Lett. 433:63-67(1998).
--- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
EMBL; U61843; AAC61295.1; --
HSSP; Q12959; 1PDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PD2.
InterPro; IPR000408; Reg_chr_condens.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                 FlyBase, FBGN0032363, CG6509.
InterPro; IPR000619; Guanylate_Kin.
InterPro; IPR001478; PDZ.
InterPro; IPR001452; SH3.
Pfam; PF00595; PDZ, 3.
SMART; SM00072; GuKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98409314; PubMed=9738934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1644 KECGIIPSOMKVEEEL 1659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 ---GTIPNYSRAQQQL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                           SMART; SM00228; PDZ; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 26; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                  HSSP; P31016; 1BE9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-BRAIN,
```

```
5,
                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-BRAIN;
MEDLINE-98290545; PubMed-9628581;
Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,
                                                                                                                                       3; Gaps
                                                                                                                        3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The complete sequences of unidentified human genes. IX. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

DNA Res. 5:31-39(1998)

-: SIMILARITY: CONTAINS 1 SH3 DOMAIN.

EMBL; AB011155; BAA25509.1; -.

HSSP; 012959; 1PDR.

InterPro; IPR001619; Guanylate_kin.
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.3%; Score 78.5; DB 4; Length 1281; 34.9%; Pred. No. 0.15; Live 10; Mismatches 28; Indels 3;
                                                                Query Match 20.3%; Score 78.5; DB 4; Length 674; Best Local Similarity 34.9%; Pred. No. 0.069; Matches 22; Conservative 10; Mismatches 28; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER 1 1 1 SEQUENCE 1281 AA; 140286 MW; 4CC150D03F3ED8B9 CRC64;
                                        674 AA; 74892 MW; C4C006B0A4F7E8E8 CRC64;
                                                                                                                                                                                                                                                                                  0374E3.
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
KIAA0583 protein (Fragment).
                                                                                                                                                                                                                                                                           PRT; 1281 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001468, Reg.chr_condens.
InterPro; IPR001452, SH3.
Pfam; PF00555, Guanylate_kin; 1.
Pfam; PF00189; 8H3.
Pfam; PF00189; SH3. 1.
PRINTS; PR00452; SH3DOMAIN.
SMART; SM00072; GuKc; 1.
SMART; SM00326; SH3; 1.
PROSTITE; PS50052; GUANYLATE_KINASE_2; 2.
PROSTITE; PS50106; PDZ; 4.
PROSTITE; PS50106; PDZ; 4.
PROSTITE; PS50106; PDZ; 4.
PROSITE; PS00626; RCC1_2; UNKNOWN_1.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 20.3%
Best Local Similarity 34.9%
Matches 22; Conservative
                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                              11:
406 IPS 408
            PROSITE; PS5
SH3 domain.
SEQUENCE 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 IPN 62
                                                                                                                                                                             60 IPN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SH3 domain.
                                                                                                                                                                                                                                                                         Q9Y4E3
                                                                                                                                                                                                                                           g
                                                                                                                         ò
                                                                                                                                                 q
                                                                                                                                                                              οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
```

```
Db 1013 IPS 1015
```

Search completed: January 22, 2003, 08:56:45 Job time: 13.914 secs

THIS PREE BLANK WARTON

```
January 22, 2003, 08:49:35; Search time 34.8857 Seconds (without alignments) 683.714 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | SIDS2/gcgdata/geneseq/geneseqp-embl/Aa1980.DaT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/Aa1981.DaT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/Aa1981.DaT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/Aa1983.DaT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/Aa1983.DaT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/Aa1986.DaT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/Aa1986.DaT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/Aa1986.DaT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/Aa1980.DaT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/Aa1990.DaT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/Aa1990.DaT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/Aa1991.DaT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/Aa1991.DaT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/Aa1992.DaT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/Aa1993.DaT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/Aa1993.DaT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/Aa1993.DaT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/Aa1993.DaT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/Aa1993.DaT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/Aa1993.DaT:*
                                                                                                                                                                                                                                                                                                                                                                    US-09-767-215-2_COPY_826_1004
930
1 RPRPVLLVPRAVGKILSEKL.....vRQAIADEQKKVVWTEQSPR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS2/gcgdata/geneseg/genesegp-embl/AA2000.DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA2001.DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA2002.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS2/gcgdata/geneseq/genesegp-emb1/AA1999.DAT
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          908470 segs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A_Geneseq_101002
                                                                                                                                                                                                                                                                                                                                                                                                                   score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                            Title:
Perfect sc
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database
                                                                                                                                                                                                                       Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Human caspase recr	Human predicted ca	Human caspase recr	Human polypeptide	Human polypeptide,	Human plakoglobin	Human caspase recr	Human P-dlq protei	Mouse quanylate ki	AA sequence (III)
QI	AAE07164	AAE07165	AAU01207	AAM38934	AAM93822	AAU73247	AAU01206	AAW72748	AAR93137	AAP70243
	22	22	22	22	22	23	22	19	16	8
% Query Match Length DB	1004	1139	1147	350	746	1032	1032	674	198	197
% Ouery Match	100.0	95.1	26.1	18.9	18.9	18.9	18.2	13.8	13.4	13.1
Score	930	884	242.5	175.5	175.5	175.5	169.5	128.5	124.5	121.5
Result No.	1	7	m	4	ស	9	7	80	σ	10

Mouse guanylate ki Mouse guanylate ki Sequence of a poly Human guanylate ki AA sequence (VII) AA sequence (VII) AA sequence (VII) AA sequence (VIII) AA sequence (VII	d; Protein; 1004 AA.  irst entry)  cruitment domain-14 (CARD-14).  ecruitment domain-14; CARD-14; chromosome 17;  ecruitment domain-14; CARD-14; call death; cancer; therapy; der; system; lupus erythematosus; neurological disorder; der; system; sidease; inflammatory disorder; anaemia; lisorder; myclodysplastic syndrome; mycloardial infarction; disorder; Crohn's disease; allergic rhinitis; infection; disorder; crotostatic; immunosuppressive; nootropic; antiviral; antibacterial.  Location/Qualifiers 69  Location/Qualifiers 69  Those="camp-and cGMP-dependent protein kinase phosphorylation site" 1016  Those="casein kinase II phosphorylation site" 7016  Those="casein kinase II phosphorylation site" 7016  1215  Anote="casein kinase II phosphorylation site" 7016  7016  7016  7016  7016  7017
AAV07443 AAW97135 AAW97135 AAR96478 AAR91316 AAR97134 AAP07134 AAP0627 AAP0624 AAP70245 AAP70245 AAP70246 AAP70246 AAP80628 AAP70246 AAP80628	domain-14 (CA domain-14) C. domain-14; C. domain-14; C. r.kb; cell gromaic lupus ery mic lupus ery mic lupus ery cohostatic; in cohostatic; in antibacteri; antibacteri; antibacteri; antibacteri; antibacteri; selion site"  NRD_domain ssein kinase I ssein kinase I
2 44444444 770310000000000000000000000000000000000	in; 1  t dom  t dom  t dom  t dom  t dom  y)  y)  t dom  you  you  you  ylati  cAMP.  CAMP.  CAMP.  CAMP.  CAMP.
11990 11990 11990 11990 11990 11990 11990 11990 11990 11990 11990 11990 11990 11990 11990	first entry)  recruitment domain-14 -reappa B; NF-kB; cell order; systemic lupus sease; Parkinson's dis disorder; nayelodyspla disorder; cytostatic g disorder; cytostatic e; antiviral; antibac Location/Qualifiers 6.9 Locat
11112222222222222222222222222222222222	standard  Ol (fir  pase rec  spase re  actor.ka  actor.ka  site 6  site 1  site 1  site 2
111 121 121 121 121 121 121 121 121 121	1 4 AE07164 LE07164; NOV-20 Inman cas Incomparation Incomp
	RESULT AAADOTIC AAAADOTIC AAAADOTIC AAAADOTIC AAAADOTIC AAAAADOTIC AAAAADOTIC AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

```
note= "cAMP- and cGMP-dependent protein kinase ohosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Casein Kinase ....
926. 929
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                    844
.e= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                       "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Protein kinase C phosphorylation site"
                                                                                                   "Casein kinase II phosphorylation site"
                                                                                                                                                                             "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Protein kinase C phosphorylation site"
                          "Casein kinase II phosphorylation site"
                                     637
2= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         An isolated caspase recruitment domain polypeptide useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "RGD cell cl.".
893..896
/note= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 863
.e- "Casein kinase II phosphorylation
                                                              .655
e= "Protein kinase C phosphorylation
                                                                                                                                                                                                     "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .949
.e= "Peroxisomal targetting signal"
                                                                                                                                                                                                                                                                                                                                             /note="Peroxisomal targetting signal"
196..799
                                                                                                                                                                                                                                                                                                                                                                                                                          label= Guanylate_kinase_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "N-myristoylation site"
1002..1004
                                                                                                                                                                                                                                                                                                                                                                                                "N-myristoylation site"
                                                                                                                                                                                                                             "N-myristoylation site"
                                                                                                                                                     "N-myristoylation site"
                                                                                                                                                                                                                                                        "N-glycosylation site"
  "N-glycosylation site"
                                                                                                                          /label= SH3_domain
714..719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-FEB-2000; 2000US-0181159.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JAN-2001; 2001WO-US02087
                                                                                                                                                                                                                                                                                                                                                                                            /note= "N--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Pt
044..947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "C
868..870
                                                                                                                                                                                                                .738
                                                                                                                                                                                                                                                                                  /note= "P
760..763
                                                                                                                                                                                                                                                                                                                                                                                ..805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .985
                                                                                                                                                        /note= "N
725..727
                                                                                                                                                                                         .728
                                                                                                                                                                                                                                            740
                                                                                       ...677
                                                                                                                                                                                                                                                                 759..761
/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note=
                                                                                                                                                                                                                                                                                                                                                                          'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note=
                                                                                                                                                                               "note=
                                                                                                                                                                                                        'note=
                                                                                                                                                                                                                                 note=
                                                                                                      'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-497073/54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAD13447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200159065-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                           Andified-site
                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
              Modified-site
                                                               Modified-site
                                                                                        Modified-site
                                                                                                                                          Andified-site
                                                                                                                                                                                           Modified-site
                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bertin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                               отаіп
                                                                                                                   Domain
   .466
e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .472
e "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .504
e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                              .262
e- "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                      .283
e- "Casein Kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .310
e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .386
e= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..452
te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .465
.e- "Protein kinase C phosphorylation site"
                                                                                       'note= "N-myristuj......
134..137
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                    /note= "N-myristoy.co...
165..168
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                           .252
e- "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Protein kinase C phosphorylation site"
                                       'note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                    rnote= "Tyrosine Alusso".
221. 224
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                   .243
.e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .365
e= "Tyrosine kinase phosphorylation site"
               /note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                        .227
.e= "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .381
.e= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                   "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .406
e= "Leucine zipper pattern"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "N-myristoylation site"
589..592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .516
e= "N-myristoylation site"
                                                                                                                                                     ..135
te= "N-myristoylation site"
                                                                            .122
ce= "N-myristoylation site"
                                                                  'note= "N-glycosylation site"
                                                                                                                               126..420
/label= Coiled_Coil_domain
                                                                                                                                                                                                                                                                                                                         'label= k-Box_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68..660
label- PDZ_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .368
                                                                                                                                                                                                                                                                                                                                                                                                                              note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                        Modified-site
                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mod1fled-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
      Modified-site
                             Modified-site
                                                      Modified-site
                                                                               Modified-site
                                                                                                        Modified-site
                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                  Domain
```

m

```
AAU01207;
                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               966
                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU01207
  à
                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; caspase recruitment domain-14; CARD-14; chromosome 17; nuclear factor kappa B; NN-kB; cell growth; cell death; cancer; therapy; autoimmune disorder; systemic lupus erythematosus; neurological disorder; Alzheimer's disease; Parkinson's disease; inflammatory disorder; anaemia; haematological disorder; myelodysplastic syndrome; myocardial infarction; stroke; immune disorder; Crohn's disease; allergic rhinitis; infection;
                                                      The present sequence is human caspase recruitment domain-14 (CARD-14). The CARD-14 gene is located on chromosome 17. The CARD-14 is used for the detection of modulators that modulates the ability of CARD-14 to bind to Bcl-10 and stimulates phosphorylation of Bcl-10 or activation of nuclear factor-kappa B (NF-kB). The CARD-14 is useful for regulating growth and cell death and useful for the treatment of cancer. It is also useful for the treatment of cancer. It is also useful for the treatment of autoimmune disorders (e.g., systemic lupus erythematosus), neurological disorders e.g., Alzheimer's and Parkinson's disease, inflammatory disorders, haematological disorders (e.g., anaemia, myelodysplastic syndromes), myocardial infarctions, strokes, immune disorders (e.g., Crohn's disease, allergic rhinitis), cell signalling disorders and certain viral and bacterial infections.
regulating growth and cell death and useful for the treatment of cancer
                                                                                                                                                                                                                                                                                                          VTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRLGTS 120
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                           EEQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTEQSPR 179
                                                                                                                                                                                                                                                                                             1 RPRPVLLVPRAVGKILSEKLCLLQGFKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGRCW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell signalling disorder; cytostatic; immunosuppressive; nootropic;
neuroprotective; antiviral; antibacterial.
                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                             Length 1004;
                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human predicted caspase recruitment domain-14 (CARD-14).
                                                                                                                                                                                                                                             Score 930; DB 22;
Pred. No. 2.2e-91;
                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Encoded by TGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE07165 standard; Protein; 1139 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..., Location/Qualifiers Misc-difference 700
                                  Claim 1; Fig 1A-1E; 109pp; English.
                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JAN-2001; 2001WO-US02087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-FEB-2000; 2000US-0181159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 179; Conservative
                                                                                                                                                                                                                   1004 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200159065-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOMO sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-AUG-2001
                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE07165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bertin J;
                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                   826
                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                   988
                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                  946
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE07165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                           ò
```

```
(CARD-14). The CARD-14 gene is located on chromosome 17. The CARD-14 is used for the detection of modulators that modulates the ability of CARD-14 to bind to Bcl-10 and stimulates phosphorylation of Bcl-10 or activation of nuclear factor-kappa B (NF kB). The CARD-14 is useful for regulating growth and cell death and useful for the treatment of cancer. It is also useful for the treatment of autoimmune disorders (e.g., systemic lupus erythematosus), neurological disorders e.g., Alzheimer's and Parkinson's disease, inflammatory disorders, haematological disorders strokes, immune disorders (e.g., and and parkinson) any elodysplastic syndromes), myocardial infarctions, strokes, immune disorders (e.g., Crobn's disease, allergic rhinitis), cell signalling disorders and certain viral and bacterial infections.
                                                                                             An isolated caspase recruitment domain polypeptide useful for regulating growth and cell death and useful for the treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRLGTS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence is predicted human caspase recruitment domain-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RPRPVLLVPRAVGKILSEKLCLLQGFKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGRCW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         apoptosis; hyperproliferative disorder; autoimmune; neurological; inflammatory disorder; viral infection; stress-related response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Protein kinase C phosphorylation site" 106..109
/note= "cAMP- and cGMP-dependent protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; caspase recruitment domain; CARD-11; Bcl-10; NF-kappaB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100..102
/note= "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human caspase recruitment domain, CARD-11 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 884; DB 22;
Pred. No. 2.4e-86;
0; Mismatches 0;
                                                                                                                                                                                                                    Disclosure; Fig 2A-2C; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "CARD domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU01207 standard; Protein; 1147 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.08; F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 100.
Matches 171; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100..103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105..107
WPI; 2001-497073/54.
N-PSDB; AAD13448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1139 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
```

ö

```
/note= "Casein kinase II phosphorylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 9; Fig 14A-14C; 145pp; English.
                "SH3 domain"
                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0507533.
2000US-0513904.
2000US-0685791.
                                                                                                                                                                                                                                                                                                                                                                                                                                               (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2000; 2000WO-US32716.
                                                                                                                                                                                                                                                                                                                                                                                                       99US-0168780
                                                /note= "Ca
787 789
                                                                                                                                                                           .1147
                      .779
                                                                                                   note=
                                                                                                                                    'note=
                                                                                                                                                    'note=
                                                                                                                                                                                     /note=
                                                                                                                                                                                                                      note=
                                                                   note=
                                                                                   'note=
                                                                                                                                                                                                      note=
                                  'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-367809/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAS05389
                                                                                                                                                                                                                                                                                                                                                      WO200140468-A2
                                                                                                                                                                                                                                                                                                                                                                                                              18-FEB-2000;
25-FEB-2000;
10-OCT-2000;
                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                              Modified-site
                         Modified-site
                                         Modified-site
                                                         Modified-site
                                                                          Modified-site
                                                                                          Modified-site
                                                                                                          Modified-site
                                                                                                                          Modified-site
                                                                                                                                          Modified-site
                                                                                                                                                           Modified-site
                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                       03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                       07-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bertin J;
                                                                                                                                                                            Domain
         Domain
 /note="cAMP- and cGMP-dependent protein kinase
phosphorylation site"
459..461
                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "cAMP- and cGMP-dependent protein kinase
  phosphorylation site"
                                                                                                                                                                                                                                                                                                                               /note= "cAMP- and cGMP-dependent protein kinase
phosphorylation site"
                                                                                                                                                                                                                                                                                     476.479 3.77 Anote= "Casein kinase II phosphorylation site" 508.510 (2005) Anote= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Casein kinase II phosphorylation site"
761..766
701..767
764..767
                                                                                                                                                                                                                                            note= "Protein kinase C phosphorylation site" 71..474
note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         592..695
/note= "Casein kinase II phosphorylation site"
698..703
                                                                                                                                                                          .. 292
te= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                       'note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                       "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         897..689 '
note= "Protein Kinase C phosphorylation site"
                        ..165
re= "Casein kinase II phosphorylation site"
                                         ..171
te- "Casein kinase II phosphorylation site"
                                                                        . 245
te= "Protein kinase C phosphorylation site"
                                                                                                                                                          ..789
te= "Casein kinase II phosphorylation site"
                                                        183
te- "Tyrosine kinase phosphorylation site"
                                                                                          .195
.e= "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .641
:e= "Glycosaminoglycan attachment site"
                                                                                                                                                                                                     "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                               /note= "N-myristoylation site" 634..637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "N-myristoylation site"
                                                                                                                                                                                                                                                                              "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                       "N-glycosylation site"
                                                                                                         ..244
te= "N-glycosylation site"
phosphorylation site"
                  "Coiled coil domain"
                                                                                                                                         ...285
re= "Amidation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "MAGUK domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "PDZ domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "N
710..715
                                                                                                                                                                                                                                                                                                                                                                                                                                                        535..1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..728
                                                                                                                                                                                                            .432
                                                                                                                                                                                                                                                                     ..475
                                                                                                                                                                                                                                                                                                                       .513
                                                                                                                                                                                                                                                                                                                                                                               ..587
                                                                                                                                                                                                                                                                                                                                              558..560
                                                                                                                                                                                                                                                                                                                                                             578..581
                                                                                                                                                                                                                                                                                                                                                                                                                                       535..748
         .431
                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note=
                                                                                                                    'note=
                                                                                                                                                                                                                                                                              'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note=
                                                                                                                                                                                                                                                                                                                                                                                        'note=
                                                                                                   'note=
                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                    'note-
                                                                    'note-
                                                                                    'note=
                                                                                                                                                                      'note=
                                                                                                                                                                                     'note-
                                                                                                                                     note=
                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                          Modified-site
                                          Modified-site
                                                          Modified-site
                                                                           Modified-site
                                                                                           Modified-site
                                                                                                           Modified-site
                                                                                                                            Modified-site
                                                                                                                                            Modified-site
                                                                                                                                                            Modified-site
                                                                                                                                                                             Modified-site
                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
          Domain
```

```
Novel caspase recruitment domain (CARD) proteins, CARD-9, CARD-10, CARD-11, useful as targets for therapy, as immunogens, and in screening and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents novel human caspase recruitment domain, CARD-11. The polynucleotide encoding this sequence was isolated from a human T-cell cDNA library. Also described are novel human sequences for CARD-9 and CARD-10 (AAU01205, AAU01206) and rat CARD-9 (AAU01204). CARD-9, CARD-10 and CARD-11 interact with Bcl-10 which is thought to activate nuclear factor (NF)-kappaB and apoptosis. The sequences of the invention can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "N-myristoylation site"
1088..1091
/note= "Casein kinase II phosphorylation site"
1120..1123
/note= "Casein kinase II phosphorylation site"
                     782
e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                             147.850
"note= "Casein kinase II phosphorylation site"
153.858
                                                                                                                                                                                                                                                                                                                                ..859
ce= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                372.875
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           926..929
/note= "Casein kinase II phosphorylation site"
935..937
                                                                                                  "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anote- "Casein kinase II phosphorylation site' (1010. 11018
Anote- "Tyrosine kinase phosphorylation site" (1050. 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .819
e= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "Protein kinase C phosphorylation
.003..1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Guanylate kinase (GUK) domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..922
.te- "N-myristoylation site"
                                                                                                                                                                        .828
e= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                           "N-myristoylation site"
"N-glycosylation site"
```

```
treating a disorder associated with abnormal levels of apoptosis by modulating the expression or activity of CARD-9, CARD-10, or CARD-11.

They can be used for the treatment of hyperproliferative disorders (e.g. cancer), autoimmune disorders (e.g. systemic lupus erythematosus), neurological disorders (e.g. Alzheimer's disease), inflammatory disorders (e.g. Crohn's disease), and viral infection (e.g. HIV). The CARD polypeptide, polynucleotide and an antibody which selectively binds to CARD can be used in screening and detection assays (e.g. chromosomal, monitoring clinical trials, and therapy (treatment and prophylaxis). The CARD polypeptide may be used to screen for drugs that bind to and/or modulate it. CARD sequences are potential targets for regulating and outlarmation, cancer, NF-kappaB signalling, stress-related response and apoptosis in human disease. A host cell containing a polynucleotide encoding CARD can be used to create transgenic animals.
                                                                                                                                                                                                                                                                                                                                        4,
                                                                                                                                                                                                                                                                                                                                                                                            Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 GGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 RLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTE 175
                                                                                                                                                                                                                                                                                                                                       7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peripheral nervous system; neuropathy; central nervous system; CNS; Alzhehmer's; Parkinson's disease; hademostatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic; chemotactic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                       1 RPRPVLLVPRAVGKILSEKLCLLQG---FKKCLAEYLSQEEYEAWSQRGDII--QEGEVS
                                                                                                                                                                                                                                                                                                        Length 1147;
                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                                                                        DB 22;
                                                                                                                                                                                                                                                                                                      26.1%; Score 242.5; DB 31.5%; Pred. No. 5.8e-17
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 31.5%; Pred. No. 5.8e-Matches 57; Conservative 41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM38934 standard; Protein; 350 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human polypeptide SEQ ID NO 2079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200005-0598042.
200005-0598042.
200005-0653450.
200005-0663191.
200005-0693036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0488725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0552317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                       1147 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1144 E 1144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 0 176
                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM38934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
```

```
ñ
                                                                                                                                                                                                                 The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous system, such as peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and thrombolytic activity, arthritis and inflammation, leukaemias and constructions.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed
                               ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 CWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRLG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 RPVLLVPRAVGKILSEKLCLLOG----FKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGR 58
                               Wang
                                                                                                                                        Novel nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 TSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    281 WRDSELLRQCRGSEQVLWGLPCSWVQVPAHEWGHAEELAKVVRGRILQEQARLVWVE 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 175.5; DB 22; Length 350;
; Pred. No. 2.1e-10;
24; Mismatches 88; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; full length cDNA; cDNA synthesis; oligo-capping.
                               Qian XB,
Yang Y,
                            nen R, Ma Y, C
tu C, Xue AJ,
Drmanac RT;
                                                                                                                                                                                     Example 3; SEQ ID NO 2079; 10078pp; English.
                                                                                                                                                         such as central nervous system injuries
                            Chen R,
                                              Xu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human polypeptide, SEQ ID NO: 3879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM93822 standard; Protein; 746 AA
                            Asundi V, Che
Wehrman T, Xu
Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.9%;
32.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99JP-0194486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000JP-0118774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUL-2000; 2000EP-0114089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58; Conservative
                                                                                          WPI; 2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            350 AA;
(HYSE-) HYSEQ INC.
                                                           Zhou P,
                             Liu C,
Wang Z,
                                                                                                           N-PSDB; AAI58090
                                                                                                                                                                                                                                                                                                                                                                                                                                                           specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP1130094-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM93822;
                            YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                           Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                               Tang
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

```
AAU01206;
                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                              Query Match
                       Van Roy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU01206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q
                                                                                                                                                                                                                                                                                                                                                                                       3;
                                                                                                                                                                    The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been solutionide sequences of 5'— and 3'—ends of the cDNA molecules have been determined. For and 3'—ends of the CDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; plakoglobin; cytostatic; osteopathic; dermatological; cardiant; plakoglobin related disease; skin carcinoma; acantholytic disease; basal cell carcinoma; squamous cell carcinoma; Naxos disease; extramammary paget's disease; hart disease; skin blistering; subcorneal acantholysis; Grover's disease; Hailey'Hailey's disease; Darier's disease; ectodermal dysplasia; skin fragility syndrome.
                                                                                                          830\ \mathrm{Primers} useful for synthesizing full length cDNA clones and their use in genetic manipulation -
                                                                                                                                                                                                                                                                                                                                                                                                                              58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 TSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            677 WRDSELLRQCRGSEQVLWGLPCSWVQVPAHEWGHAEELAKVVRGRILQEQARLVWVE 733
                                              Ë
                                                                                                                                                                                                                                                                                                                                                                                                              3 RPVLLVPRAVGKILSEKLCLLOG----FKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 CWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kawai Y;
T, Koga
                                                                                                                                                                                                                                                                                                                                                             Length 746;
                                                                                                                                                Claim 8; SEQ ID NO 3879; 1380pp + sequence listing; English.
                                   Isogai T, Hayashi K, Ishii S,
T, Nagai K, Kojima S, Otsuki
                                                                                                                                                                                                                                                                                                                                                             DB 22;
                                                                                                                                                                                                                                                                                                                                                             18.9%; Score 175.5; DB 2
32.8%; Pred. No. 5.7e-10;
iive 24; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human plakoglobin interacting protein #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU73247 standard; Protein; 1032 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-MAY-2000; 2000EP-0201668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-MAY-2001; 2001WO-EP04872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                 Sugiyama
          (HELI-) HELIX RES INST
                                    Nishikawa T,
                                                                       2001-524255/58.
                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
Les 58, Conserv
                                                                                                                                                                                                                                                                                                                                     746 AA;
                                                                                    N-PSDB; AAK94778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200185933-A2.
                                                Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-NOV-2001
                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                              Query Match
                                    Ota T,
                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                ô
```

```
The invention relates to an isolated plakoglobin interacting polypeptide (I). (I) is useful as a medicament and in the manufacture of a medicament for treating plakoglobin related diseases, such as skin carcinoma or an acantholytic disease, and to screen compounds that interfere with the interaction of the polypeptide with plakoglobin The plakoglobin related diseases include basal cell carcinoma, squamous cell carcinoma, extramammary Paget's disease, Naxos disease, heart diseases, skin blistering and acantholytic diseases such as subcorneal acantholysis, Grover's disease, Hailey's disease or Darier's disease, and ectodermal dysplasia/Skin fragility syndrome. Auv73245-AAV73254 represent novel human plakoglobin interacting protein amino acid sequences and related sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            846 RPVVLLPECLAPRLIRNLLDLPSSRLDFQVCPAESLSGEELCPSSAPGAPKAQPATPGLG 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 CWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRLG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 RPVLLVPRAVGKILSEKLCLLQG----FKKCLAEYLSQEEYEAWSQRGDI1QEGEVSGGR 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polypeptide, useful for treating skin carcinoma or acantholyti
disease such as Grover's and Darier's disease, comprises a protein
interacting with human plakoglobin and involved in transduction of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 TSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; caspase recruitment domain; CARD-10; Bcl-10; NF-kappaB; apoptosis; hyperproliferative disorder; autoimmune; neurological; inflammatory disorder; viral infection; stress-related response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 23; Length 1032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Protein kinase C phosphorylation site"
76..79
/note= "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            caspase recruitment domain, CARD-10 polypeptide.
(VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 175.5; DB 2
Pred. No. 8.8e-10;
; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15..20
/note= "N-myristoylation
                                                                    Vanlandschoot A;
                                                                                                                                                                                                                                                                                                                                 plakoglobin related signal to nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23..123
/note= "CARD domain"
68..70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU01206 standard; Protein; 1032 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Figure 3; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.9%;
32.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                    Bonne S,
                                                                                                                                 WPI; 2002-062246/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1032 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 58; Conserv
                                                                                                                                                                                                                              New polypeptide,
disease such as G
                                                                                                                                                                   N-PSDB; AAS98203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                    [1
```

ñ

7

```
"Casein kinase II phosphorylation site"
        . 739
                                                                                                                                                                                                                                                                                             /note=
  /note=
                                                                                            note-
                                                                                                                                       note=
                                                                                                                                                      note-
                                                                                                                                                                                    'note=
                                                                                                                                                                                                                                 'note=
                /note=
                                                                            note=
                                                                                                         'note=
                                                                                                                        'note=
                                                                                                                                                                     'note=
                                "note=
                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-367809/38.
N-PSDB; AAS05388.
                                                                                                                                                                                                                                                                                                            WO200140468-A2
                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                     Modified-site
        Modified-site
                                                    Modified-site
                                                                   Modified-site
                                                                                                                              Modified-site
                                                                                                                                            Modified-site
                                                                                                                                                            Modified-site
                                                                                                                                                                           Modified-site
                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                      Modified-site
                       Modified-site
                                     Modified-site
                                                                                  Modified-site
                                                                                                 Modified-site
                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                              10-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                        03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                               18-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                      25-FEB-2000
                                                                                                                                                                                                                                                                                                                           07-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                             Bertin J;
                                                                                                                Domain
 fnote= "N-myristcytuct.....510..513
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                site"
                                                                                                       ..245
te= "Casein kinase II phosphorylation site"
                                                                                                                     . 295
.e= "Protein Kinase C phosphorylation site"
                                                                                                                                    . 296
te= "Casein kinase II phosphorylation site"
                                                                                                                                                                  .315
ce= "Protein Kinase C phosphorylation site"
                                                                                                                                                                                                                                             ..441
te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                     .552
.e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                    ..560
te= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..644
te= "Protein kinase C phosphorylation site"
        phosphorylation site"
                                                                                                                                                                                ..334
te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                         site"
                                                                                                                                                                                                                                                                                          ..481
te- "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                  .573
.te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                         "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphorylation site"
                              ..115
:e= "Casein kinase II phosphorylation site"
                                                                                 "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                       ..514
ce= "Protein kinase C phosphorylation
                                                                                                                                                                                                                        "Casein kinase II phosphorylation
                                                                                                "Leucine zipper homology region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Glycosaminoglycan attachment
                                                                                                                                                                                                                                       "Leucine zipper homology
                                                                                                                                                                                                                                                                                                         ..492
te= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                            "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "N-myristoylation site"
                                                    "N-myristoylation site"
                                                                                                                                                            "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           704..772
/note= "SH3 domain"
712..715
/note= "N-glycosylation site"
714..717
                                                                                                                                                                                                                                                                                     "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                          "N-glycosylation site"
                                                         .457
.e- "Coiled coil domain"
                                                                                                                                                                                                166..398
'note= "Tropomyosin domain"
        "Protein kinase C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΙΙ
                      'note= "Amidation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
.693
re= "Casein kinase
                                                                                                                                                                                                                                                                      "MAGUK domain"
                                                                                                                                            /note= "C
                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "N
303..605
                                                                                                                                                                                                                ..415
                                                                                                                                                                                                                                .447
                                                                                                                                                                                                                                                                             .475
                                                                                                                                                                                                                                                                                                                                                                                                                                                 .641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..684
                                                                                         .251
                                                                                                                                                                                                                                                                      'note=
                                                                                                                                                                                                                                                        'note=
                                      'note=
                                                                                                                                                             'note=
                                                                                                                                                                                           'note=
                                                                                                                                                                                                                        'note=
                                                                                                                                                                                                                                                                                                                                                                'note=
                                                                                                                                                                                                                                                                                                                                                                                                             'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note=
                                                                                                 'note=
                                                                                                                                                                            'note=
                                                                                                                                                                                                                                        'note=
                                                                                                                                                                                                                                                                                                                                                 'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                           'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note=
                                                    'note=
                                                                                  'note=
                                                                                                                'note=
                                                                                                                               'note=
                                                                                                                                                                                                                                                                                     'note=
                                                                                                                                                                                                                                                                                                     'note-
                                                                                                                                                                                                                                                                                                                                                                               note=
                                                                                                                                                                                                                                                                                                                                                                                             'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note=
                                                                    'note=
Modified-site
               Modified-site
                                                                         Modified-site
                                                                                                        Modified-site
                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                             Modified-site
                                            Modified-site
                                                                                                                      Modified-site
                                                                                                                                    Modified-site
                                                                                                                                                    Modified-site
                                                                                                                                                                  Modified-site
                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                        Region
                                                                                                                                                                                                 Domain
                                                            Domain
                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                Region
```

```
The present sequence represents novel human caspase recruitment domain, CARD-10. The polynucleotide encoding this sequence was isolated from a human skin cDNA library. Also described are novel human sequences for CARD-9 and CARD-11 (AAV01205, AAV01207) and rat CARD-9 (AAV01204). CARD-9, CARD-10 and CARD-11 interact with Bcl-10 which is thought to activate nuclear factor (NF)-kappaB and apoptosis. The sequences of the invention can be used for treating a disorder associated with abnormal levels of apoptosis by modulating the expression or activity of CARD-9, CARD-10, or CARD-11. They can be used for the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel caspase recruitment domain (CARD) proteins, CARD-9, CARD-10, CARD-11, useful as targets for therapy, as immunogens, and in screening and detection assays -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "N-myristoylation site"
1021. 1026
/note= "N-myristoylation site"
/note= "Protein kinase C phosphorylation site"
1028. 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                     ..832
te= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Protein kinase C phosphorylation site"
                   .751
-- "Casein Kinase II phosphorylation site"
                                                                                                                                                                                                          784
ce= "Protein Kinase C phosphorylation site"
                                                                                              site"
                                                                                                                                         "Casein kinase II phosphorylation site"
                                                                .756
:e- "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                             .870
ce= "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                               ...872
te- "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .885
te= "Casein kinase II phosphorylation
"Tyrosine kinase phosphorylation
                                                                                                                                                                                                                                                                                                      .
.e= "Guanylate kinase (GUK) domain"
                                                                                                                                                             .766
e= "N-myristoylation site"
                                                                                                                                                                                                                                                                                     "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "N'...,
915..918
...+a= "Amidation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 9; Fig 10A-10C; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0168780.
2000US-0507533.
2000US-0513904.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2000; 2000WO-US32716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0685791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..986
                                                                                                                  54..757
```

```
3,
hyperproliferative disorders (e.g. cancer), autoimmune disorders (e.g. systemic lupus erythematosus), neurological disorders (e.g. Alzheimer's disease), inflammatory disorders (e.g. Crohn's disease), and viral infection (e.g. HY). The CARD polypeptide, polynucleotide and an antibody which selectively binds to CARD can be used in screening
                                                                          and detection assays (e.g. chromosomal mapping, tissue typing), predictive medicine (prognostic assays, monitoring clinical trials, and therapy (treatment and prophylaxis). The CARD polypeptide may be used to screen for drugs that bind to and/or modulate it. CARD sequences are potential targets for regulating inflammation, cancer, NF-kappaB signalling, stress-related response and apoptosis in human disease. A host cell containing a polynucleotide encoding CARD can be used to create transgenic animals.
                                                                                                                                                                                                                                                                                                                                                  846 RPVVLLPECLAPRLIRNLLDLPSSRLDFQVCPAESLSGEELCPSSAPGAPKAQPATPGLG 905
                                                                                                                                                                                                                                                                                                                                                                                   59 CWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRLG 118
                                                                                                                                                                                                                                                                                                                                                                                                     SRI-RAIQESVGKK--HCLLELGARGVRERVONEIXPIVIHVEVTEKNVREVRGLLGRPG 962
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                      58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  963 WRDSELLRQCRGSEQVLWGLPCSWVQVPAHEWGHAEELAKVVRGRILQEQARLVWVE 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     family protein - used for, e.g. investigation of tumour suppression and for development of anticancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                119 TSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTE 175
                                                                                                                                                                                                                                                                                                                       3 RPVLLVPRAVGKILSEKLCLLQG----FKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGR
                                                                                                                                                                                                                                                         Length 1032;
                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-dlg; dlg family; detection; carcinostatic mechanism; cer; tumour suppressor; embryogenesis; regulation.
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                       DB 22;
                                                                                                                                                                                                                                                       18.2%; Score 169.5; DB 32.2%; Pred. No. 3.9e-09
                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "encoded by WAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW72748 standard; Protein; 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= unknown
                                                                                                                                                                                                                                                                                        24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SUME ) SUMITOMO ELECTRIC IND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-JP01611.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97JP-0111846.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakata M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-568727/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human P-dlg protein
                                                                                                                                                                                                                         1032 AA;
                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAV67191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human dlg
mechanisms of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09846745-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakamura H,
                                                                                                                                                                                                                                                                                      57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anticancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-OCT-1998
                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW72748;
                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human;
                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW7274
   2222222222222
                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                    δ
```

Claim 1; Page 29-32; 55pp; Japanese.

```
10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the amino acid sequence of the mouse guanylate kinase. The gene was isolated from a lambda-gtl0 CDNA library of mouse 702/3 B lymphoma cells, using the corresp, human gene (AAT17148) as a probe. The isolated gene fragment (800 bp) was cloned into pUC118. These proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Herpes simplex virus; thymidine kinase; mutant; random library; vector; nucleotide binding site; inhibition; pathogenic agent; virus; bacterium; warm blooded animal; parasite; tumour cell; autoreactive immune cell; primer; PCR; amplification; mouse; human; guanylate kinase.
       The present sequence is a human protein belonging to the dlg family (P-dlg). P-dlg is recognised by an antibody binding to the epitope: KEQRDETYLRDKYTORHSKE. The dlg family of proteins is involved in regulation of embryogenesis and in tumnour suppression. P-dlg, and its associated polynucleotides and antibodies are useful in investigating mechanisms of tumour suppression and in the design and screening of potential anticancer agents.
                                                                                                                                                                                                                                                        495 RPVLILGPLLDVVKEMLVNEAPGKFCRCPLEVMKASQQAIERGVKDCLF----VDYKRR 549
                                                                                                                                                                                                                                                                                       SQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSV 102
                                                                                                                                                                                                                                                                                                          -----KGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSD 152
                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid molecules encoding Herpes virus thymidine kinase enzyme - useful for inhibiting a pathogenic agent, a tumour cell or an auto:reactive immune cell
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                            ----ILSEKLCLLQGFKKCLAEYLSQEEYEAW 42
                                                                                                                                                                                           57;
                                                                                                                                                              Length 674;
                                                                                                                                                                                              Indels
                                                                                                                                                                DB 19;
                                                                                                                                                                                           64;
                                                                                                                                                              Score 128.5; DB Pred. No. 6e-05; ); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 9; Page 90-92; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                             LDGLLSCVRQAIADEQKKVVWTEQSP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                       LSSICTOILAMVNOEQNKVLWIPACP 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA.
                                                                                                                                                                13.8%; Scc
26.7%; Pre
Live 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR93137 standard; Protein; 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse guanylate kinase protein.
                                                                                                                                                                                                                            ---LVPRAVGK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95WO-US05561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94US-0237592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-403866/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Loeb LA;
                                                                                                                                                                              Best Local Similarity
Matches 55; Conserv
                                                                                                                                   674 AA;
                                                                                                                                                                                                                                                                                                                                                   103 NEKMAKKLK--
                                                                                                                                                                                                                            RPVL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9530007-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-NOV-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Black ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR93137;
                                                                                                                                     Sequence
                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                               596
                                                                                                                                                                                                                                                                                                                                                                                                                                          648
                                                                                                                                                                                                                            m
                                                                                                                                                                                                                                                                                                                     550
                                                                                                                                                                                                                                                                                        43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                        δy
                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                 QY
                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                             ά
                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

Wed Jan 22

```
7;
     for ease
were fused to a hexa-His/thrombin cleavage site peptide sequence for ease of purification. The human and mouse guanylate kinase genes can be used to construct dual expression vectors confg. the human or mouse sequences and novel Herpes simplex virus (HSV) type-1 thymidine kinase mutants (AATO5187-91) which contain mutations in the region encoding residues 165-175. Vectors confg. the mutant and normal kinase sequences can be used to inhibit a pathogenic agent in a warm blooded animal e.g. viruses, bacteria or parasites, or a tumour cell or autoreactive immune
                                                                                                                                                                                                                                                                                                                                                      102 VNEKMAKKLKKGLQRLGTSEEQLLE---AARQEEGDLDRAPCLYSSLAPDGWSDLDGLLS 158
                                                                                                                                                                                                                                                                              42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVS 101
                                                                                                                                                                                                                                                                                                        DIAAGDFIEHAEFSGNLYGTSKEAVRAVQAMNRICVLDVDLQGVRSIKKTDLCP--IYIF 121
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                        2 PRPVLLV-PRAVGK-ILSEKL----CLLQGFKKCLAE-------YLSQEEYEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA sequence (III) of a polypeptide having human haematopoietic cell growth potentiating factor (HCGPF) activity.
                                                                                                                                                                                               27;
                                                                                                                                                                   DB 16; Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        growth potentiating factor - prepd. from human peripheral blood derived
                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hiroshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Autoimmune disease therapy; immunodeficient disease;
                                                                                                                                                                                             82;
                                                                                                                                                                 13.4%; Score 124.5; DB 1
25.5%; Pred. No. 3.2e-05;
iive 37; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shinsuke T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP70243 standard; protein; 197 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 13; Page 62; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'n,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86JP-0002633.
87JP-0002521.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87EP-0100107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86JP-0302698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Junji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human haematopoietic cell from gene obtd. using RNA mononuclear cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                          159 CVRQAIADEQKKVVWT 174
                                                                                                                                                                                             50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               180 TLKQALSEEIKKAQGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 marrow transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gen Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AJIN ) AJINOMOTO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1987-229568/33
                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                        198 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAN70355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tadatsugu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JAN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JAN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-DEC-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JAN-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-AUG-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nobukazu K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP232707-A.
                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAP70243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pone
                                                                                                                                                                                                                                                                                                           64
                                                                                                                                                                                             Matches
  8X3333333X8
                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

```
.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSV-1; thymidine kinase; mutation; DRH nucleoside binding site; enzyme; stathogen; tumout; hyperkeratosis; psoriasis; prostate hypertrophy; PCR; hyperthyroidism; endocrinopathy; autoimmune disease; allergy; restenosis; viral disease; AIDS; hepatitis; parasite; bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents the mouse guanylate kinase (GK) protein. The invention relates to the generation of novel HSV-1 thymidine kinase (TK) or GK genes with a mutation upstream, within or downstream from a DRH nucleoside binding site. The TK enzymes can be used for inhibiting pathogenic agents, e.g. tumours, hyperkeratosis, psoriasis, prostate hypertrophy, hyperthyroidism, endocrinopathies, autoimmune diseases, allergies, restenosis, viral diseases such as AIDS, hepatitis,
The HCGPF exhibits immune control and haematopietic control functions over a wide range and may be used in the fields of immunodeficient diseases, autoimmune diseases, infectious diseases, hepatitis, nephritis, cancers and bone marrow transplantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVS 101
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
                                                                                                                                                                                                                                                                                                                                                                                        -----YLSQEEYEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VNEKMAKKLKKGLQRLGT-SEEQLLE--AARQEEGDLDRAPCLYSSLAPDGWSDLDGLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                              4 PRPVVLSGPSGAGKSTLLKRLLQEHSGIFGFSVSHTTRNPRPGEENGKDYYFVTREVMQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIAAGDFIEQAEFSGNLYGTSKVAVQAVQAMNRICVLDVDLQGVRNIKATDLRP--IYIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Herpesviridae thymidine kinase mutants - useful for treating
prostate hypertrophy, allergies, cystic fibrosis and Alzheimer's
                                                                                                                                                                                                                                            DB 8; Length 197;
                                                                                                                                                                                                                                     13.1%; Score 121.5; DB 8; 25.5%; Pred. No. 6.7e-05; tive 39; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                             2 PRPVLLV-PRAVGKILSEKLCLLQ....-GFKKCLAE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 25; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY07443 standard; Protein; 198 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse guanylate kinase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DARW-) DARWIN MOLECULAR CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US21672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 CVRQAIADEQKK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :::|:::| ||
180 ELKEALSEEIKK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-277631/23.
                                                                                                                                                                                                                                                                         Local Similarity
nes 49; Conserv
                                                                                                                                                                        197 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAX57669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9919466-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-APR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY07443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Black ME;
                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus sp.
                                                                                                                                                                                                                                                                                Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY07443
   2222XX
                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A X D X D X D X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X
```

DB 20;

```
(AJIN ) AJINOMOTO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1988-199153/29.
                              Similarity
198 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAN81032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Taniquchi T,
                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-JAN-1987;
                                                                                                                                                                                                                                                                                                           15-0CT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUL-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP274560-A.
                                         53;
                                                                                                                                                                                                                                                                                      AAP80478;
Sequence
                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                102
                                                                                                                                                                                           158
                                         Matches
                                                                                                                                                                                                                                                        AAP80478
ğ
                                                                                                                           QQ
                                                                                                                                                                    qq
                                                                                                                                                                                                              QD
                                                                                                                                                                                                                                                                            g
                                                                                                        δλ
                                                                                                                                                ŏ
                                                                                                                                                                                           ŏ
                                                              Ω
                                                              6
                                                                                                                                                                                                                                                                                                                                                                       HSV-1; thymidine kinase; mutation; DRH nucleoside binding site; enzyme; pathogen; tumour; hyperkeratosis; psoriasis; prostate hypertrophy; PCR; hyperthyroidism; endocrinopathy; autoimmune disease; allergy; restenosis; viral disease; AIDS; hepatitis; parasite; bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the mouse guanylate kinase (GK) protein. The invention relates to the generation of novel HSV-1 thymidine kinase (TK) or GK genes with a mutation upstream, within or downstream from a DRH nucleoside binding site. The TK enzymes can be used for inhibiting pathogenic agents, e.g. tumours, hyperkatosis, psoriasis, prostate allorgies, restenosis, viral diseases such as AIDS, hepatitis, intracellular parasitic diseases or bacterial infection.
                                                                                                                                                                                    64 DIAAGDFIEHAEFSGNLYGTSKEAVRAVQAMNRICVLDVDLQAVRSIKKTDLCP--IYIF 121
                                                                                                                                                                     102 VNEKMAKKLKKGLQRLGT-SEEQL---LEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLL 157
                                                                                                                            42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVS 101
                                                               Gaps
                                                                                   ---YLSQEEYEA 41
                                                                                                        4 PRPVVLSGPSGAGKSTLLKKLFQEHSSIFGFSVSHTTRNPRPGEEDGKDYYFVTREMMQR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 develop products for treating e.g. tumours, autoimmune diseases, allergies, restenosis or viral, bacterial or parasitic diseases
                                                              29;
                                        Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Herpesviridiae thymidine kinase mutant nucleic acids
                                                               Indels
or bacterial infection
                                          DB 20;
                                         13.1%; Score 121.5; DB 2 26.9%; Pred. No. 6.8e-05;
                                                                                   2 PRPVLLV-PRAVGK-ILSEKL----CLLQGFKKCLAE-
                                                              37; Mismatches
                                                                                                                                                                                                                                                                                       AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 22; 72pp; English.
 intracellular parasitic diseases
                                                                                                                                                                                                                                                                                      AAW97135 standard; Protein; 198
                                                                                                                                                                                                                                                                                                                                                    Mouse guanylate kinase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-0432871
94US-0237592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0432871
                                                                                                                                                                                                                           : ::||:::| || |
179 ATLKQALSEEIKKAQGT 195
                                                                                                                                                                                                               SCVRQAIADEQKKVVWT 174
                                                                                                                                                                                                                                                                                                                               (first entry)
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-189650/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Loeb LA;
                                                    Local Similarity
                     198 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAX15377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAY-1994;
                                                                                                                                                                                                                                                                                                                               22-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5877010-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAR-1999
                                                               53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Black ME,
                                                                                                                                                                                                                                                                                                          AAW97135;
                     Sequence
                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                              Mus sp
                                                                                                                                                                                                               158
                                                               Matches
                                                                                                                                                                                                                                                                   RESULT 12
                                                                                                                                                                                                                                                                              AAW9713
                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                          q
                                                                                                                                                                                                                ò
SXC
                                                                                                       g
                                                                                                                             ò
                                                                                                                                                g
                                                                                                                                                                     ò
```

```
ġ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A polypeptide with this sequence and a gene encoding it are claimed. Also claimed is a vector DNA capable of replication in prokaryotes and eukaryotes, the transformed prokaryotes and eukaryotes and a polypeptide having HCGPF activity. The HCGPF potentiates the growth of haematopoietic cells. It exhibits immune control and haematopoietic control functions.
                                                                                                                                                                                                                                                   Human haematopoietic cell growth potentiating factor; immune control; haematopoietic control functions; immunodeficient diseases;
                                                                                                                                                                                                                    42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVS 101
                                                                                                                                                                                                                                                                                                                               VNEKMAKKLKKGLQRLGT-SEEQL---LEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLL 157
                                                           Gaps
                                                                                                                                                              4 PRPVVLSGPSGAGKSTLLKKLFQEHSSIFGFSVSHTTRNPRPGEEDGKDYYFVTREMMQR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19..197 /note="A polypeptide with this sequence and a gene encoding it are claimed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence of a polypeptide having human haematopoietic cell growth potentiating factor (HCGPF) activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant human haematopoietic cell growth potentiating factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kashima
                                                     29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used for immuno:deficient, auto:immune or infectious diseases,
Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 13, claim 34; Fig 2 and Fig 5 and Fig 8; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hepatitis, nephritis, cancer or bone marrow transplantation
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matsui
Score 121.5; DB 20;
Pred. No. 6.8e-05;
7; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŝ
                                                                                                              2 PRPVLLV-PRAVGK-ILSEKL----CLLQGFKKCLAE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Taki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune diseases; infectious diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hamuro J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="As above"
                                                  37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAP80478 standard; protein; 197
  13.1%;
26.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87EP-0108782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87JP-0002521
                                                                                                                                                                                                                                                                                                                                                                                                                                        SCVRQAIADEQKKVVWT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 ATLKQALSEEIKKAQGT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <sub>ن</sub>
```

Length 197;

DB 16;

```
used to inhibit a pathogenic agent in a warm blooded animal e.g. vi
bacteria or parasites, or a tumour cell or autoreactive immune cell
                                                                      Similarity
                                      AA;
                                     197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200252036-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                              03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-JUL-2002.
                                                                                                                                                                                                                                                                                                                                                                       AA015490;
                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jung B,
                                                              Query Match
                                                                                  Matches
                                                                                                                                                                                                          102
                                                                                                                                                                                                                                                                                                                        RESULT 15
 SSSSS
                                                                                                                                                                                                                                                                                 Сp
                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                  q
                                                                                                                                                                                 Pp
                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                          δλ
                                                                                                                                                           δ
                                                                                                                                                                                                          δ
                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is the amino acid sequence of the human guanylate kinase. The gene was isolated from a proliferating B lymphocyte cDNA library with primers AAT/150-1. The resulting fragment (600 bp) was cloned into pUC118.

The human gene was used to isolate the gene encoding the mouse guanylate kinase gene (AAT/149). These proteins were fused to as the hear-His/thrombin cleavage site peptide sequence for eas of purification. The human and mouse guanylate kinase gene can be used to construct dual expression vectors contg. the human or mouse sequences and novel Herspes simplex virus (HSV) type-1 thymidine kinase mutants (AAT/05187-91) which contain mutations in the region encoding residues 165-175. Vectors contg. the mutant and normal kinase sequences can be
                                                                                                                                                                                                                                                                                                                                                                                                                 Herpes simplex virus; thymidine kinase; mutant; random library; vector; nuclectide binding site; inhibition; pathogenic agent; virus; bacterium; warm blooded animal; parasite; tumour cell; autoreactive immune cell; primer; PCR; amplification; mouse; human; guanylate kinase.
                                                                                                                                                                                                VNEKMAKKLKKGLQRLGT-SEEQLLE--AARQEEGDLDRAPCLYSSLAPDGWSDLDGLLS 158
                                                                                                                                                 64 DIAAGDFIEHAEFSGNLYGTSKVAVQAVQAMNRICVLDVDLQGVRNIKATDLRP--1Y1S 121
                                                                                                                                  42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFFIVIHVS 101
                                                                                                        4 PRPVVLSGPSGAGKSTLLKRLLQEHSGIFGFSVSHTTRNPRPGEENGKDYYFVTREVMQR 63
                                                             Gaps
                                                                                 -----YLSQEEYEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid molecules encoding Herpes virus thymidine kinase enzyme

    useful for inhibiting a pathogenic agent, a tumour cell or an
auto:reactive immune cell

                                                          27;
                                  Length 197;
                                                           Indels
                                                           78;
                                   DB 9;
                                  12.8%; Score 119.5; DB 9 25.5%; Pred. No. 0.00011;
                                                                                 2 PRPVLLV-PRAVGKILSEKLCLLQ-----GFKKCLAE--
                                                          38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 9; Page 87-88; 124pp; English.
                                                                                                                                                                                                                                                                                                                      AAR93136 standard; Protein; 197 AA.
                                                                                                                                                                                                                                                                                                                                                                                             Human guanylate kinase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95WO-US05561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94US-0237592
                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                          49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                               :::|:::| ||
180 ELKEALSEEIKK 191
                                                                                                                                                                                                                                CVRQAIADEQKK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-403866/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Loeb LA;
                                                Similarity
           197 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAT17148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9530007-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                     04-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Black ME,
           Sequence
                                                                                                                                                                                                                                                                                                                                             AAR93136;
                                   Query Match
                                                Local
                                                                                                                                                                                 102
                                                           Matches
                                                                                                                                                                                                                                159
                                                                                                                                                                                                                                                                                             RESULT 14
                                                                                                                                                                                                                                                                                                          AAR93136
                                                                                                                                                                                                       Dp
                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                  ò
                                                                                                                                                      g
                                                                                                                                                                                ò
                                                                                                                                                                                                                                ò
```

```
7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention comprises a method for determining whether a substance is an activator or an inhibitor of a DHAM-kinase (deregulated in hyperactive macrophage kinase). DHAM-kinases used in the invention include guanylate kinase I (GUKI), serin-threonin-kinase PAK2 and serin-threonin-kinase PRK2. The method of the invention is useful for identifying substances that influence inflammatory conditions of chronic inflammatory airway diseases (e.g. chronic bronchitis or chronic obstructive pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Determining activators or inhibitors of 'deregulated in hyperactive macrophage' (DHAM)-kinase for treating chronic inflammatory airway diseases, by measuring DHAM-kinase function after it is contacted with
                                                                                                                                                                                                                                                                                                                                                                                                                                   VNEKMAKKLKKGLQRLGT-SEEQLLE--AARQEEGDLDRAPCLYSSLAPDGWSDLDGLLS 158
                                                                                                Gaps
                                                                                                                                                                                                                                                                            42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVS 101
                                                                                                                                                         -----YLSQEEYEA 41
                                                                                                                                                                                                                 4 PRPVVLSGPSGAGKSTLLKRLLQEHSGIFGFSVSHTTRNPRPGEENGKDYYFVTREVMQR 63
                                                                                             27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; DHAM-kinase inhibitor; guanylate kinase 1; PRK2; deregulated in hyperactive macrophage kinase inhibitor; GUK1; serin-threonin-kinase; PAK2; inflammatory condition; chronic inflammatory airway disease; chronic bronchitis; chronic obstructive pulmonary disease; COPD.
                                                                                                Indels
Score 119.5; DB 10,
                                                                                                                                                         2 PRPVLLV-PRAVGKILSEKLCLLQ-----GFKKCLAE-----
                         12.8%; Score 11....
25.5%; Pred. No. 0.00(
+ive 38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BOEH ) BOEHRINGER INGELHEIM PHARMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Page 47-48; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA015490 standard; Protein; 197 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human guanylate kinase 1 (GUK1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kraut N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-2001; 2001WO-EP14844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-DEC-2000; 2000US-257854P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                              Local Similaricy --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159 CVRQAIADEOKK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 ELKEALSEEIKK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mueller S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-583570/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAL44148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a test substance
```

```
7;
                                                                                                                                                                                                                   102 VNEKMAKKLKKGLQRLGT-SEEQLLE--AARQEEGDLDRAPCLYSSLAPDGWSDLDGLLS 158
                                                                                                                                                                                                                                  disease - COPD). The present amino acid sequence represents the human quanylate kinase 1 (GUK1).
                                                                                                                                                                  42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVS 101
                                                                                                                                                                                  Query Match
12.8%; Score 119.5; DB 23; Length 197;
Best Local Similarity 25.5%; Pred. No. 0.00011;
Matches 49; Conservative 38; Mismatches 78; Indels 27; Gaps
                                                                                                               159 CVRQAIADEQKK 170
                                         197 AA;
                                          Sequence
   SXCC
                                                                                                                                                                                      qq
                                                                                                                                       Dp
                                                                                                                                                                  δ
                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                        ŏ
                                                                                                                    δy
```

Search completed: January 22, 2003, 08:52:22
Job time : 35.8857 secs

:::|:::| || 180 ELKEALSEEIKK 191

```
71.5
71.5
71.5
70.5
70.5
70.5
70.7
70.7
70.7
70.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4008, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 51, App.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Appl
                                                                                                                                                                                                                                                                        (without alignments) 429.229 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                            January 22, 2003, 08:52:30 ; Search time 12.2702 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RPRPVLLVPRAVGKILSEKL......VRQAIADEQKKVVWTEQSPR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sednence Sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-289-709-1
US-08-602-656-1
US-09-20-646-1
US-09-20-641-5
US-07-894-212A-2
US-07-894-212A-2
US-08-961-083-200
US-08-961-083-200
US-08-961-083-200
US-08-961-083-200
US-08-961-083-200
US-08-961-083-200
US-08-961-083-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-270-956-51

US-08-430-871C-49

US-09-270-956-49

US-09-150-460B-8

US-09-150-460B-7

US-09-150-460B-7

US-09-150-460B-6

US-09-150-460B-6

US-09-150-460B-6

US-09-150-460B-6

US-09-150-460B-6

US-08-352-737-24

US-08-353-700-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -09-562-737-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-511-477-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262574 segs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                    US-09-767-215-2_COPY_826_1004
930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                        protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1997

1997

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

1009

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121.5
121.5
118.5
118.5
118.5
86.5
86.5
86.5
84
88.8
80
80
80
80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.5
76.5
76.5
75
75
73
73.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB
Maximum DB
                                                                                                                                                        OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database
                                                                                                                                                                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Result
No.
```

```
8, Appli
8, Appli
5492, Ap
2, Appli
30, Appli
                                                                                                                                                                                                                              2, Appli
2, Appli
2, Appli
22, Appli
22, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVS 101
                                                      sequence 23, p. Sequence 28, p. Sequence 2, p. Sequence 2, p. Sequence 2, p. Sequence 2, p. Sequence 8, p. Sequence 2, p. Sequence 23, p. Sequence 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER FALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,871C
FILING DATE: 02-MAY-1995
CLEASIFICATION: 102-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: MCMASters David D.
REGISTATION NUMBER: 34,963
REFERENCE/POCKET NUMBER: 34,0052,409C1
TELECOMMUNICATION INFORMATION:
                                                US-09-562-737-23

US-08-562-737-28

US-08-660-326-40

US-08-361-611-2

US-08-361-611-2

US-08-946-967-2

US-08-946-967-2

US-09-134-001C-5492

US-09-134-001C-5492

US-09-085-199B-2

US-09-085-199B-4

US-09-088-199B-4

US-09-088-1898-4

US-09-088-489-23

US-09-088-489-24

US-09-088-489-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 PRPVLLV-PRAVGK-ILSEKL----CLLQGFKKCLAE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Loeb, Lawrence A.
APPLICANT: Black, Margaret E.
TITLE OF INVENTION: THYMIDINE KINASE MUTANTS
CORRESPONDENCE: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 121.5; DB
Pred. No. 1e-05;
'; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 51, Application US/08432871C; Patent No. 5877010; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.1%; Sco:
26.9%; Pre
ative 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 51:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 198 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 26.9
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
976
724
1094
1094
4900
4900
1066
1066
1066
1066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
11066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-432-871C-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-432-871C-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
2223
3333
3333
3333
3333
3333
4444
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
443
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
443
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
443
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
443
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
443
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
443
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
443
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
4433
443
4433
4433
4433
4433
4433
4433
443
443
443
443
443
443
443
443
46
```

ó

```
RESULT 3
US-08-432-871C-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ōλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 DIAAGDFIEHAEFSGNLYGTSKEAVRAVQAMNRICVLDVDLQAVRSIKKTDLCP--IYIF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 VNEKMAKKLKKGLQRLGT-SEEQL---LEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLL 157
                                                                              12 WSORGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVS 101
64 DIAAGDFIEHAEFSGNLYGTSKEAVRAVQAMNRICVLDVDLQAVRSIKKTDLCP--IYIF 121
                                                         102 VNEKMAKKLKKGLQRLGT-SEEQL---LEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLL 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----YLSQEEYEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 PRPVVLSGPSGAGKSTLLKKLFQEHSSIFGFSVSHTTRNPRPGEEDGKDYYFVTREMMOR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,956
FILIG DATE: 17-MAR-1999
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.1%; Score 121.5; DB 4;
26.9%; Pred. No. 1e-05;
tive 37; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                   Sequence 51, Application US/09270956
Patent No. 6451571
GENERAL INFORMATION:
APPLICANT: Loeb, Lawrence A.
APPLICANT: Black, Margaret E.
TITLE OF INVENTION: THYMIDINE KINASE MUTANTS
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 PRPVLLV-PRAVGK-ILSEKL----CLLQGFKKCLAE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: MCMASters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : ::||:::| || |
179 ATLKQALSEIKKAQGT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 SCVRQAIADEQKKVVWT 174
                                                                                                                                          SCVRQAIADEQKKVVWT 174
                                                                                                                                                                                     179 ATLKQALSEEIKKAQGT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 13.18
Best Local Similarity 26.98
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-09-270-956-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 6300 Colum
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
ZIP: 98104-7092
                                                                                                                                                                                                                                                                    US-09-270-956-51
                                                                                                                                            158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                             ò
                                                                                                    g
                                                                                                                                            ò
```

```
,,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 VNEKMAKKLKKGLQRLGT-SEEQLLE--AARQEEGDLDRAPCLYSSLAPDGWSDLDGLLS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 DIAAGDFIEHAEFSGNLYGTSKVAVQAVQAMNRICVLDVDLQGVRNIKATDLRP--IYIS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 PRPVVLSGPSGAGKSTLLKRLLQAHSGIFGFSVSHTTRNPRPGEENGKDXYFVTREVMQR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARES PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,871C
FILING DATE: 02-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MCMASLES, DAY'd D.
REGISTRATION NUMBER: 34.963
REFERENCE/DOCKET NUMBER: 24.0052.409C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                              IE: Seed and Berry LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.7%; Score 118.5; DB 2;
llarity 25.5%; Pred. No. 2.2e-05;
Conservative 38; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
US-09-270-956-49
Sequence 49, Application US/09270956
Sequence 49, Application US/09270956
Patent No. 6451571
GENERAL INFORMATION:
APPLICANT: Locb, Lawrence A.
APPLICANT: Black, Margaret E.
TITLE OF INVENTION: THYMIDINE KINASE MUTANTS
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                      APPLICANT: Loeb, Lawrence A.
APPLICANT: Black, Margaret E.
TITLE OF INVENTION: THYMIDINE KINASE MUTANTS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 PRPVLLV-PRAVGKILSEKLCL----LQGFKKCLAE---
                                                                                                                                                                                                                                                                                                                                                                E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Sequence 49, Application US/08432871C
Patent No. 5877010
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 372836
INFORMATION FOR SEQ ID NO: 49:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 197 amino acids amino acid
                                                                                                                                                                                                                                              CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-432-871C-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159 CVRQAIADEQKK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :::|:::| ||
180 ELKEALSEEIKK 191
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
```

us-09-767-215-2\_copy\_826\_1004.rai

```
SEQ ID NO 7
LENGTH: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                  Qγ
                                                                                                                                                                qq
                                                                                                                                                                                                δ
                                                                                                                                                                                                                              QQ
                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 VNEKMAKKLKKGLQRLGT-SEEQLLE--AARQEEGDLDRAPCLYSSLAPDGWSDLDGLLS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 PRPVVLSGPSGAGKSTLLKRLLQAHSGIFGFSVSHTTRNPRPGEENGKDYYFVTREVMQR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/09150460B
Patent No. 6190882
GENERAL INFORMATION:
APPLICANT: Labe Cheng-Chi
APPLICANT: Bichele, Gregor
APPLICANT: Sun, Zhong Sheng
TITLE OF INVERFORE: D6399
FILE REPERENCE: D6399
                                                                      COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,956
FILING DATE: 17-MAR-1999
CLASSIFICATION: 433
ATCARREY/AGENT INFORMATION:
NAME: MCMASTERS, David D.
REGISTRATION NUMBER: 33,963
**TORNEY/AGENT NUMBER: 240052.409C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 PRPVLLV-PRAVGKILSEKLCL----LQGFKKCLAE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: D6039
CURRENT APPLICATION NUMBER: US/09/150,460B
CURRENT FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: US 60/058,256
PRIOR FILING DATE: 1997-09-09
NUMBER OF SEQ ID NOS: 21
SEED and BERRY LLP
                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 34,90
REFERENCE/DOCKET NUMBER: 240
TELECOMMUNICATION INFORMATION:
TELERAX: (206) 682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 49: SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-09-270-956-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 CVRQAIADEQKK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 ELKEALSEEIKK 191
                                              Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                             COUNTRY: US
ZIP: 98104-7092
        STREET: booverITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
US-09-150-460B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 8
LENGTH: 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pp
```

```
.;
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
6
                                                                                                                                                                                                                                                                                                                                                        66 VESLMEKNTHALLDVQ-LDSVCTLHRMDIFPI-----VIHVSVNEKMAKKLKKGLQR 116
                                                                                                                                                                                                                                                                                                                                                                                                195 ----ADMSTYTLEELEHITSEYTLQNQDTFSVAVSFLTGRIVYISEQAAVLLKCKRDVFR 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 LPPERRGKGRSGTLATLQYALACVKQVQANQEYYQQWS-----LEEGEPCS----- 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 VESLMEKNTHALLDVQ-LDSVCTLHRMDIFPI-----VIHVSVNEKMAKKLKKGLQR 116
                                                                                                                                                                                                                                   7 LVPRAVGKILSEKLCLLQGFKKCLAE-YLSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 LVPRAVGKILSEKLCLLQGFKKCLAE-YLSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHA 65
; OTHER INFORMATION: Peptide sequence of largest deduced open reading; OTHER INFORMATION: frame from RIGUI 3.0 US-09-150-460B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: Peptide sequence of largest deduced open reading COTHER INFORMATION: frame from RIGUI 6.6 US-09-150-460B-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 875;
                                                                                                                    Length 798;
                                                                                                                                                                                                                                                                                              149 LPPERRGKGRSGTLATLQYALACVKQVQANQEYYQQWS----LEEGEPCS---
                                                                                                                                                                         51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/09150460B
Patent No. 6190882
GENERAL INFORMATION:
APPLICANT: Lee, Cheng-Chi
APPLICANT: Bichel, Urs
APPLICANT: Bichele, Gregor
APPLICANT: Sun, Zhong Sheng
TITLE OF INVENTION: Mammalian Circadian Rhythym-Like Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalian Circadian Rhythym-Like Gene
                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 9.3%; Score 86.5; DB 4; Best Local Similarity 25.8%; Pred. No. 0.63; Matches 39; Conservative 24; Mismatches 51;
                                                                                                                 Query Match 9.3%; Score 86.5; DB Best Local Similarity 25.8%; Pred. No. 0.55; Matches 39; Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lee, Cheng-Chi
APPLICANT: Albrecht, Urs
APPLICANT: Bichele, Gregor
APPLICANT: Bichele, Gregor
APPLICANT: Sun, Zhong Sheng
TITLE OF INVENTION Mammalian Circadian Rhytl
FILE REPERENCE: D6039
CURRENT APPLICATION NUMBER: US/09/150,460B
CURRENT FILING DATE: 1998-09-09
FRIOR FILING DATE: 1997-09-09
NUMBER: OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 LGTSEEQLLEAARQEEGDLDRAPCLYSSLAP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               || :|| || || || 251 -CTRFSELL--APQDVG-----VFYGSTAP 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 LGTSEEQLLEAARQEEGDLDRAPCLYSSLAP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/09150460B Patent No. 6190882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
US-09-150-460B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-150-460B-7
```

```
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8;
                                                                                                                                                                                                                                                                                                                               .;
ω
                                                                                                                                                                                                     OTHER INFORMATION: Protein sequence corresponding to RIGUI 4.7; Gene Bank OTHER INFORMATION: Accession Number: AF022991
                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 VESLMEKNTHALLDVQ-LDSVCTLHRMDIFPI-----VIHVSVNEKMAKKLKKGLQR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            535 RPIIILGPTKDRANDDLLSE---FPDKFGSCVPHTTRPKREYEIDGRDXHFVSSREKMEK 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHV- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----SVNEKMA-KKLKKGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWS 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   652 PRSLENVLEINKRITEEQARKAFDRATKLEQEFTE--------CFSAIVEGDSFE 698
                                                                                                                                                                                                                                                                                                                                                                                               50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----LSQEEYEA 41
                                                                                                                                                                                                                                                                                                                                                                   7 LVPRAVGKILSEKLCLLQGFKKCLAE-YLSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Sequence US-09-562-737-21
                                                                                                                                                                                                                                                                                   Length 1290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 9.0%; Score 84; DB 4; Length 724; Best Local Similarity 19.2%; Pred. No. 0.91; Matches 40; Conservative 37; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21, Application US/09562737

Patent No. 6428967

GENERAL INFORMATION:
APPLICANT: Herz, Joachim
APPLICANT: Herz, Joachim
TITLE OF INVENTION:
CURRENT APPLICATION US/09/562,737

CURRENT FILING DATE: 2000-05-01

NUMBER OF SEQ ID NOS: 132

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 21

LENGTH: 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 RPVLLV----PRAVGKILSEKLCLLQGFKKCL-----AEY--
                                                                                                                                                                                                                                                                                   9.3%; Score 86.5; DB 4;
25.8%; Pred. No. 1.1;
tive 24; Mismatches 51;
CURRENT APPLICATION NUMBER: US/09/150,460B CURRENT FILING DATE: 1998-09-09 PRIOR APPLICATION UNMBER: US 60/058,256 PRIOR FILING DATE: 1997-09-09 NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 LGTSEEQLLEAARQEEGDLDRAPCLYSSLAP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 -GTRFSELL--APQDVG-----VFYGSTAP 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 DLDGLLSCVRQAIADEQKKVVWTEQSPR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 699 E---IYHKVKRVIEDLSGPYIWVPARER 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                        Best Local Similarity 25.8%
Matches 39; Conservative
                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                     SEQ ID NO 6
LENGTH: 1290
                                                                                                                                                                                                                                               US-09-150-460B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-562-737-21
                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                       õ
```

```
585 SREKKEKDIQAHKFLEAGOYNSHLMGTSVQSVRENAEQGKHCILQVSANAVRRLRAAHLH 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95 PIVIHV-----SVNEKMAKKL-KKGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  645 PIAISIRPRSLENVTEINKRITEEVARKAFDRATWLEQEFTE--------CFYAI 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35 SQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIF 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5710022el Nuclear Mitotic Phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Sequence
; OTHER INFORMATION: Sequence
15.09-562-737-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATOMIN RC-BOS/MS-DOS
SOFTWARE: PATOMIN RC-BOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,254
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION MATA:
APPLICATION NUMBER: US 08/141,239
FILING DATE: 22-OCT-1993
ATTOMIN MATA:
A
                                                                                                        APPLICANT: NFORMATION:
APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REPERENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/09/562,737
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Campbell and Flores 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 83; DB 4;
Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 LAPDGWSDLDGLLSCVRQAIADEQKKVVWTEQSPR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.9%; Score 83; UB *
Best Local Similarity 18.7%; Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815 REFERENCE/DOCKET NUMBER: P-CJ 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08328254
Patent No. 5710022
GENERAL INFORMATION:
APPLICANT: Lee, Wen-Hwa
TITLE OF INVENTION: A No. 57100226
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Flores
US-09-562-737-29
; Sequence 29, Application US/09562737
; Patent No. 6428967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            San Diego
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
US-08-328-254-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
```

4

```
Вp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        œ
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHV- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --SVNEKMAKKLKKGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          652 PROLENVLEINKSITEEQARKATDRATKL --- EQEVTEC -------FSAIVE 693
                                                                                                                                                                                                                                                                                                                          92 DIFPIVIHVSVNEKMAKKLK------KGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 RPVLLV----PRAVGKILSEKLCLLQGFKKCL-----AEYL------SQEEYEA 41
                                                                                                                                                                                                                                                                                                   ----THALLDVQLDSVCTLHRM 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-562-737-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26;
                                                                                                                                                                                                                 8.7%; Score 81; DB 1; Length 2482;
23.7%; Pred. No. 11;
tive 21; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 8.6%; Score 80; DB 4; Length 724; Best Local Similarity 18.5%; Pred. No. 2.5; Matches 39; Conservative 36; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Herz, Joachim
APPLICANT: Herz, Joachim
APPLICANT: Gothardt, wilchael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708
CURRENT FAPPLICATION NUMBER: US/09/562,737
CURRENT FILIKG DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 24
LENGTH: 724
                                                                                                                                                                                                                                                                                                 44 QRGDII----QEGEVSGGRCWVTRHAVESLMEKN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    963 -------DCLRKQYLSENEQ--WQQK 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                         145 LAPDGWSDLDGLLSCVRQAIADEQKKVVWTEQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 GWSDLDGLLSCVRQAIADEQKKVVWTEQSPR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -WDSFEEIYHKYKRVIEDLSGAYIWVPARER 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24, Application US/09562737 Patent No. 6428967
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 2482 amino acids
                                                                                                                                                                                                                                                          Matches 36; Conservative
                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
US-09-562-737-24
                                                                                                                                                                  ; MULECULE II
US-08-328-254-6
                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          694
                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

RESULT 12 US-08-353-700-1

```
۲;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Yen, Timothy J.
APPLICANT: Rattner, Jorone B.
TITLE OF INVENTION: Nucleic Acid Encoding a Transiently
TITLE OF INVENTION: Expressed Kinetochore Protein, and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1598 QTGDMSLLSNLEGVVSANQCSVDEVFCSSLQEENLTRKETPSAPAKGVEELESLCEVYRQ 1657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92 DIFPIVIHVSVNEKMAKKLK------KGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 QRGDII----QEGEVSGGRCWVTRHAVESLMEKN-----THALLDVQLDSVCTLHRM 91
                                                                   APPLICANT: YEN, TIMOTHY J.
APPLICANT: RATTWER, JEROME B.
TITLE OF INVENTION: NUCLEIC ACID ENCODING A
TITLE OF INVENTION: TRANSIENTLY-EXPRESSED KINETOCHORE PROTEIN,
TITLE OF INVENTION: AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 3248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
                                                                                                                                                                                                                              ADDRESSEE: DANN, DORFMAN, HERRELL AND SKILLMAN
STREET: 1601 MARKET STREET, SUITE 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 8.6%; Score 80; DB Best Local Similarity 23.7%; Pred. No. 21; Matches 36; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1691 ------LDCLRKQYLSENEQ--WQQK 1708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 LAPDGWSDLDGLLSCVRQAIADEQKKVVWTEQ 176
                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08353700 Patent No. 5599919 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: REED, JANET E.
REGISTRATION NUMBER: 36,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 3248 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 09-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Dann, Dor
                                                                                                                                                                                                                                                                          CITY: PHILADELPHIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT-US95-16216-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-353-700-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
```

```
87 TLHRMDIFPIVIHVS---VNEKMAKKLKKGLQRLGTSEEQ--LLEAARQEEGDLDRAPCL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 KKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVC 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08602656
| Patent No. 5679571
| GENERAL INFORMATION:
| TILLE OF INVENTION: Recombinant D-Hydantoinase, A Process For the TITLE OF INVENTION: Production and Use TITLE OF SEQUENCES: 4
| CORRESPONDENCE ADDRESS: ADDRESSE: Felfe & Lynch STREET: 805 Third Avenue CITY: New York City STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : DB 1; Length 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
8.2%; Score 76.5; DB
Best Local Similarity 24.8%; Pred. No. 3.3;
Matches 32; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: P 43 28 829.4 FILING DATE: 27-AGGUST-1993 ATTORNEY. AGENT INFORMATION: NAWE: Hanson, No. 5679571man D. REGISTRATION NUMBER: 30,946 REPRENCE/DOCKET NUMBER: BOER 1041 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 688-9200
                    PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PTLING DATE: 27-AUGUST-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 552324man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 30,946
REFERENCE/COCKET NUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WOrdperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,656
FILING DATE: 16-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08/289,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-AUGUST-1994
12-AUGUST-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 12-AUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
US-08-289-709-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 YSSLAPDGW 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                287 WSPPLREKW 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-08-602-656-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1598 QTGDMSLLSNLEGVVSANQCSVDEVFCSSLQEENLTRKETPSAPAKGVEELESLCEVYRQ 1657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 DIFPIVIHVSVNEKMAKKLK-----KGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 QRGDII----QEGEVSGGRCWVTRHAVESLMEKN-----THALLDVQLDSVCTLHRM 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BUTLSCHEY, Helmut; Lang, Gunter; Popp, Friedrich
TITLE OF INVENTION: Recombinant D-Hydantoinase, A Process For the
TITLE OF INVENTION: Production and Use
TITLE OF INVENTION: Production and Use
CORRESPONDENCE: 4
ADDRESSE: ADDRESS:
ADDRESSE: Relfe & Lynch
STREET: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1658 SL-----EKLEEKMESQGIMKNKEIQEL----EQLLSSERQE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

8.6%; Score 80; DB 5; Length 3248;
Best Local Similarity 23.7%; Pred. No. 21;
Matches 36; Conservative 21; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1691 ------WQQK 1708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 LAPDGWSDLDGLLSCVRQAIADEQKKVVWTEQ 176
                                                                                                                                                                                                                                                                                                                                     APPLICALLOND
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 09-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3248 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/289,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08289709
Patent No. 5523224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SS: not relevant not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
                                                                COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
          Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ANTI-SENSE:
PCT-US95-16216-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-289-709-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

```
4;
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                          27 KKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVC 86
                                                                                                                                   Query Match

8.2%; Score 76.5; DB 1; Length 460;
Best Local Similarity 24.8%; Pred. No. 3.3;
Matches, 32; Conservative 21; Mismatches 43; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                        Search completed: January 22, 2003, 08:57:42 Job time: 15.2702 secs
TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 460 amino acids
TYPE: amino acid
STRANDEDNESS: single
COPOLOGY: linear
                                                                                                                                                                                                                                                                                                                142 YSSLAPDGW 150
                                                                                                                                                                                                                                                                                                                                     : | : 1
287 WSPPLREKW 295
                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                          QQ
```

OLISO) XINTE BY WK (ORALO)

Sequence 152, App

Sequence

Sequence 409, App Sequence 10062, A Sequence 12540, A Sequence 12540, A Sequence 4, Appli Sequence 574, Ap Sequence 574, Ap Sequence 374, Ap Sequence 52, Appl Sequence 52, Appl Sequence 9, Appli Sequence 9, Appli Sequence 13, Appli Sequence 12, Appli Sequence 9, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13262, A Sequence 13262, Appli Sequence 1326, Appli Sequence 13262, Appli Sequence 13262, Appli Sequence 13262, Appli Sequence 13262, Appli

Sequence 2, Appli

Title: Perfect score:

Run on:

Scoring table: Sequence:

Minimum DB seq Maximum DB seq

Database

```
61 VTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRLGTS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RPRPVLLVPRAVGKILSEKLCLLQGFKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGRCW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 EEQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTEQSPR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09767215
Patent No. US20020081636A1
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-142001
CURRENT APPLICATION NUMBER: US/09/767,215
CURRENT FILING DATE: 2001-01-22
PRIOR PILING DATE: 2000-02-09
PRIOR FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
0 US-09-783-320-46

0 US-09-994-288-5

0 US-09-72-200

2 US-10-078-929-152

0 US-09-815-242-10062

0 US-09-815-242-10062

0 US-09-815-242-10662

0 US-09-815-242-10540

0 US-09-73-68-88

0 US-09-73-68-88-88

0 US-09-73-626-4244

0 US-09-73-626-5074

0 US-09-73-626-5074

0 US-09-73-626-5074

0 US-09-913-75-938

0 US-09-913-76-938

0 US-09-919-172-29

0 US-09-919-172-29

0 US-09-911-72-29

0 US-09-911-72-29

0 US-09-813-74-86-9

0 US-09-911-72-29

0 US-09-813-74-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 930; DB 10; Best Local Similarity 100.0%; Pred. No. 7e-87; Matches 179; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                            US-10-023-437-9
US-09-895-913A-326
US-09-925-301-1335
US-09-866-582-39
US-09-978-729A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
   576
576
1614
1004
1004
336
336
336
336
336
336
336
634
443
441
441
1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-09-767-215-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 2
LENGTH: 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-767-215-2
   TYPE: PRT
   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Óχ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Appli
Sequence 12, Appli
Sequence 59, Appli
Sequence 2, Appli
Sequence 358, Appli
Sequence 26, Appli
Sequence 27, Appli
Sequence 34, Appli
Sequence 34, Appli
Sequence 36, Appli
Sequence 36, Appli
Sequence 36, Appli
Sequence 37, Appli
Sequence 36, Appli
Sequence 37, Appli
Sequence 48, Appli
Sequence 48, Appli
Sequence 48, Appli
Sequence 48, Appli
Sequence 38, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Appli
Sequence 5, Appli
                                                                                                                          (without alignments) 500.428 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                            January 22, 2003, 08:49:35; Search time 7.21774 Seconds
                                                                                                                                                                                                    1 RPRPVLLVPRAVGKILSEKL......VRQAIADEQKKVVWTEQSPR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO0_UBCOMB.pep:*
//cgn2_6/ptodata/2/pubpaa/USO0_UBCW_PUB.pep:*
//cgn2_6/ptodata/2/pubpaa/USO0_UBCW_PUB.pep:*
//cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
                 GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-767-215-2
US-10-032-159A-8
US-110-032-905-12
US-010-032-159A-8
US-010-039-905-12
US-09-919-497-98
US-09-919-497-98
US-09-919-497-59
US-09-919-497-59
US-09-919-497-59
US-09-918-320-36
US-09-783-320-42
US-09-783-320-44
US-09-783-320-44
US-09-783-320-44
US-09-783-320-40
US-09-783-320-40
US-09-783-320-40
US-09-783-320-40
US-09-783-320-40
US-09-783-320-40
US-09-783-320-30
                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                             122226 seqs, 20178551 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                          US-09-767-215-2_COPY_826_1004
930
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                          length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1004
11138
11247
1736
669
669
867
1155
1195
2240
2240
2240
2240
2240
225
2260
236
236
250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101
111:::1
```

ö

Gaps

0

Sequence 5, Application US/09767215 Patent No. US20020081636A1

RESULT 2 US-09-767-215-5

Score

Result δ. Θ a

176 0 176

```
δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 GGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 RLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 VTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRLGTS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                994
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RPRPVLLVPRAVGKILSEKLCLLQG---FKKCLAEYLSQEEYEAWSQRGDII--QEGEVS 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RPRPVLLVPRAVGKILSEKLCLLQGFKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGRCW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 8, Application US/10032159A; Sequence 8, Application US/10032159A; Patent No. US20020164703A1; GENERAL INFORMATION: PAPLICANT: Pawlowski, Krzysztof; APPLICANT: Pawlowski, Krzysztof; APPLICANT: Reed, John C.; APPLICANT: Godzik, Adam; TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES, TITLE OF INVENTION: ENCODING NUCLEIC ACIDS, AND METHODS OF USE; FILE REFERENCE: P-LJ 5100; CURRENT APPLICATION NUMBER: US/10/032,159A; CURRENT FILING DATE: 2001-12-19; PRIOR APPLICATION NUMBER: US 60/257,457; PRIOR FILING DATE: 2000-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 EEQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                   APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: 07334-142001
CURRENT APPLICATION NUMBER: US/09/767,215
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 60/181,159
PRIOR FILING DATE: 2000-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 26.1%; Score 242.5; DB 9; Best Local Similarity 31.5%; Pred. No. 1.7e-16; Matches 57; Conservative 41; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                               Query Match 95.1%; Score 884; DB 10; Best Local Similarity 100.0%; Pred. No. 4.2e-82; Matches 171; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens US-10-032-159A-8
                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-09-767-215-5
  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1247
                                                                                                                                                                                                                                                        SEQ ID NO 5
LENGTH: 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-032-159A-8
                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 DIAAGDFIEHAEFSGNLYGTSKVAVQAVQAMNRICVLDVDLQGVRNIKATDLRP--IYIS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 VNEKMAKKLKKGLQRLGT-SEEQLLE--AARQEEGDLDRAPCLYSSLAPDGWSDLDGLLS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFFIVIHVS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 EYLSQEE---YE-AWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 PRPVVLSGPSGAGKSTLLKRLLQEHSGIFGFSVSHTTRNPRPGEENGKDYYFVTREVMQR 63
                                                                                                    Sequence 12, Application US/10029905

Patent No. US20020160438A1

GENERAL INFORMATION:

APPLICANT: Boehringer Ingelheim Pharma KG

TITLE OF INVENTION: Method for identifying compounds which positively

TITLE OF INVENTION: influence inflammatory conditions

FILE REFERENCE: 1/1177

CURRENT APPLICATION NUMBER: US/10/029,905

CURRENT FILING DATE: 2001-12-21

PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 98, Application US/09919497
Patent No. US20020106662a1
GENERAL INFORMATION:
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR FILING DATE: 2000-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 11.1%; Score 103.5; DB 10; Length Best Local Similarity 21.2%; Pred. No. 0.044; Matches 35; Conservative 36; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.8%; Score 119.5; DB 9; 25.5%; Pred. No. 5.6e-05; iive 38; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 PRPVLLV-PRAVGKILSEKLCLLQ-----GFKKCLAE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 25.5%
                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 CVRQAIADEQKK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-09-919-497-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens US-10-029-905-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :::|:::| ||
180 ELKEALSEEIKK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-919-497-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 98
LENGTH: 1736
1244 E 1244
                                                                                        US-10-029-905-12
                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 12
LENGTH: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ÓΫ
```

```
ω
,
                                                                                                                                                                                                                                         US-09-19-497-59

Sequence 59, Application US/09919497

Patent No. US-0020106662A1

SEQUENCE 59, Application US/09919497

Patent No. US-0020106662A1

SEQUENCE TOWNERMATION:

APPLICANT: Mutter, George L.

TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER

FILE REFERENCE: B0801/7225

CURRENT APPLICATION NUMBER: US/09/919,497

CURRENT FILING DATE: 2001-07-31

PRIOR APPLICATION NUMBER: US 60/221,735

PRIOR APPLICATION NUMBER: US 60/221,735

PRIOR SEQ ID NOS: 100

SOFTWARE: Patentin version 3.0

SEQ ID NO 59

LENGTH: 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09807721

Patent No. US2002017445341

GENERAL INFORMATION:
APPLICANT: UNIVERSITY
APPLICANT: UNIVERSITY OF CENTRAL FLORIDA
TILE OF INVENTION: PRODUCTION OF ANTIBODIES IN TRANSGENIC PLASTIDS
FILE REFERENCE: 1463-PCT-US-00
CURRENT APPLICATION NUMBER: 2001-12-21
FRICH APPLICATION NUMBER: PCT/US01/06274
PRIOR APPLICATION NUMBER: PCT/US01/06274

PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 2
LENGTH: 669
                                                                578 RPIIILGPTKDRANDDLLSE---FPDKFGSCVPHTTRPKREYEIDGRDYHFVSSREKMEK 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . : : | :
------CFSAIVEGDSFE 741
647 EKLAREEPDIYQIAKSEPRDAGTDQRSSG---YIRLHTIKQIIDQDKHALLDVTPNAVDR 703
                                           --AKKLKKGLORLGTSEEQLLEAARQE 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHV- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----SVNEKMA-KKLKKGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWS 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 RPVLLV----PRAVGKILSEKLCLLQGFKKCL-----AEY------LSQEEYEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81; Indels
                                                                                                                                                132 EGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTEQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          695 PRSLENVLEINKRITEEQARKAFDRATKLEQEFTE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 84;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : : | :: | . : | E---IYHKVKRVIEDLSGPYIWVPARER 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152 DLDGLLSCVRQAIADEQKKVVWTEQSPR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 19.29
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-919-497-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
US-09-807-721-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-807-721-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                         88
                                                                                                                                                                761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            742
                                                                             g
                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      οŻ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                         δ
                                                                                                                       οχ
```

```
APPLICANT: Turner C. Alexander Jr
APPLICANT: Zambrowicz, Brian
TITLE OF INVENTION: NO. US20020038011A1el Human Kinases and Polynucleotides Encodi
FILE REFERENCE: LEX-0137-USA
CURRENT APPLICATION NUMBER: US/09/783,320
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Al-Garawi, Amal APPLICANT: Al-Garawi, Amal APPLICANT: Miller, Charles APPLICANT: Miller, Charles APPLICANT: Miller, Charles APPLICANT: Tomb, Jean Francois APPLICANT: Oomen, Raymond P.

TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Encoding No. US20020160456Alel Helicobacter Polypeptides in tTITLE OF INVENTION: Genome FILE REFERENCE: 06132/043002
CURRENT APPLICATION NUMBER: US09/895,913A
CURRENT FILING DATE: 2001-06-29
PRIOR FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 368
SOFTWARE: FastSEQ for Windows Version 4.0
                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                   66 VESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRLGTSE---- 121
                                           Gaps
                                                                              1 RPRPVLLVPRAVGKILSEKL---CLLQGF--KKCLAEYLS-----QEEYEAWSQRGDII 49
                                                                                                                                                            -- EGEVSGGRCWV-----TRHAVESLMEKNTHALLDV- 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 LLVPRAVGKILSEKLCLLQGFKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 -- EQLLEAARQEEGDLDRAPCLYSSLAPD-----GWSDLDGLLSCVRQAIADEQKK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 9; Length 867;
Length 669;
                                         Indels
                                         44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63;
  DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 LLTPEA-KKLLEEAKESLKAYKDCLSQARNEEE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 6.3;
                                       19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28; Mismatches
                                                                                                                                                                                                                                                                 81 -- QLDSVCTLHRMDIF----PIVIHVSVNEKM 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.4%; Score 78.5; 22.0%; Pred. No. 6.
8.6%; Score 80;
25.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 358, Application US/09895913A
; Patent No. US200201060456A1
GENERAL INFORMATION:
; APPLICANT: Kleanthous, Harold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 26, Application US/09783320
Patent No. US20020038011A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hu, Yi
APPLICANT: Nepomnichy, Boris
                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 22.0%
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Walke, D. Wade
                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-895-913A-358
                                                                                                                                                                                                                                                                                                                                                            US-09-895-913A-358
                                       39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-783-320-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
  Query Match
                                                                                                                                                          20
                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
                                                                                                                 q
                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                       Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                              ò
                                                                                                                                                          ŏ
                                                                                                                                                                                                                                        öλ
```

```
APPLICANT: Walke, D. Wade
APPLICANT: Walke, D. Wade
APPLICANT: Walke, D. Wade
APPLICANT: Hu, Yi
APPLICANT: Hu, Yi
APPLICANT: Turner, C. Alexander Jr
APPLICANT: Zambrowicz, Brian
TITLE OF INVENTION: No. US20020038011A1e1 Human Kinases and Polynucleotides Encodi
FILE REFERENCE: LEX-0137-USA
CURRENT APPLICATION NUMBER: US/09/783,320
CURRENT FILING DATE: 2001-02-15
PRIOR PRIOR APPLICATION NUMBER: US 60/183,582
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-2
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FRASEQ for Windows Version 4.0
SEQ ID NO 42
LENGTH: 211
                              APPLICANT: Zambrowicz, Brian
TITLE OF INVENTION: No. US20020038011A1el Human Kinases and Polynucleotides Encodi
FILE REPERENCE: LEX.0137-USA
CURRENT ELILOS DATE: 2001-02-15
CURRENT FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-22
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 4.0
SED ID NO 34
LENGTH: 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 FISKHLFETDVQNNKFIEYGEYKNNYYGTSIDSVRSVLAKNKVCLLDVQPHTVKHLRTLE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 FISKHLFETDVQNNKFIEYGEYKNNYYGTSIDSVRSVLAKNKVCLLDVQPHTVKHLRTLE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 YLSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 YLSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10; Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10; Length 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 FKPYVIFIK------PPSIERLRETRKNAKIISSRDDQG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 IFPIVIHVSVNEKMAKKLKKGLQRL-GTSEEQLLEAARQEEG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 IFPIVIHVSVNEKMAKKLKKGLQRL-GTSEEQLLEAARQEEG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
8.3%; Score 77; DB 1
Best Local Similarity 24.5%; Pred. No. 1.4;
Matches 25; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
8.3%; Score 77; DB 1
Best Local Similarity 24.5%; Pred. No. 1.2;
Matches 25; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
US-09-783-320-36
; Sequence 36, Application US/09783320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-783-320-42; Sequence 42, Application US/09783320; Patent No. US20020038011A1; GENERAL INFORMATION:
   Turner, C. Alexander Jr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: homo sapiens
US-09-783-320-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CRGANISM: homo sapiens
US-09-783-320-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hu, YI, APPLICANT: Nepomnichy, Boris
APPLICANT: Turner, C. Alexander Jr
APPLICANT: Zambrowicz, Brian
TITLE OF INVENTION: NO. US20020038011A1e1 Human Kinases and Polynucleotides Encoding
FILE REPERENCE: LEX-0137-USA
CURRENT APPLICATION NUMBER: US/09/783,320
CURRENT FILING DATE: 2000-02-15
PRIOR FILING DATE: 2000-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 FISKHLFETDVQNNKFIEYGEYKNNYYGTSIDSVRSVLAKNKVCLLDVQPHTVKHLRTLE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 FISKHLEFETDVQNNKFIEYGEYKNNYYGTSIDSVRSVLAKNKVCLLDVQPHTVKHLRTLE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 YLSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 YLSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.3%; Score 77; DB 10; Length 155; Best Local Similarity 24.5%; Pred. No. 0.9; Matches 25; Conservative 21; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 FKPYVIFIK------PPSIERLRETRKNAKIISSRDDQG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 IFPIVIHVSVNEKMAKKLKKGLQRL-GTSEEQLLEAARQEEG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 IFPIVIHVSVNEKMAKKLKKGLQRL-GTSEEQLLEAARQEEG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.3%; Score 77; DB 24.5%; Pred. No. 1.1; tive 21; Mismatches
CURRENT FILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: US 60/183,582
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: US 60/184,014
PRIOR FILING DATE: 2000-02-22
NUMBER OF SEQ ID NOS: S0
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 34, Application US/09783320
Patent No. US20020038011A1
GENERAL INFORMATION:
APPLICANT: Hu, Yi
APPLICANT: Nepomnichy, Boris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 28, Application US/09783320
Patent No. US2002038011A1
GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 24.5
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: homo sapiens
US-09-783-320-28
                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: homo sapiens
US-09-783-320-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
US-09-783-320-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-783-320-34
                                                                                                                                                                                                                                                                        LENGTH: 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ολ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ç
```

```
APPLICANT: Neybonnichy, Boris
APPLICANT: Turner, C. Alexander Jr
APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
TITLE OF INVENTION: No. US20020038011A1el Human Kinases and Polynucleotides Encodi
FILE REFREBROE: LEX-0137-USA
CURRENT APPLICATION NUMBER: US 60/183,582
PRIOR APPLICATION NUMBER: US 60/183,582
PRIOR PILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 YLSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.3%; Score 77; DB 10; Length 296; 24.5%; Pred. No. 2.1;
Live 21; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 IFPIVIHVSVNEKMAKKLKKGLQRL-GTSEEQLLEAARQEEG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       255 FKPYVIFIK-------PPSIERLRETRKNAKIISSRDDQG 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: January 22, 2003, 08:52:55
Job time : 8.21774 secs
                                                                                                                                                                       Sequence 32, Application US/09783320 Patent No. US20020038011A1 GENERAL INFORMATION:
APPLICANT: Walke, D. Wade APPLICANT: Hu, Y1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 24.59
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: homo sapiens
                                                                                                                         us-09-783-320-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-783-320-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                            APPLICANT: Mall No. Made
APPLICANT: Mel, N. Made
APPLICANT: Nepomnichy, Boris
APPLICANT: Nepomnichy, Boris
APPLICANT: Turner. C. Alexander Jr
APPLICANT: Lambrowicz, Brian
TITLE OF INVENTION: No. US20020038011A1e1 Human Kinases and Polynucleotides Encoding
FILE REFERENCE: LEX-0137-USA
CURRENT FILING UNMBER: US 60/183,520
CURRENT FILING DATE: 2000-02-15
PRIOR PILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-22
NUMBER OF SEQ ID NOS: 50
SOFTHARE: PEASESEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Nepomnichy, Boris
APPLICANT: Turner, C. Alexander Jr
APPLICANT: Turner, C. Alexander Jr
APPLICANT: Turner, C. Alexander Jr
TITLE ON INVENTION: No. US20020038011A1e1 Human Kinases and Polynucleotides Encoding
FILE REFERENCE: LEX-0137-USA
CURRENT APPLICATION NUMBER: US/09/783,320
CURRENT FILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: US 60/183,582
PRIOR APPLICATION NUMBER: US 60/184,014
PRIOR FILING DATE: 2000-02-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 FISKHLFETDVQNNKFIEYGEYKNNYYGTSIDSVRSVLAKNKVCLLDVQPHTVKHLRTLE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::|: :| | |: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 YLSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 YLSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 8.3%; Score 77; DB 10; Length 240; Best Local Similarity 24.5%; Pred. No. 1.6; Matches 25; Conservative 21; Mismatches 46; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.3%; Score 77; DB 10; Length 22. Best Local Similarity 24.5%; Pred. No. 1.5; Matches 25; Conservative 21; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 FKPYVIFIK------PPSIERLRETRKNAKIISSRDDQG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 IFPIVIHVSVNEKMAKKLKKGLQRL-GTSEEQLLEAARQEEG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 FKPYVIFIK------PPSIERLRETRKNAKIISSRDDQG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 IFPIVIHVSVNEKMAKKLKKGLQRL-GTSEEQLLEAARQEEG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 44
LENGTH: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 44, Application US/09783320 Patent No. US20020038011A1
                                        GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Hu, Yi
US20020038011A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: homo sapiens
US-09-783-320-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-783-320-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-09-783-320-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
```

5

10;

THIS PAGE BLANK (USPIO)

```
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
```

- protein search, using sw model OM protein January 22, 2003, 08:49:35; Search time 13.7137 Seconds (without alignments) 1254.807 Million cell updates/sec Run on:

US-09-767-215-2\_COPY\_826\_1004 score: Title:

930 1 RPRPVLLVPRAVGKILSEKL.....VRQAIADEQKKVVWTEQSPR 179 Perfect sc Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 DB Minimum Maximum

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

Database

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
1: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		dip			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
	130.5	14.0	1281		T00346	hypothetical prote
2		13.2	198		539447	
m	119.5	12.8	197		S68864	
4		12.4			KIPGGU	
5		ч	-		T13703	(1)
9		11.1	1736		A47747	uo
7		•	1745	~	A46431	junction-
8	94.5	10.2		7	T22166	
6		9.6		7	146236	0
10	88	9.5		~	JE0366	junction
11	86.5	9.3		~	T00018	j protein
12	98	9.5		~	H69378	conserved hypothet
13	84.5	9.1		7	F82679	
14	84			7	JH0800	postsynaptic densi
15	84	9.0		7	T09599	
16	83.5	•	646	~	T02643	hypothetical prote
17	83		911	7	156552	υ
18	82	80 .00	849	-	S64732	scaffold attachmen
19	82	-	1225	~	A49464	chromosome segreda
20	80.5		1047	7	G90684	ATP-dependent dsDN
21		8.7	1047		C85535	ATP-dependent dsDN
22	80		414		C69530	3-ketoacyl-CoA thi
23	80	8.6	720		A45436	synapse-associated
24	79.5		920		C96831	hypothetical prote
25	79	٠	1744		F86161	F1003.10 protein -
26	78.5	8.4	379		T10588	
27	78.5	8.4	92	~	A53188	pericentrin - mous
28	78.5	8.4	1927	~	G64585	cag pathogenicity
29	78	8.4	467	7	A57627	p55 erythrocyte me

oxidoreductase, ac	channel associated	KIAA0013 protein (	G1/S transition co	gene X104 protein	hypothetical prote	orotidine-5'-phosp	casein kinase II (	human homolog of D	helicase, UvrD/Rep	guanylate kinase U	probable UDPglucos	class I major hist	cellulose synthase	endopeptidase Clp	hsdR protein - Kle
D82101	T10811	A59431	T02749	154378	T48362	I39845	A54907	G02165	н87687	G82920	T00467	B35878	T02560	AI1720	T30818
~	7	~	~	7	~	7	7	~	7	7	~	7	7	7	~
814	852	1023	471	1116	170	239	258	585	1203	191	375	406	748	866	1013
	4	₹.	٣.	٣.	٣.	٣.	٣.	٠.	٣.	7.	7	. 2	3.2	8.2	3.2
8.4	ω.	œ	8	8	æ	æ	∞	ж	æ	80	œ	ω	w	~	~
	78 8.							77 8		76.5 8					

## ALIGNMENTS

C. Accession: T00346
R. Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, DNA Res. 5, 31-39, 1998
A. Title: Prediction of the coding sequences of unidentified human genes. IX. The comp A. Reference number: 214086; MUID: 98290545; PMID: 9628581
A. Accession: T00346
A. Status: preliminary: translated from GB/EMBL/DDBJ
A. Molecule type: mRNA
A. Molecule type: mRNA
A. Residues: 1-1281
A. Molecule type: mRNA
A. Residues: L-1281
A. Molecule type: mRNA
A. Residues: L-1281
A. hypothetical protein KIAA0583 - human (fragment) C;Species: Homo sapiens (man) C;Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 21-Jul-2000 X)NOTE: KIAA0583 C;Superfamily: guanylate kinase homology F;1102-1270/Domain: guanylate kinase homology <GKI> . '

10; 43 SQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSV 102 Gaps 3 RPVL------LVPRAVGK-----ILSEKLCLLQGFKKCLAEYLSQEEYEAW 42 57; Query Match
14.0%; Score 130.5; DB 2; Length 1281;
Best Local Similarity 26.7%; Pred. No. 0.0018;
Matches 55; Conservative 31; Mismatches 63; Indels 57; g δλ ò

103 NEKMAKKLK------KGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSD 152 1157 qq ŏ Q

LDGLLSCVRQAIADEQKKVVWTEQSP 178 153 1255 g ò

RESULT 2

guanylate kinase (EC 2.7.4.8) - bovine
G'Species: Bos primigenius taurus (cattle)
C'Species: Bos primigenius taurus (cattle)
C'Date: 07-Oct-1994 #sequence\_revision 05-May-1995 #text\_change 19-Jan-2001
C'Accession: 339447, 339448
R'Gaidarov, I.O.; Suslov, O.N.; Abdulaev, N.G.
FEBS Lett. 335, 81-84, 1993
A;Title: Enzymes of the cyclic GMP metabolism in bovine retina. I. Cloning and expres A;Reference number: S39448; MUID:94063086; PMID:8243671

a

```
A;Gene: tamou (tam)
A;Cross-references: FlyBase:FBgn0003177
                                                                                                                                                         quanylate kinase (EC 2.7.4.8) - pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
159 CVROAIADEOKK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                              180 ELKEALSEEIKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: T13703
                                                                                                                                                                                                                                                                                                                  A; Accession: S23776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Simi
Matches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T13703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                         g
    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Fitzgibbon, J; Katsanis, N.; Wells, D.; Delhanty, J.; Vallins, W.; Hunt, D.M. FEBS Lett. 365, 185-188, 1996
A;Title: Human guanylate kinase (GUK1): CDNA sequence, expression and chromosomal localing a Reference number: 568864; MUID:96213684; PMID:8647247
A;Recession: S68864
A;Status: preliminary
A;Moceache Eyps: mRNA
A;Residues: 1-197 <FTT>
A;Cross-references: EMBL:L76200; NID:g1196435; PIDN:AAC37598.1; PID:g1196436
C;Genetics:
A;Gene: GDB:GUK1
A;Cross-references: GDB:119289; OMIM:139270
A;Map position: 1432-1442
C;Superfamily: guanylate kinase; guanylate kinase homology
C;Seyworfs: nucleotide binding: P-loop; Phosphotransferase
F;5-189/Domain: guanylate kinase homology <GKL>
F;11-18/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                             phos
A; Accession: S39447
A; Molecule type: mmNA
A; Residues: 1-198 cGAI>
A; Coss-references: EMBL:X67029; NID:g433073; PIDN:CAA47423.1; PID:g433074
A; Cross-references: EMBL:X67029; NID:g433073; PIDN:CAA47423.1; PID:g433074
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 10-17;24-32;35-82;90-97;121-126;139-146;149-154;178-182 cGA2>
C; Superfamily: guanylate kinase; guanylate kinase homology
C; Keywords: ATP; Dlocked amino end; magnesium; monomer; nucleotide binding; P-loop; P; 5-189/Domain: guanylate kinase homology cGKI>
F;1-18/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Homo sapiens (man)
:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 19-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 DIAAGDFIEHAEFSGNLYGTSKVAVQAWORICVLDVDLQGVRNIKATDLRP--IYIS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 VNEKMAKKLKKGLQRLGT-SEEQLLE--AARQEEGDLDRAPCLYSSLAPDGWSDLDGLLS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 VTREVMORDIAAGDFIEHAEFSGNLYGTSKAAVRAVQAMNRICVLDVDLOGVRNIKKTDL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FPIVIHVSVN--EKMAKKLKKGLQRLGTSEEQLLE--AARQEEGDLDRAPCLYSSLAPDG 149
                                                                                                                                                                                                                                                                                                                                                                                                        55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----YLSQEEYEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 PRPVVLSGPSGAGKSTLLKRLLQEHSGIFGFSVSHTTRNPRPGEENGKDYYFVTREVMOR 63
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                              .---Y 33
                                                                                                                                                                                                                                                                                                                                                                                                     4 PRPVVLSGPSGAGKSTL-----LKKLLQEHGSIFGFSVSHTTRDPRPGEENGKDYYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 LSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27;
                                                                                                                                                                                                                                                                                                                  45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 197;
                                                                                                                                                                                                                                                                        Length 198;
                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5;
                                                                                                                                                                                                                                                                   ; Score 122.5; DB 2;
; Pred. No. 0.001;
35; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 PRPVLLV-PRAVGKILSEKLCLLQ-----GFKKCLAE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.8%; Score 119.5; DB 25.5%; Pred. No. 0.0019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38; Mismatches
                                                                                                                                                                                                                                                                                                                                                              2 PRPVLLV-PRAVGKILSEKLCLLQGFKKCLAE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 -DSLDKAYWALKEALSEEIKKAQGTGQS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 WSDLDGLLSCVRQAIADEQKKVVWTEQS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      guanylate kinase (EC 2.7.4.8) 1 - human
                                                                                                                                                                                                                                                                      13.2%; 24.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 12.8°
Best Local Similarity 25.5°
Matches 49; Conservative
                                                                                                                                                                                                                                                                                             1 Similarity 24.5 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: S68864
                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                               Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94
                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                  á
                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
```

ì

```
tamA protein - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000

C;Accession: T13703

R;Takahisa, M.; Togashi, S.; Suzuki, T.; Kobayashi, M.; Murayama, A.; Kondo, K.; Miya

Genes Dev. 10, 1783-1795, 1996

A;Title: The Drosophila tamou gene, a component of the activating pathway of extramac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Molecule type: protein
A.Residues: 1-197 <282>
C.Superfamily: quanylate kinase; quanylate kinase homology
C.Keywords: acetylated amino end; ATP; magnesium; monomer; nucleotide binding; P-loop
F;4-188/Domain: guanylate kinase homology <GKI>
F;10-17/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 1-197 -2550-
R;Zschocke, P.D.; Schiltz, E.; Schulz, G.E.
Eur. J. Blochem. 213, 263-269, 1993
A;Title: Purification and sequence determination of guanylate kinase from pig brain.
A;Reference number: $32545; MUID:93238695; PMID:8097461
A;Reference number: $32545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL: D83477; NID: 91498136; PIDN: BAA11923.1; PID: 91498137 C; Genetics:
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 19-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FPIVIHVSVN--EKMAKKLKKGLQRLGTSEEQLLE--AARQEEGDLDRAPCLYSSLAPDG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPIXIFVQPPSLDVLEQRLR---QRNTETEESLARRLAAARADMESSKEPGLFDLIIN- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VIREVMORDIAAGDFIEHAEFSGNLYGTSKAAVRAVQAMNRICVLDVDLQGVRNIKKTDL 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 LSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F:35-82/Region: GMP binding #status predicted F:1/Modified site: acetylated amino end (Gly) #status experimental F;16/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                   C;Accession: S23776; S32545
R;Zschocke, P.D.; Schiltz, E.; Schulz, G.E.
submitted to the Protein Sequence Database, September 1992
A;Reference number: S23776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1367 <TAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.4%; Score 115.5; DB 24.0%; Pred. No. 0.0044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 PRPVLLV-PRAVGKILSEKLCLLQGFKKCLAE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 WSDLDGLLSCVRQAIADEQKKVVWTEQS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 -DSLDKAYWALKEALSEEIKKAQATGHS 197
```

```
A. Residues: 1-1745 <ITO>
A. Cross-references: GB:D14340; NID:g303709; PIDN:BAA03274.1; PID:d1003784; PID:g30371
A. Cross-references: GB:D14340; NID:g303709; PIDN:BAA03274.1; PID:d1003784; PID:g30371
A. Experimental source: F9 cells
A. Note: sequence extracted from CRBI backbone (NCBIN:131200, NCBIP:131201)
C. Superfamily: quanylate kinase homology; GLGF domain homology
F:27-106/Domain: GLGF domain homology <GLGI>
F:428-498/Domain: GLGF domain homology <GLGI>
F:645-794/Domain: quanylate kinase homology <GKI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: I46236
R;Jesaitis, L.A.; Goodenough, D.A.
J. Cell Biol. 124, 949-961, 1994
A;Title: Molecular characterization and tissue distribution of 20-2, a tight junction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    980/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 4
A;Introns: 46/2; 105/3; 187/3; 283/1; 365/3; 444/2; 501/2; 605/1; 688/1; 922/2;
                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:268298; PIDN:CAA92607.1; GSPDB:GN00022; CESP:F44D12.1 A;Experimental source: clone F44D12 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F44D12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T22166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tight junction protein - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 16-Dec-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 TRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKK-----GLQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 RLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLS----CVRQAIADEQKKV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 LHRMDIFPIVIHVSVNEKMAKKL------KKGLQRLGTSEEQLLEAARQEEGDLDRA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      32 EYLSQEE---YE-AWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
                                                                                                                                                                                                                                                                                                                                                                 Indels 27;
                                                                                                                                                                                                                                                                                                      Length 1745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47;
                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                              58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTEQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :::|| ::|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ricoles, L. State and Labrary, December 1995 A; Reference number: 219525 A; Reference number: 219525 A; Accession: T22166 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: 0.1034 < WILD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.2%; Score 94.5; D
25.6%; Pred. No. 2.4;
ive 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                              35; Mismatches
                                                                                                                                                                                                                                                                                                  Score 100.5;
                                                                                                                                                                                                                                                                                                                                  Pred. No.
                                                                                                                                                                                                                                                                                                      10.8%;
24.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 25.69
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                 38; Conservative
   A; Molecule type: nucleic acid A; Residues: 1-1745 <ITO>
                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: CESP: F44D12.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1025 VWVQR 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 VWTEQ 176
                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        716
                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T22166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δλ
                                                                                                                                                                                                                                                                                                                                                                                                                            Öλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: The 220-kD protein colocalizing with cadherins in non-epithelial cells is ident
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S.; Kitani-Yasuda, T.; Tsukita, S.; Tsukita,
                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46431
tight junction-associated protein 20-1 - mouse
tight junction-associated protein 20-1 - mouse
C;Species: Mus musculus (house mouse)
C;Species: 21.5ep-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A46431
R;Itch, M: Nagafuchi, A:; Yonemura, S:; Kitani-Yasuda, T.; Tsukita, S:; Tsi
J; Cell Biol. 121, 491-502, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tight junction protein ZO-1 - human
C;Species: Homo sapiens (man)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 05-Nov-1999
                                                                                                                                                            | ::||| :: |:| :| :| :| :| :| SKKLLEQCQK----LERV-----WSHIFSTQIALSDEESWYRKLRDSIDLQQS 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     647 EKLAREEPDIYQIAKSEPRDAGTDQRSSG---YIRLHTIKQIIDQDKHALLDVTPNAVDR 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----AKKLKKGLQRLGTSEEQLLEAARQE 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            704 LNYAQWYPIVVFLNPDSKQGVKTMRMRLCPESRKSARKLYERSHKLAKNNHHLFTTT--- 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                              Gaps
                                                                                                                   3 RPVLLVPRAVGKILSEKLCLLQGFKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGRCWVT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 EYLSQEE---YE-AWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCT 87
                                                                                                                                                                                                                                          RHA-VESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEK-MAKKLKKGLQRLG-T
                                                                                                                                                                                                                                                                                                                                                           SEEQLLEAARQEEGDLDRAPCLYSSLAPDGW-----SDLDGLLSCVRQAIADEQK
   Length 1367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTEQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----INLNSMNDGW----YGALKEAVQQQQNQLVWVSE 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    py.
A;Reference number: A46431; MUID:93252986; PMID:8486731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53;
   DB 2;
                                                           64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
11.9%; Score 110.5; DE 23.4%; Pred. No. 0.12; iive 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.1%; Score 103.5; DE ilarity 21.2%; Pred. No. 0.69; Conservative 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 LHRMDIFPIVIHVSVNEKM-----
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 35; Conserv
                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 KVVWTEQS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          782 GAVWMSES 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A46431
A; Status: preliminary
         Local St...
      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
                            Best Loca
Matches
                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                                                                                           120
                                                                                                                                                                                                                                                                                                                                                                                                                      737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                            Q
                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                           ò
```

4

g

ò

qq ò Dp δ g

à

```
Conserved hypothetical protein AF1032 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Accession: H69378
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
T; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes,
Smith, H.O.; Woese, C.R.; Venter, J.C. C
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-886 <KLE>
A;Cross-references: GB:AE001032; GB:AE000782; NID:92689355; PIDN:AAB90211.1; PID:9264
C;Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032
Nature 389, 512-516, 1997
A;Title: Circadian oscillation of a mammalian homologue of the Drosophila period gene
A;Reference number: 214056; MUID:97472418; PMID:9333243
A;Accession: T00018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         conserved hypothetical protein XF1453 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1290 <TEL>
A;Cross-references: EMBL:AB002107; NID:q2506044; PIDN:BAA22633.1; PID:q2506045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VESLMEKNTHALLDVQ-LDSVCTLHRMDIFPI-----VIHVSVNEKMAKKLKKGLQR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----MDMSTYTLEELEHITSEYTLQNQDTFSVAVSFLTGRIVYISEQAAVLLRCKRDVFR 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 THALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRLGTSEEQLLEAARQEE- 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 KILSEKLCILQGFKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 LVPRAVGKILSEKLCLLQGFKKCLAE-YLSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 SEEVRNLE-----SRLKELEEHKSRLESLRKQESSVLQEVRGLEEKLRELEKQLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149 LPPERRGKGRSGTLATLQYALACVKQVQANQEYYQQWS-----LEEGEPCS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 ----GDLDRAPCLYSSLAP--DGWSDLDGLLSCVRQAIADEQKK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VYERIEDLEKKAKEVKELKPKAERYSILEKLLSEINQALRDVEKR 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51;
                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 9.2%; Score 86; DB 2; 1 Similarity 26.1%; Pred. No. 12; 43; Conservative 33; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 9.3%; Score 86.5; D
Best Local Similarity 25.8%; Pred. No. 16;
Matches 39; Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 LGTSEEQLLEAARQEEGDLDRAPCLYSSLAP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: brain C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 17q12-13.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 43; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
F82679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Light junction protein, ZO-2 - chicken
C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Accession: J5-30-1-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jul-2000
C; Accession: J5036
R; Collins, J.R.; Rizzolo, L.J.
Biochem. Biophys. Res. Commun. 252, 617-622, 1998
A; Title: Protein-binding domains of the tight junction protein, ZO-2, are highly conservence number: J50366; MuID: 99057550; PMID: 9837755
A; Reference number: J50366
A; Status: preliminary
A; Residues: preliminary
A; Wolecule type: mRNA
A; Residues: 1-1163 <COL>
A; Cross-references: GB: AF085184; NID: 93820579; PIDN: AAC95469.1; PID: 93820580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  period protein homolog - human
C;Species: Homo Sapiens (man)
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000
C;Accession: T00018
R;Tei, H.; Okamura, H.; Shigeyoshi, Y.; Fukuhara, C.; Ozawa, R.; Hirose, M.; Sakaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 CWYTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRLG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 TSEEQLLEAARQEEGDLDRAPCLY-----SSLAPDGWSDLDGLLSCVRQAIADEQKKV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                415 PTSNKSSRKLYDQANKLKKT-CAHLFTATINLNSANDSW-----FGSLKDTIQHQQGEA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 VTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRL--- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 -GTSEEQLLEAARQEEGDLDR--APCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       801 SNKSSRKLYEQANKLKKTCSHLFTATINLNSANDSW-----YGSLKDTIQQQQGEAVWV 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 RPVLL----VPRAVGKILSEKLCLLQGFKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGR 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316 RPVVLFGPIADIALEKLANELPDLFQTAK-----TEPKDAGSEKSSGV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39;
                                                                                                                                                                                                                                                                                                                                                                                                 Length 775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 9.5%; Score 88; DB 2; Length 1163; Best Local Similarity 25.4%; Pred. No. 11; Matches 31; Conservative 21; Mismatches 56; Indels
                A;Reference number: A54475; MUID:94179414; PMID:8132716
A;Accession: 146236
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-775 <JES>
A;Cross-references: GB:L27152; NID:9463047; PID:9507892
C;Genetics:
A;Gene: ZO-2
C;Genetics:
A;Gene: ZO-2
C;Genetics:
A;Gene: ZO-2
F;101-171/Domain: GLGF domain homology; GLGF domain homology
F;101-171/Domain: guanylate kinase homology <GKI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              74;
                                                                                                                                                                                                                                                                                                                                                                                                    ;
;
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.6%; Score 89.5; D
Best Local Similarity 22.7%; Pred. No. 4.9;
Matches 42; Conservative 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 11;
21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              Score 89.5;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       468 VWVSE 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SE 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
```

ò g ò à

```
Search completed: January 22, 2003, 08:54:45
Job time : 16.7137 secs
                                                                                                                                                                                                                                                                            101 ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSD95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   742
                                                                                                                                                                                                                                                                                                                                                                                                             152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΩD
                                                                          qq
                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δy
                                                                                                                                              ò
C:Accession: F82679
Ranonyous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequer Ranonyous, The Xylella fastidiosa of the plant pathogen Xylella fastidiosa.
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: F82679
A:Status: preliminary
A:Residues: 14-29 <SINA
A:Residues: 14-29 <SINA
A:Residues: 14-29 <SINA
A:Residues: 14-20 <SINA
A:Cross-references: GB:AE003975; GB:AE003849; NID:g9106468; PIDN:AAF84262.1; GSPDB:GN001
A:Rexperimental source: strain 95c
R:Simpson, A.J.G: Renneoth, R.P.; Camargo, A.P.; Ferreira, A.J.S.
B:Riomeson, A.J.G.; Renneoth, R.P.; Camargo, A.P.; Ferreira, A.J.S.
B:Riomeson, A.J.G.; Renneoth, R.P.; Camargo, L.E.A.; Kuranae, B.E.; Laigr Chado, M.A.; Madelra, A.M.B.N.; Madelra, H.M.F.; Marcoa, B.C.; Miyaki, C.Y.; Frohm
J.D.; Junqueira, M.L.; Renneor, B.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, B.E.; Laigr Chado, M.A.; Madelra, A.M.B.N.; Madelra, M.P.; Marcoa, B.C.; Miyaki, C.Y.; Rosa, A.J. de M.; de Rosa Jr. V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A; Authors: da Silva, A.C.R.; da Silva, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: Ap9328
A:Genetics:
A:Genetics:
A:Genetics:
A:Genetics:
A:Gene: XF1453
C:Superfamily: Haemophilus influenzae conserved hypothetical protein H11590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Postsynaptic density protein PSD-95 - rat

N.Alternate names: brain specific PSD-95 protein; discs-large tumor suppressor protein P
C.Species: Rattus norvegicus (Norway rat)
C.Spate: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C.Accession: JH0800; S26407
R.Ch. K.O.; Hunt, C.A.; Kennedy, M.B.
R.Cho, K.O.; Hunt, C.A.; Kennedy, M.B.
A.Title: The rat brain postsynaptic density fraction contains a homolog of the drosophil A; Reference number: JH0800; MUID:93040233; PMID:1419001
A; Reference number: JH0800
A; Molecule type: mRNA
A; Residues: 1-724 cCHO>
A; Roberfamily: discs-large tumor suppressor; GLGF domain homology cGLG1>
F; 70-148 / Domain: GLGF domain homology cGLG2>
F; 716-243 / Domain: GLGF domain homology cGLG2>
F; 435-493 / Domain: guanylate kinase homology cGKI>
F; 535-712 / Domain: guanylate kinase homology cGKI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ъ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 FPIVIHVSVNEKMAKKLKKGL--QRLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWS 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 LSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDI 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 9.0%; Score 84; DB 2; Length 724; Best Local Similarity 19.2%; Pred. No. 14; Matches 40; Conservative 37; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 9.1%; Score 84.5; DE Local Similarity 24.1%; Pred. No. 6.8; es 34; Conservative 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 DLDGLLSC--VRQAIADEQKK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | | | :: : | :| :: | 205 DEDGQMTADLLSQVLADRSRR 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
GLGF domain homology; guanylate kinase h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         postsynaptic density protein 95 - human
C;Species: Homo sapiens (man)
C;Date: 16-Jul.1999 #sequence_revision 16-Jul-1999 #text_change 21-Jan-2000
C;Accession: T05599
R;Stathakls, D.G.; Hoover, K.H.; You, Z.; Bryant, P.J.
submitted to the EMBL Data Library, July 1998
A;Reference number: 216761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHV- 100
                               42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHV- 100
                                                                                                                                        ---SVNEKMA-KKLKKGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWS 151
                                                                                                                                                                                                                                                                        652 PRSLENVLEINKRITEEQARKAFDRATKLEQEFTE-----------CFSAIVEGDSFE 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----SVNEKMA-KKLKKGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWS 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----CFSAIVEGDSFE 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
--LSQEEYEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-767 <STA>
A;Cross-references: EMBL:U83192; NID:g3318652; PID:g3318653
A;Experimental source: mammary
C;Genetics:
3 RPVLLV----PRAVGKILSEKLCLLQGFKKCL-----AEY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 RPVLLV----PRAVGKILSEKLCLLQGFKKCL----AEY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       695 PRSLENVLEINKRITEEQARKAFDRATKLEQEFTE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 9.0%; Score 84; DB 2; Best Local Similarity 19.2%; Pred. No. 15; Matches 40; Conservative 37; Mismatches 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Superfamily: discs-large tumor suppressor; GLGF F; 208-28/Domain: GLGF Gomain homology <GLG> F; 478-755/Domain: S13 homology <SH3> F; 578-755/Domain: guanylate kinase homology <GKI>
                                                                                                                                                                                                                                                                                                                                                                  DLDGLLSCVRQAIADEQKKVVWTEQSPR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLDGLLSCVRQAIADEQKKVVWTEQSPR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E---IYHKVKRVIEDLSGPYIWVPARER 766
```

THIS PAGE BLANK (USPTO)

-

```
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

January 22, 2003, 08:49:35 ; Search time 6.97715 Seconds (without alignments) 1064.082 Million cell updates/sec Run on:

US-09-767-215-2\_COPY\_826\_1004 930 1 RPRPVLLVPRAVGKILSEKL.....VRQAIADEQKKVVWTEQSPR 179 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result		% Query			SUMMAKIES	
No.	Score	Match	Length	DB	ID	Description
1	m	100.0	1004	П	CARE_HUMAN	Q9bx16 homo sapien
7		6	666	П	CARE_MOUSE	mus m
٣		9	1147	П	CARB_HUMAN	Q9bx17 homo sapien
4	185.5	19.9	1021	٦	CARA_MOUSE	mus n
S		₩.	1032	Н	CARA_HUMAN	Q9bwt7 homo sapien
9		ω.		ч	KGUA_MOUSE	mus m
7		13.2		П	KGUA_BOVIN	P46195 bos taurus
æ		ς.		П	KGUA_HUMAN	Q16774 homo sapien
6		ć.		7	KGUA_PIG	s sns
10		ij		П	ZO1_HUMAN	Q07157 homo sapien
11		٥.		Н	ZO1_MOUSE	mus m
12		。		П	ZO2_MOUSE	mus m
13	91			~	DLG3_HUMAN	Q92796 homo sapien
14	06			-	DLG3_MOUSE	mus m
12	g			П	DLG3_RAT	
16	89.5			Н	ZOZ_CANFA	Q95168 canis famil
17		٠		П	ZO2_HUMAN	
18	∞			<del>-</del>	ZO3_CANFA	canis
19	86.5			-	PER1_HUMAN	
20	98			П	RA50_ARCFU	
21	84			П	DLG4_MOUSE	
22	84			П	DLG4_RAT	
23	84	٠		П	DLG4_HUMAN	рошо
24	83	٠		П	MTTF_HUMAN	homo
25	83			-	DLG1_RAT	rattn
56	æ			П	SMC1_YEAST	
27	81.5			П	KGUA_RALSO	Q8xxf9 ralstonia s
78	81	٠		П	ZO3_MOUSE	Q9qxy1 mus musculu
59	80	•		П	CENF_HUMAN	homo
30	7	•		-	ZO3_HUMAN	95049 homo
31	78.5	8.4	1920	Н	- 1	48725 mus n
32	78	8.4	467	Н	EM55_FUGRU	Įп
33	78	8.4	852	٦	DLG2_RAT	3622

P25971 bacillus su P38930 saccharomyc Q13368 homo sapien Q9pqs9 ureaplasma P13215 simian cyto Q35973 mus musculu P53016 caenorhabdi P24708 actus trivi Q15700 homo sapien Q64311 mus musculu O94916 homo sapien Q64311 mus musculu	TS	004 AA. ddate) update) (CARD-containing MAGUK protein	Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.	MEDLINE=21192234; PubMed=11278692; MEDLINE=21192234; PubMed=11278692; Bertin J., Wang L., Guo Y., Jacobson M.D., Poyet JL., Srinivasula S.M., Merriam S., Distefano P.S., Alnemri E.S.; CARD11 and CARD14 are novel caspase recruitment domain (CARD)/membrane-associated guanylate kinase (MAGUK) family members that interact with Bc110 and activate NF-kappaB."; J. Biol. Chem. 276:11877-11882(2001).	et D., Thome M., Tschopp J.; ner of Bcll0, induces Bcll0 n.";	et D., Thome M., Tschopp J.;	vix, and Colon; R.; (DEC-2000) to the EMBL/GenBank/DDBJ databases. (NS Activates NF-kappaB via Bcl10 and IKK. Stimulates the orylation of Bcl10. T: CARD14 and Bcl10 bind to each other by CARD-CARD	- INTERECTION.  - SUBCELLULAR LOCATION: Cytoplasmic.  - TISSUE SPECIFICITY: Expressed in placenta. Also detected in HeLa S3 cells, but not in the other cancer cell lines tested.  - SIMILARITY: CONTAINS 1 CARD DOMAIN.  - SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.  - SIMILARITY: CONTAINS 1 GUANYLATE KINASE-LIKE DOMAIN.  - CAUTION: Supposed to contain a SH3 domain which is not detected by PROSITE, Pfam or SWART.	ht. It is produced through a collaboration Bioinformatics and the EMBL outstation-iltute. There are no restrictions on its is as long as its content is in no way
PYRE_BACSU KC2C_YEAST MMP3_HUMAN KGUA_UREPA DNBI_SCMVC PERI_MOUSE PERI_MOUSE DLG2_CAEEL INVO_AOTTE DLG2_HUMAN DLG3_HUMAN DLG1_HUMAN PNAD_MOUSE	ALIGNMENTS	PRT; 1( lence up otation	Sraniata; Satarrhir	592; cobson M. Distefanc aspase re nylate ki ctivate N	195; O., Bonr Jing part activatic	O., Bonnet	COM N.A.  Colon;  to the EMBL/GenBar  tes NF-kappaB via F  of Bcl10.  and Bcl10 bind to e	plasmic. sed in pl ther canc D DOMAIN. ZDHR DOMAIN. NYLATE K1 in a SH3	OT entry is copyright. It is Swiss Institute of Bioinform Bioinformatics Institute. T profit institutions as long
		DARD; I, Created) 1, Last sequil, Last anno domain proj	ta; (es; (	1278 , Jac S., Jac S., Jac S., Jac gual nd a	1356 heau bin paB	Micheau 3(2001).	 - kap 10.	Cytol pressible of CARI PDZ, GUAL	opyr te o s In
<b>ненененене</b>		; rea ast ast	rda nat	d≈1 Y. Y. am nov ced ted 7-1	d=1 Mic ing kap kap	Mic 200	N.A. on; o the s NF. BCl]	S C T S T S T S T S T S T S T S T S T S	is c titu atic nsti
233 258 585 1191 1291 1291 334 870 904 309 1531		STANDARD; 1. 41, Cr 1. 41, La 1. 41, La ment doma	an). a; Chordata; a; Primates;	Pubmec., Guo Merrid 4 are psecial ssocial h Bcl1(6:1187)	PubMed PubMed PubMed Pontain PubMed NF-1	n F., 1 8-198(;	FROM 1 d Color 00) to ivates on of 1 14 and	DCATION ICITY: not in DNTAIN: DNTAIN: DNTAIN: DSGG to OI SMI	OT entry is copy Swiss Institute Bioinformatics profit institut
8888888888888		ST, VB5; (Rel. (Rel. (Rel.	ARMA2. s (Hum: Metazo: utheri	OM N.A 92234; Wang L S.M., CARD1. rane-a ct wit	OM N.A 55663; artinol CARD-c tion al	Martinon F., 505:198-198	or 1-40 From N. ervix, and Colon; rg R.; d (DEC-2000) to t TION: Activates N phorylation of BC NIT: CARD14 and B	TIOD.  ULAR LA SPECIF S, but ITY: CI I	S-PROT ent the Swiss ean Bioinf non-profit
144 777 76.5 777 76.5 777 76.5 777 76.5 76.5		LT 1 CARE_HUMAN CARE_HUMAN QBAKLG; QBBVBS; 15-JUN-2002 (Rel. 41,	Z) (Calma z CARD14 OR C Homo sapien: Eukaryota; B Mammalia; E: NCBI_TaxID='	MEDLINE-211 BETLIN J., Bertin J., Srinivasula "CARD11 and (CARD)/memb that intera J. Biol. Ch	SEQUENCE FROM N.A. MEDEL SEGUENCE FROM N.A. MEDEL SEGUENCE TATTON F., Micheau O., Bonnet D., Caide O., Marthon F., Micheau O., Bonnet D., Carmal, a CARD-containing binding partner of phosphorylation and NF-kappaB activation."; FEBS Lett. 496:121-127(2001).	ERRATUM. Gaide O., M FEBS Lett.	SEQUENCE OF 1-740 FROM OSCILLARY SEQUENCE OF STRANSBERG (DEC-2000) to 1-FUNCTION: Activates phosphorylation of EUSBUNIT: CARD14 and	Interaction of the state of the	This SWISS-Pl between the the European use by non
		25 S.	2 X X C C C C Z Z					22222222222	38888

```
Q9BXL7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARB_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                      δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΩD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                ó
modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 14 (Bcl10-interacting MAGUK protein
                                                                                                                                                                                                                 GUANYLATE KINASE.
DYEASEPLFKAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTD
                                                                                                                                                                                                                                        GYKRLLQDLEAK -> SRARPLLSPGLLMGTVAAGGVTQAD
                                                                                                                                                                                                                                                                                                                                                                               61 VTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRLGTS 120
                                                                                                                                                                                                                                                                                                                                                                                          2
                                                                                                                                                                                                                                                                                                                                                                                                                       121 EEQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTEQSPR 179
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                    1 RPRPVLLVPRAVGKILSEKLCLLQGFKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGRCW 60
                                                                                                                                                                                                                                                 FTSPRRCRSTLGWASALSWADVKRSAHL (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Binnl, a MAGUK family member linking protein kinase C activation Bcll0-mediated NF-kappa B induction."; J. Biol. Chem. 276:30589-30597(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                         Length 1004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=21391892; PubMed=11387339;
MCAllister-Lucas L.M., Inohara N., Lucas P.C., Ruland J., Be
Li Q., Chen S., Chen F.F., Yamaoka S., Verma I.M., Mak T.W.,
Nunez G.;
                                                                                                                                                                                                                                                                                          Score 930; DB 1; Length 1
Pred. No. 2.9e-73;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Activates NF-kappaB via Bcll0 and IKK.
                                                                                                                                                                                                                                                                      7469B8B56BE06073 CRC64;
                                                                                                                                                                                    CARD. COILED COIL (POTENTIAL).
                                                                                                                             PROSITE; PS50209; CARD; 1.
PROSITE; PS00856; GUANYLATE_KINASE_1; FALSE_NEG.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  999 AA
                                                                                                                                                                                                                                                             AAH01326)
                                                   EMBL: AY032927; AAK54453.1; -.
EMBL: BC08142; AAH8142.1; -.
EMBL: BC081326; AAH01326.1; ALT_INIT.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PD2.
SMART; SM00072; GUK; 1.
SMART; SM00228; PD2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                       1004 AA; 113299 MW;
                                          EMBL; AF322642; AAG53403.1; -.
                                                                                                                                                                                                                                                                                          100.08;
                                                                                                                                                                                                                                                                                                    100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 82-743 FROM N.A.
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                    107
409
658
990
671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARD14 OR BIMP2.
                                                                                                                                                                                    15
128
568
858
619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Breast;
                                                                                                                                                                           Coiled coil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARE_MOUSE

    (Bimp2)

                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                         원
                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                 þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 VTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRLGTS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             882 ITRHAVESLMNMSTHALLDVRLDSVRVLHRMDMFPIIIHVSVNEKTAKKLRKGLHRLGSS 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 11 (CARD-containing MAGUK protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RPRPVLLVPRAVGKILSEKLCLLQGFKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGRCW 60
                       121 EEQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTEQSP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  942 EEQFLEVARQEEGELDRVPCLYSSLAPDSWSDLDSLLSCVRLAIADEQKKVVWTE-SP 998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

BEDLINE-2192234, PubMed=11278692;
Bertin J., Wang L., Guo Y., Jacobson M.D., Poyet J.-L.,
Srinivasula S.M., Merriam S., Distefano P.S., Alnemri E.S.;
Srinivasula S.M., Merriam S., Distefano P.S., Alnemri E.S.;
Srinivasula S.M., Merriam S., Distefano P.S., Alnemri CARDI and CARDIJ are novel caspase recruitment domain
(CARD)/membrane-associated quanylate kinase (MAGUK) family members
that interact with Boll0 and activate NF-kappaB.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QAQQQLLA -> HLLEDHRS (IN REF. 2).
SUBUNIT: CARD14 and Bc110 bind to each other by CARD-CARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D18350DA12430255 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF363457; AAK60137.1; -.
EMBL; BC004692; AAH04692.1; -.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
Pfam; PF00595; PDZ, 1.
PROSTIE; PS50209; CARD; 1.
PROSTIE; PS500856; GUANYLATE_KINASE_1; FALSE_NEG.
PROSTIE; PS50052; GUANYLATE_KINASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.4%; Score 738.5; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.3e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GUANYLATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113496 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last seq
15-JUN-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 80.39
Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15
125
572
854
736
736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARDII OR CARMAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coiled coil.
DOMAIN
DOMAIN
DOMAIN
55
DOMAIN
8
CONFLICT
7

    (Carma 1)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARB_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
```

ij

 $\sim$ 

```
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
                                                                                                                                                                                                                                                                                                                                                                -:- SUBCELLULAR LOCATION: Cytoplasmic.
-:- TISSUE SPECIFICITY: Detected in adult peripheral blood leukocytes, trysue Specificity: Detected in adult peripheral blood leukocytes, trymus, spleen and liver. Also found in promyelocytic leukemia HL-60 cells, chronic myelogenous leukemia K562 cells, Burkitt's Iymphoma Raji cells and colorectal adenocarcinoma SW480 cells. Not detected in HeLa S3, Molt-4, A549 and G431 cells. Not detected in HeLa S3, Molt-4, A549 and G431 cells.
-:- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
-:- SIMILARITY: CONTAINS 1 GUANYLATE KINASE-LIKE DOMAIN.
-:- CAUTION: Supposed to contain a SH3 domain which is not detected by PROSITE, Ffam or SMART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1026 AFEC-IAPANIEAVAAKNKHCLLEAGIGCTRDLIKSNIYPIVLFIRVCEKNIKRFRKLLP 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPRPVLLVPRAVGKILSEKLCLLQG---FKKCLAEYLSQEEYEAWSQRGDII--QEGEVS 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                          Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.;
Carmal, a CARD-containing binding partner of Bcll0, induces Bcll0
phosphorylation and NF-kappaB activation.";
FEBS Lett. 496:121-127(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 26.1%; Score 242.5; DB 1; Length 1147; 1 Similarity 31.5%; Pred. No. 2.1e-13; 57; Conservative 41; Mismatches 76; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            > L (IN REF. 2).
913A4B015D2B36CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50209; CARD; 1.
PROSITE; PS00856; GUANYLATE_KINASE_1; FALSE_NEG.
PROSITE; PS50052; GUANYLATE_KINASE_2; FALSE_NEG.
PROSITE; PS50106; PDZ; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GUANYLATE KINASE.
  Biol. Chem. 276:11877-11882(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew, HGNC:16393; CARD11.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PD2.
SMART; SM00228; PD2; 1.
                                           SEQUENCE FROM N.A. MEDLINE-21255663; PubMed-11356195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 103 CARD.
123 442 COILEG
673 748 PDZ.
96 GUANY
808 808 P ->
1147 AA; 132641 MW; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF322641; AAG53402.1; -.
                                                                                                                                                                                                                                                                                                                                                    interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coiled coil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1144 E 1144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 0 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                         ERRATUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
NAME OF THE STATE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ογ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ŋ,
                                                            15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 10 (Bcl10-interacting MAGUK protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                942 IRGLIGRPGWRDSELLRQCRGSEQWLWGLPCSWVQVPAHAWGHAEELAKVVRGRILQEQA 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interaction. They both participate in a complex with MALT1, where MALT1 binds to Bc110.
--- TISSUE SPECIFICITY: Highly expressed in kidney, heart followed by brain, lung, liver, skeletal muscle and testis.
--- SIMILARITY: CONTAINS I CARD DOMAIN.
--- CAUTION: Supposed to contain a SH3, a PDZ and a guanylate kinase-like domain. But none of these 3 domains are detected by PROSITE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      834 RPVVLLPECLAPRLIRNLLDLPSSRLDFQVCPAESLSGEEQCTSSAPGAPKAWPATAGL- 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 QEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       893 -----GSR---IRAIQESVGKK--HCLLELGARGVRELVHSEVYPIVIHVEVTEKNVRE 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 LKKGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQK 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Binpl, a MAGUK family member linking protein kinase c activation to Bcll0-mediated NF-kappa B induction.",
J. Biol. chem. 276:30589-397(2001).
-: FUNCTION: Activates NF-kappaB via Bcll0 and IKK.
-: SUBUNIT: CARD10 and Bcll0 bind to each other by CARD-CARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 RPVLLVPRAVGKILSEKLCLLQG----FKKCLAEYLSQEEY------EAWSQRGDII 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lucas P.C., Ruland J., Benito A.,
                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.9%; Score 185.5; DB 1; Length 1021; 31.0%; Pred. No. 1.6e-08; trive 25; Mismatches 79; Indels 25;
                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=21391892; PubMed=11387339;
MCAllister-Lucas L.M., Inohara N., Lucas P.C., Ruland J., Ber
M. J. C., Chen S., Chen F.F., Yamaoka S., Verma I.M., Mak T.W.,
Nunez G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 450 COILED COIL (POTENTIAL).
558 565 POLY-SER.
1021 AA; 114413 MW; 4811A09BDBBF792C CRC64;
1021 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF363456; AAK60136.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS50209; CARD; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115
450
565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam or SMART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::|| |:
RLVWVER 1008
                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170 KVVWTEQ 176
                                                                                                                                                                                                                                  CARDIO OR BIMPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ma.
Local Sim
58;
   CARA_MOUSE
                                                                                                                                                                                                         (Bimpl)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
```

RESULT

```
RRADA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RP MAINTE-2005/155; Pubbed-10591208;

RM MAINTE-2005/155; Pubbed-10591208;

RM Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,

RA BURDINE-2005/155; Pubbed-10591208;

RA BURDINE-2005/155; Pubbed-10591208;

RA BITG C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,

Burd C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,

Burd C.P., Blakey S.E., Raidgeman A.M., Buck D., Chen Y., Clark G.,

RA BITG C.P., Davkore C., Coller C., Collier R.E., Chenor R.,

RA Clegg S.M., Cobley V.E., Coller G.G., Collier R.E., Chenor R.,

RA Clegg S.M., Cobley V.E., Coder G.G., Collier R.E., Chenor R.,

RA Clegg S.M., Cobley V.E., Carafham D.V., Garner A.A.,

Gibert J.G., Machan M.E., Grafham D.V., Garner A.A.,

RA BURN K.L., Fey J.M., Flenning K.J., Fernorb L., Garner A.A.,

RA Laird G.K., Langford C.F., Leversha M.A., Libyd C., Libyd D.M.,

RA Laird G.K., Langford C.F., Leversha M.A., Libyd C., Libyd D.M.,

RA Martyn I.D., Machan M.C., Skreward C.A., Sulston D., Phillimore B.J.C.F.,

RA Dottl C.N., Pavitt R., Paracce A.V., Pearson D., Phillimore B.J.C.F.,

RA Soderlund C., Spragon L., Skuce C.D., Smalley S., Smith M.L.,

RA Soderlund C., Spragon L., Stleward C.A., Sulston J.E., Wann R.M.,

Williams L., Williams S.A., Williamson H., Willew J.D.E.,

Williams L., Williams S.A., Williamson H., Willew J., Shimizu N.,

RA Minoshima S., Kawasaxi K., Sasaxi T., Abakawa S., Rodon J., Shimizu N.,

RA Dorman A., Fang F., Fu Y. Hu P., Hu P., Hua A., Kenton S., Lai H., Lao D.T.,

RA Dorman A., Fang F., Fu Y. Will P., Hua A., Kenton S., Lai H., Lao H.I.,

RA Dorman A., Pang G., Wang Z., White J., Williams D., Wu H., Yao Z.,

RA Dorman A., Pang C., Wang Z., White J., Williamsu D., Wu H., Yao Z.,

RA Dorman A., Pang G., Lin S.-P., Loh P., Wallay E., Naghaba H., Bohner S., Oldes M., Oldsson D., Benils G., Benley D., Bradshaw H., Bohner S., Classe S., Mutray J., Miller S., Budarf M., Langell P., Walker C., Wang S., White J., Walker S., Budarf M., R.,

Rocket D., Wang C., Wang C., White J., Walker S., Budarf M., R.,

Rocket 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-21292987; PubMed-11259443; Wang L., Manji G.A., Wang L., Guo Y., Huang W.-J., Ke X., Poyet J.-L., Manji G.A., Bertin J.; Merriam S., Glucksmann M.A., DiStefano P.S., Alnemri E.S., Bertin J.; "CARD10 is a novel caspase recruitment domain/membrane-associated guanylate kinase family member that interacts with Bcl10 and activates
                                                                  09BWT7; 09UGR5; 09UGR6; 09Y3H0; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Caspase recruitment domain protein 10 (CARD-containing MAGUK protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-21255663; PubMed=11356195;
Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.;
"Carmal, a CARD-containing binding partner of Bcll0, induces Bcll0
phosphorylation and NF-KappaB activation.";
FEBS Lett, 496:121-127(2001).
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp FEBS Lett. 505:198-198(2001).
                                   PRT; 1032 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol. Chem. 276:21405-21409(2001)
                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

    Carma 3).
    CARD10 OR CARMA3.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NF-kappa B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERRATUM.
CCARA_HUMAN

AC CORRA_HUMAN

DT AC COBWATTO

DT 15-JUN

DE 15-JUN

DE 30 (Caspas

DE 3) (Caspas

COC CORRALIO

COC CORRALIO

COC CORRALIO

COC CORRALIO

COC COCCO

COC COCCO

CO
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation her Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                               interaction. They both participate in a complex with MALT1, where MALT1 binds to B0110 (By similarity).
SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).
TISSUE SPECIFICITY: Detected in adult heart, kidney and liver:
Inwer levels in intestine, placenta, muscle and lung. Also found in fetal lung, liver and kidney.
SIMILARITY: CONTAINS 1 CARD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 CWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRLG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   846 RPVVLLPECLAPRLIRNLLDLPSSRLDFQVCPAESLSGEELCPSSAPGAPKAQPATPGLG 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRI-RAIQESVGKK--HCLLELGARGVRERVQNEIYPIVIHVEVTEKNVREVRGLLGRPG 962
Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D.
E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                             CAUTION: Supposed to contain a SH3, a PDZ and a guanylate kinase-like domain. But none of these 3 domains are detected by PROSITE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 RPVLLVPRAVGKILSEKLCLLQG----FKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGR 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra l
Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,
Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 TSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAUTION: Ref.4 sequence differs from that shown due to various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 169.5; DB 1; Length 1032; Pred. No. 4.1e-07;
                                                                                                                                                                         -i- FUNCTION: Activates NF-kappaB via Bcl10 and IKK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89 Q -> R (IN REF. 4).
17 K -> KQ (IN REF. 4).
32 R -> L (IN REF. 4).
115946 MW; 8377319AB82A0949 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COILED COIL (POTENTIAL). POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Guanylate Kinase (EC 2.7.4.8) (GMP Kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197 AA
                                                                                                                 "The DNA sequence of human chromosome 22.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL: AY032928; AAK54454.1; -1.2ED.
EMBL: AL0449851; CAB63075.1; ALT_SED.
EMBL: AL049851; CAB63076.1; ALT_SED.
EMBL: AL022315; CAB42832.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene identification problems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AY028896; AAK26165.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50209; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                 Nature 402:489-495(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115
456
574
289
917
932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  917
932
932
932
933
933
                                                                                            Tilahun Y., Wright H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam or SMART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GUK1 OR GMK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KGUA_MOUSE
Q64520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
KGUA_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
```

ä;

S

```
MEDLINE=94271265; PubMed=7911663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GUK1 OR GMK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KGUA_HUMAN
Q16774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hunt D.M.;
                                                                                                                                                                                                                                                                                                                        INIT_MET
NP_BIND
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KGUA_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
  δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       òγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license alreaner (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                 MEDLINE-96279248; PubMed-8663313;
Brady W.A., Kokoris M.S., Fitzgibbon M., Black M.E.;
"Cloning, characterization, and modeling of mouse and human guanylate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 DIAAGDFIEHAEFSGNLYGTSKEAVRAVQAMNRICVLDVDLQGVRSIKKTDLCP--IYIF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 VNEKMAKKLKKGLQRLGTSEEQLLE···AARQEEGDLDRAPCLYSSLAPDGWSDLDGLLS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 PRPVLLV-PRAVGK-ILSEKL----CLLQGFKKCLAE------YLSQEEYEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                  J. Biol. Chem. 271:16734-16740(1996).
-i- FUNCTION: ESSENTIAL FOR RECYCLING GMP AND INDIRECTLY, CGMP-1- CATALYTIC ACTIVITY: ATP + GMP = ADP + GDP.
                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 197;
                                                                                                                                                                                                                                                                                                                                                          Transferase; Kinase; ATP-binding; Acetylation.
INIT_MET 0 0 BY SIMILARITY.
NP_BIND 10 17 ATP (BY SIMILARITY).
MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
SEQUENCE 197 AA; 21767 MW; 332403BF0DICCFB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                  -!- SIMILARITY: BELONGS TO THE GUANYLATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                      13.4%; Score 124.5; DB 1
25.5%; Pred. No. 0.00051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Guanylate kinase (EC 2.7.4.8) (GMP kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            37; Mismatches
                                                                                                                                                                                                                                                                                                                                   PS00856; GUANYLATE_KINASE_1; 1. PS50052; GUANYLATE_KINASE_2; 1.
                                                                                                                        SUBUNIT: MONOMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                   MGD; MGI:95871; Gukl.
InterPro; IPR000619; Guanylate_kin.
Pfam; PF00625; Guanylate_kin; 1.
SMART; SM00072; GuKc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                            EMBL; U53514; AAC52652.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 CVRQAIADEQKKVVWT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 TLKQALSEEIKKAQGT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GUK1 OR GUK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KGUA_BOVIN
P46195;
                                                           "Cloning, c
kinases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                     PROSITE;
 ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             임
```

```
between the Swiss Institute of Bioinformatics and the EMBL outstation-
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 FPIVIHVSVN--EKMAKKLKKGLQRLGTSEEQLLE--AARQEEGDLDRAPCLYSSLAPDG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 PRPVVLSGPSGAGKSTL-----LKKLLQEHGSIFGFSVSHTTRDPRPGEENGKDYYF 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 LSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDI 93
Gaidarov I.O., Suslov O.N., Ovchinnikova T.V., Abdulaev N.G.;
"Guanylate kinase from bovine retina: isolation, primary structure,
and expression in E. coli.",
and expression in E. coli.",
-:- FUNCTION: ESSENTIAL FOR RECYCLING GMP AND INDIRECTLY, CGMP.
-:- CATALYTIC ACTIVITY: ATP + GMP - ADP + GDP.
-:- SUBBUNT: MONOMER (BY SIMILARITY).
-:- SUBBUNT: BELONGS TO THE GUANYLATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-96213684; PubMed-8647247;
Fitzgibbon J., Katsanis N., Wells D., Delhanty J., Vallins W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Human guanylate kinase (GUK1): cDNA sequence, expression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP (BY SIMILARITY).
ACETYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 AA; 21778 MW; 5CB5DD007BC15C62 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 122.5; DB 1
Pred. No. 0.00076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transferase; Kinase; ATP-binding; Acetylation. INIT_MET 0 0 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-2002 (Rel. 41, Last annotation update)
Guanylate kinase (EC 2.7.4.8) (GMP kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              196 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR000619; Guanylate_kin.
Pfam; PF00625; Guanylate_kin; 1.
SMART; SM00072; GuKc; 1.
PROSITE; PS00856; GUANYLATE_KINASE_1; 1.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 WSDLDGLLSCVRQAIADEQKKVVWTEQS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171 -DSLDKAYWALKEALSEEIKKAQGTGQS 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X67029; CAA47423.1; -. HSSP; P15454; 1GKY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosomal localisation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
```

```
NCBI_TaxID=9823;
                                                                          TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TJP1 OR ZO1
                                                                                                                                                                                                                                                                                                                                                20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZO1_HUMAN
Q07157;
                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                   brain.";
                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
ZO1_HUMAN
                                                                                                                                                                                                                                                                                                                                                Matches
Qγ
                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                              δŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                        δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                             MEDINE-96279248; PubMed-8663313;
Brady W.A., Kokoris M.S., Fitzgibbon M., Black M.E.;
"Cloning, characterization, and modeling of mouse and human guanylate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 DIAAGDFIEHAEFSGNLYGTSKVAVQAWNRICVLDVDLQGVRNIKATDLRP--IYIS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 VNEKMAKKLKKGLQRLGT-SEEQLLE--AARQEEGDLDRAPCLYSSLAPDGWSDLDGLLS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 PRPVVLSGPSGAGKSTLLKRLLQEHSGIFGFSVSHTTRNPRPGEENGKDYYFVTREVMQR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----YLSQEEYEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27;
                                                                                                                  DB 1; Length 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                  10 17 ATP (BY SIMILARITY).

1 1 ACETYLATION (BY SIMILARITY).

196 AA: 21594 MW. C4727A7E2AA261B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.8%; Score 119.5; DB 1;
25.5%; Pred. No. 0.0014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 PRPVLLV-PRAVGKILSEKLCLLQ-----GFKKCLAE-----
                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000619; Guanylate_kin.
Pfam; PF00625; Guanylate_kin; 1.
SMART; SM00072; GuKc; 1.
PROSITE; PS00856; GUANYLATE_KINASE_1; 1.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
Transferase; Kinase; ATP-binding; Acetylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KGUA_PIG STANDARD; PRT; 197 AA. p31006; 01-JUL-1993 (Rel. 26, Created) 01-JUL-1993 (Rel. 26, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Guanylate kinase (EC 2.7.4.8) (GMP kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
                                                                          J. Biol. Chem. 271:16734-16740(1996)
                                                                                                                                                                                                                                                                                          EMBL; BC006249; AAH06249.1; -. BEMBL; BC009944; AAH09914.1; -. HSSP; P15454; 1GKY.
                                                                                                                                                                                                                                                                               EMBL; L76200; AAC37598.1; -. EMBL; U66895; AAC50659.1; -.
Lett. 385:185-188(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                     Genew; HGNC:4693; GUK1.
MIM; 139270; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 CVRQAIADEQKK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 49; Conserv
                     SEQUENCE FROM N.A.
                                                                                                SEQUENCE FROM N.A.
                                                                                                           TISSUE-Lung
                                                                                                                                                                                                                                                                                                                                                                                                                         INIT_MET
NP_BIND
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                 kinases.
  FEBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
KGUA_PIG
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ά
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
ZSCHOCKE P.D., Schiltz E., Schulz G.E.; "Purification and sequence determination of guanylate kinase from pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 FPIVIHVSVN--EKMAKKLKKGLQRLGTSEEQLLE--AARQEEGDLDRAPCLYSSLAPDG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 PRPVVLSGPSGAGKSTL------LKKLLQEHSSIFGFSVSHTTRDPRPGEENGKDYYF 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 LSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDI 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Liver;
Willott E., Balda M.S., Fanning A.S., Jameson B., van Itallie C.,
Willott E., Balda M.S., Fanning A.S., Jameson B., van Itallie C.,
Anderson J.M.,
"The tight junction protein ZO-1 is homologous to the Drosophila
discs-large tumor suppressor protein of septate junctions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -:- FUNCTION: ESSENTIAL FOR RECYCLING GMP AND INDIRECTLY, CGMP.
-:- CATALYTIC ACTIVITY: ATP + GMP = ADP + GDP.
-:- SIMULARITY: BELONGS TO THE GUANYLATE KINASE FAMILY.
-:- SIMILARITY: BELONGS TO THE GUANYLATE KINASE FAMILY.
-:- SIMILARITY: BELONGS TO THE GUANYLATE KINASE FAMILY.
-:- FINE S23776; KIPGGU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0cT-1994 (Rel. 30, Created)
01-0cT-1994 (Rel. 30, Last sequence update)
115-JUN-2002 (Rel. 41, Last annotation update)
Tight junction protein 20-1 (Zonula occludens 1 protein) (Zona occludens 1 protein) (Tight junction protein 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP (BY SIMILARITY).
ACETYLATION.
CF492B786FCC4E6E CRC64;
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.4%; Score 115.5; DB 1; 24.0%; Pred. No. 0.0031; ative 35; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 PRPVLLV-PRAVGKILSEKLCLLQGFKKCLAE-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1736 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 WSDLDGLLSCVRQAIADEQKKVVWTEQS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 -DSLDKAYWALKEALSEEIKKAOATGHS 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem. 213:263-269(1993).
                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93238695; PubMed=8097461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
```

7;

```
132 EGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTEQ 176
                                                                                                                             ZO1_MOUSE
P39447;
                                                                                                                                                                                                                                                                                                                                                                           STRAIN-129
                                         761
                                                                                                           ZO1_MOUSE
       Óλ
                                      Db
                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                       *****************************
                                                                 MIGHT BE INVOLVED IN STABILIZING JUNCTIONS.

-!- SUBUNIT: INTERACTS WITH OCCLUDIN, CLAUDINS AND 20-3.

-!- SUBUNIT: INTERACTS WITH OCCLUDIN, CLAUDINS AND 20-3.

-!- SUBCELLULAR LOCATION: PERIPHERAL MANBRANE CYOPLASMIC SIDE.

MOVEMBRY OF 20-1 FROM THE CYTOPLASM TO MEMBRANE IS AN EARLY EVENT OCCURRING CONCURRENTLY WITH CELL-CELL CONTACT.

-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

-!- TISSUE SPECIFICITY: THE ALPHA-CONTAINING ISOFORM IS FOUND IN MOST EPITHELIAL CELLS AND THE HIGHLY SPECIALIZED EPITHELIAL JUNCTIONS.

OF RENAL GLOMERULI AND SERTOLI CELLS OF THE SEMINIFEROUS TUBULES.
                                                                                                                                                                                                                                                                              -!- SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: CONTAINS 1 GUANYLATE KINASE-LIKE DOMAIN.
-!- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LHRMDIFPIVIHVSVNEKM-------AKKLKKGLQRLGTSEEQLLEAARQE 131
Proc. Natl. Acad. Sci. U.S.A. 90:7834-7838(1993).
-!- FUNCTION: THE N-TERMINAL MAY BE INVOLVED IN TRANSDUCING A SIGNAL REQUIRED FOR TIGHT JUNCTION ASSEMBLY, WHILE THE C-TERMINAL MAY HAVE SPECIFIC PROPERTIES OF TIGHT JUNCTIONS. THE ALPHA DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EYLSQEE---YE-AWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SH3 domain; Alternative splicing; Repeat; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 1736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.1%; Score 103.5; DB 1; Length 1
21.2%; Pred. No. 0.41;
ive 36; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             508D01B7A0814FFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISSING (IN SHORT ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00856; GUANYLATE_KINASE_1; FALSE_NEG. PROSITE; PS50052; GUANYLATE_KINASE_2; 1. PROSITE; PS50106; PDZ; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SH3.
GUANYLATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro: IPR000619; Guanylate_kin.
InterPro: IPR001478; PDZ.
InterPro: IPR001452; SH3.
InterPro: IPR001452; SH3.
InterPro: IPR000906; ZUS.
IPfam: PF00625; PDZ; 3.
Ffam: PF00625; Guanylate_kin; 1.
Ffam: PF00791; ZUS; 1.
SMART: SM00726; Guanylate_kin; 1.
SMART: SM00726; SH3; 1.
SMART: SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLY-PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLY-PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDZ 1.
PDZ 2.
PDZ 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194721 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L14837; AAA02891.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50106; PDZ; 3. PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 21.2
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A47747; A47747.
HSSP; P31016; 1BFE.
Genew; HGNC:11827; TJP1.
MIM; 601009; -.
                                                                                                                                                                                                                                                                  PTM: PHOSPHORYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        782
1236
1420
989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1231 123
1414 142
910 98
1736 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tight junction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     647
     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

```
between the Swiss Institute of Bloinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cells is identical to 20-1, a tight junction-associated protein in epithelial cells: CDNA cloning and immunoelectron microscopy.";

J. Cell Biol. 121:491-502(1993).

J. Cell Biol. 121:491-502(1993).

C. I-FUNCTION: THE N-TERMINAL MAY BE INVOLVED IN TRANSDUCING A SIGNAL REQUIRED FOR TIGHT JUNCTION ASSEMBLY, WHILE THE C-TERMINAL MAY HAVE SPECIFIC PROPERFIES OF TIGHT JUNCTIONS. THE ALPHA DOMAIN MIGHT BE INVOLVED IN STABILIZING JUNCTIONS.

C. I-SUBGUILL INTERACTS WITH OCCLUDIN, CLAUDINS AND 20-3.

MOVEMBRY OF 20-1 FROM THE CYTOPLASM TO MEMBRANE IS AN EARLY EVENT OCCURRING CONCURRENTLY WITH CELL-CELL CONTACT (BY SIMILARITY).

C. I-SIMILARITY: CONTAINS 1 SH3 DOMAIN.

C. I-SIMILARITY: CONTAINS 1 SH3 DOMAIN.

C. I-SIMILARITY: CONTAINS 1 SH2 MAUK FAMILY OF CELL JUNCTION PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Itoh M., Nagafuchi A., Yonemura S., Yasuda-Kitani T., Tsukita S., Tsukita S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The 220-kD protein colocalizing with cadherins in non-epithelial
                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
1fylt junction protein 20-1 (Zonula occludens 1 protein) (Zona occludens 1 protein) (Tight junction protein 1).
----INLNSMNDGW-----YGALKEAVQQQQNQLVWVSE 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Repeat; Membrane.
PDZ 1.
PDZ 2.
                                                                                                                                                                         PRT; 1745 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00856; GUANYLATE_KINASE_1; PROSITE; PS500053; GUANYLATE_KINASE_2; PROSITE; PS50106; PDZ, 3.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:98759; Tjpl.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
InterPro; IPR001452; SH3.
InterPro; IPR000906; ZU5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93252986; PubMed=8486731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00625; Guanylate_kin; 1.
Pfam; PF00791; 2U5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D14340; BAA03274.1; -. PIR; A46431; A46431.
HSSP; P31016; 1BE9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tight junction; SH3 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00072; GUKC; 1.
SMART; SM00228; PDZ; 3.
SMART; SM00326; SH3; 1.
SMART; SM00218; ZUS; 1.
                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00018; SH3; 1.
Pfam; PF00595; PDZ; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCB1_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                     TJP1 OR ZO1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                          PHHAD DONARRANA SANGA COCCOCCOCCOCCA SANGA SANGA
```

7;

```
SMART; SM00228; PDZ; 3.
                                                                                                                                                                                                       59
                                                                                                                                                                                                                       756
                                                                                                                                                                                                                                         118
                                                                                                                                                                                                                                                                                                                       RESULT 13
                                                                                                                                                                                                                                                                                                                                                 Db
                                                                                                                                                                                                       ōλ
                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                           δλ
                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                    \delta
                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                7;
                                                                                                                                                                                                                                                                                                                                                      LHRMDIFPIVIHVSVNEKMAKKL------KKGLQRLGTSEEQLLEAARQEEGDLDRA 138
                                                                                Gaps
                                                                                                EYLSQEE---YE-AWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCT 87
                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                               27;
                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
115-JUN tinnction protein ZO-2 (Zonula occludens 2 protein) (Zona occludens 2 protein) (Tight junction protein 2).
                                                             Length 1745;
                                                                                Indels
                                             C3DA2C0A9F411F66 CRC64;
                                                            ; Score 100.5; DB 1;
; Pred. No. 0.75;
35; Mismatches 58;
                                                                                                                                                                    PCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTEQ 176
                                                                                                                                                                                     772 TINLNSM-NDGW-----YGALKEAIQQQQNQLVWVSE 802
         SH3.
GUANYLATE KINASE.
POLY-PRO.
POLY-PRO.
                                                                                                                                                                                                                                 PRT; 1167 AA
 PDZ 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1341872; Tjp2.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00018; SH3; 1.
Pfam; PF00595; PDZ; 3.
Pfam; PF00625; Guanylate_Kin; 1.
SMART; SM00072; GuKc; 1.
                                             AA; 194710 MW;
                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF113005; AAD19964.1; -.
                                                              10.8%;
24.1%;
                                                           Query Match
Best Local Similarity 24.19
Matches 38; Conservative
                                                                                                                                                                                                                                 STANDARD;
 502
584
794
1247
1430
                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P31016; 1BE9
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-10090;
         516
644
1242
1424
1745
                                                                                                                                                                                                                                                                                             TJP2 OR ZO2
                                                                                                                                                                                                                                ZOZ_MOUSE
Q9Z0U1:
                                             SEQUENCE
                           DOMAIN
DOMAIN
           DOMAIN
                    DOMAIN
                                                                                                                                                                    139
                                                                                                 32
                                                                                                                 629
                                                                                                                                   88
                                                                                                                                                                                                                RESULT 12
ZO2_MOUSE
                                                                                                                                                                                                                                          g
  FT
FT
FT
SO
                                                                                                  ò
                                                                                                                 셤
                                                                                                                                   ö
                                                                                                                                                                    ò
```

```
"prediction of the coding sequences of unidentified human genes. XV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 6:37-345(1999).
-!- FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF THE NMDA RECEPTOR SUBUNIT NR2B (8Y SIMILARITY).
-!- SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Makino K., Kuwahara H., Masuko N., Nishiyama Y., Morisaki T., Sasaki J., Nakao M., Kuwano A., Nakata M., Ushio Y., Saya H.; "Cloning and characterization of NE-dig: a novel human homolog of the Drosophila discs large (dig) tumor suppressor protein interacts with the APC protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                            713 RPVVLFGPIADIAMERLANELPDLFQTAK-----TEPKDAGSEKSSGV----- 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CWYTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRL- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -- VRLNIVRQIIEQDKHALLDVIPKAVDLLNYTQWFPIVIFFNPDSRQGVKIR--QRLS 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---GTSEEQLLEAARQEEGDLDR--APCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | :| :| :| :| :| :| 812 PISNKSSRKLFDQANKLKKTCSHLFTATINVNSANDGW-----FGSLKDSIQQQQNEAV 865
                                                                                                                                                                                                                                                                                                                                                                                                                 3 RPVLL----VPRAVGKILSEKLCLLQGFKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGR 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                   37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nagase T., Ishikawa K.-I., Kikuno R., Hirosawa M., Nomura N.,
                                                                                                                                                                                                                                                                                                                   Length 1167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein 102)
                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                     POLY-GLU.
MW; F15DA3EBC3F9434F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-Nov-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Presynaptic protein SAP102 (Synapse-associated protein (Neuroendocrine-DLG) (NE-DLG) (Discs, large homolog 3).
                                                                                                                                                                                                                                                                                                                        DB 1;
                     FALSE_NEG
                                                                                                            Repeat; Membrane. PDZ 1. PDZ 2. PDZ 3. SH3.
                                                                                                                                                                                                                          GUANYLATE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        817 AA
                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.9;
; Mismatches
                                                                                                                                                                                                                                                                                                                           Score 93.5;
              PROSITE; PS00856; GUANYLATE_KINASE_1;
PROSITE; PS50052; GUANYLATE_KINASE_2;
PROSITE; PS50106; PDz; 3.
PROSITE; PS50002; SH3; 1.
Tight junction; SH3 domain; Repeat; MeDOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-20039619; PubMed-10574462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97332623; PubMed=9188857;
                                                                                                                                                                                                                                                                                                                                                                   32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE OF 330-817 FROM N.A.
                                                                                                                                                                                                                                                                                                                        10.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oncogene 14:2425-2433(1997).
                                                                                                                                                                                                                                                                             131614
                                                                                                                                                                                                                                                                                                                                                   23.48;
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                            365
570
649
858
SM00326; SH3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Fetal brain;
                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLG3 OR KIAA1232
                                                                                                                                      10
287
489
584
678
1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                          1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DLG3_HUMAN
Q92796; Q9ULI8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 WTEQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          866 WVSE 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                           Query ...
Best Local Similary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohara O.;
                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                         DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLG3_HUMAN
```

σ

```
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLG3_RAT
   δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
                                                                                                                                                                                                                                                                                                                                                                            PDZ 1.
PDZ 2.
PDZ 3.
SH3.
SH3.
GUANYLATE KINASE.
FTALADHISHNSSLGYLGAVESKVSYPAPPQVPPTRYSPI
PRHMLABEDFT -> AARRERGAMBRARKESGSGLAMGLGS
ASASAWRRASORWAWPLRSLRPGGDA (IN REF. 2).
DFPGLSDDYYGANKL -> SIYTKRKKSFRLSRKFFFYSK
ENMAGESSTQEGGYTSNTSDSESSS (IN REF. 2).
MW; 3D7512EC4713FC4E CRC64;
-:- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-:- SIMILARITY: CONTAINS 1 GUANYLATE KINASE-LIKE DOMAIN.
-!- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          677 VSREQMEKDIQDNKFIEAGQFNDNLYGTSIQSVRAVAERGKHCILDVSGNAIKRLQQAQL 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94 FPIVIHV---SVNEKMAKKLKKGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGW 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         737 YPIAIFIKPKSIEALMEMNRRQTYEQANKIYDKAMK-LEQEFGE-----YFTAIVQG- 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 LSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDI 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUM-2002 (Rel. 41, Last annotation update)
Presynaptic protein SAP102 (Synapse-associated protein 102) (Discs, DLG3 OR DLGH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.8%; Score 91; DB 1 ilarity 19.6%; Pred. No. 2.1; Conservative 37; Mismatches
                                                                                                                                                                                                                                                                                                        SMART; SM00326; SH3; 1.
PROSITE; PS00856; GUANYLATE_KINASE_1; 1.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PD2; 3.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                InterPro; IPR000619; Guanylate_kin.
                                                                                                                                                                                                                                 Pfam; PF00018; SH3; 1.
Pfam; PF00595; PDZ; 3.
Pfam; PF00625; Garanylate_kin; 1.
ProDom; PD000065; SH3; 1.
SNART; SM00072; GuKC; 1.
SMART; SM00228; PDZ; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 SDLDGLLSCVRQAIADEQKKVVW 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 788 DSLEEIYNKIKQIIEDQSGHYIW 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               817 AA; 90344 MW;
                                                                                                                                                  EMBL; AB033058; BAA86546'1;
HSSP; Q12959; 1PDR.
Genew; HGNC:2902; DLG3.
MIM; 300189; -.
                                                                                                                                         EMBL; U49089; AAB61453.1;
                                                                                                                                                                                                            InterPro; IPR001478; PDZ.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                    SH3 domain; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLG3_MOUSE
P70175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
DLG3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                                        SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE-Brain;
STRAIN=C57BL/6; TISSUE-Brain;
Schmutz N., Makino S., Yagi T.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF THE NMDA RECEPTOR
                                                                                                                                                                                                                                                   -!- SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: CONTAINS 1 GUANYLATE KINASE-LIKE DOMAIN.
-!- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 FPIVIHVSVNEKMAKKLKKGLORLGTSEEOLLEAARQEEGD-----LDRAPCL-----Y 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 LSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDI 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLG3_RAT STANDARD; PRT; 849 AA.

Q62936; P70547;

Q1 NOV-1997 (Rel. 35, Created)

O1-NOV-1997 (Rel. 35, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Presynaptic protein SAP102 (Synapse-associated protein 102) (PSD-95/SAP90 related protein 1) (Discs, large homolog 3).
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EF3EF2D7513538EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GUANYLATE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Pred. No. 2.7; 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                813 FTAIVOG-DSLEEIYNKIKQIIEDQSGHYIW 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00856; GUANYLATE_KINASE_1; 1.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PD2; 3.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 SSLAPDGWSDLDGLLSCVRQAIADEQKKVVW 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.7%; Score 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D87117; BAA13249.1; -. HSSP; Q12959; 1PDR. MGD; MGT:188986; D1gh3. Interpro; IPR000619; Guanylate_kin. Interpro; IPR001478; PDZ. Interpro; IPR001452; SH3. Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDZ 1.
PDZ 2.
PDZ 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Guanylate_kin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93482 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similaring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00625; Guanylate
ProDom; PD000066; SH3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00072; Gukc; 1.
SMART; SM00228; PDZ; 3.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00595; PDZ; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SH3 domain; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       849 AA;
                           NCBI_TaxID=10090;
                                                                                                                                                                                                                           SUBUNIT NR2B.
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                         Irie M., Hata Y., Takai Y.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF THE NMDA RECEPTOR
                                                                                                                                                                                                                                                                                                                                         SUBUNIT NR2B.
-!- SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: CONTAINS 1 GUANYLATE KINASE-LIKE DOMAIN.
-!- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 FPIVIHVSVNEKMAKKLKKGLQRLGTSEEQLLEAARQEEGD-----LDRAPCL-----Y 142
                           Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 LSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDI 93
                                                                                                                                              Mueller B.M., Kistner D., Kindler S., Chung W.J., Kuhlendahl S., Fenster S.D., Lau L.-F., Veh R.W., Huganir R.L., Gundelfinger B.D., Garner C.C.;
                                                                                                                                                                                                  "SAF102, a novel postsynaptic protein that interacts with NMDA receptor complexes in vivo."; Neuron 17:255-265(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.7%; Score 90; DB 1; Length 849; 20.5%; Pred. No. 2.7; Azive 32; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISSING (IN SHORT ISOFORM).
34DA9C46C7BB96DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GUANYLATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERPROJUENT GUANJATE_KIN.
INTERPROJUENT GUANJATE_KIN.
INTERPROJUENT GUANJATE_KIN.
INTERPROJUENT GUANJATE_KIN.
INTERPROJUENT GUANJATE_KIN.
PÉTAM: PF00018; SH3: 1.
PF00018; PP02; 3.
PF00018; PP02; 3.
PF00018; SM00072; GUANJATE_KIN. 1.
SMART; SM00026; SH3: 1.
SMART; SM00026; SH3: 1.
PROSITE; PS00026; GUANYLATE_KINASE_1; 1.
PROSITE; PS50002; GUANYLATE_KINASE_1; 1.
PROSITE; PS50002; GUANYLATE_KINASE_2; 1.
PROSITE; PS50002; GH3: 3.
DOMAIN 149 335 PD2 1.
DOMAIN 244 330 PD2 1.
DOMAIN 444 444 PDZ 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 SSLAPDGWSDLDGLLSCVRQAIADEQKKVVW 173
                                                                                                                                   MEDLINE-96374358; PubMed-8780649;
                                                                                                                                                                                                                                                        [2]
SEQUENCE FROM N.A. (SHORT FORM).
                                                                                                 SEQUENCE FROM N.A. (LONG FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93539 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; US0147; AAA93031.1; -. EMBL; US3367; AAB48561.1; -. HSSP; Q12959; IPDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 20.5%;
Matches 31; Conservative
DLG3.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           627
849 AA;
                                                                                                                     TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
 δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
: | | : : : : | | : : : | 813 FTAIVQG-DSLEEIYNKIKQIIEDQSGHYIW 842
```

g

Search completed: January 22, 2003, 08:53:39
Job time: 8.97715 secs

```
9960n4 drosophila
994880 drosophila
994484 drosophila
997488 drosophila
99758 canis famil
P70625 rattus norv
220398 caenorhabdi
997tb3 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09y4e3 homo sapien
08tdm7 homo sapien
08tdm6 homo sapien
09ue73 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09d3x0 mus musculu
096in2 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9w7fl brachydanio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8tes3 homo sapien
                                                         January 22, 2003, 08:49:36; Search time 27.9086 Seconds (without alignments) 1321.544 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                           930
1 RPRPVLLVPRAVGKILSEKL......vRQAIADEQKKVVWTEQSPR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                           671580
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                       671580 segs, 206047115 residues
                                                                                                   US-09-767-215-2_COPY_826_1004
                                                                                                                                                                                                                                                               summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8TES3
Q9Y4E3
Q8TDM7
Q8TDM6
Q9UE73
Q9D3X0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q960N4
Q94880
Q9VHK4
Q9VKG8
Q97758
Q20398
Q9VTB3
                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                     sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                    sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
                                                                                                                                                                                                                                                                                                                                                                  sp_organelle:*
                                                                                                                                                                                                              seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                            sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11
44
11
11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13
                                                                                                                                                                                                                                                                                                                                                                                                   sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                             sp_phage:*
sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                           sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
                                                                                                                                                                                                                                                                                                                 sp_fungi:*
                                                                                                                                                                                                                                                                                                                           sp_human:*
                                                                                                                                                                                                                                                                                     SPTREMBL_21:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11171
1281
1809
1809
1809
1809
1852
1944
1945
1916
1034
233
576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                         sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.1
14.0
14.0
113.6
113.6
111.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.8
10.7
10.2
9.9
                                                                                                                                                                                                                                                                                                                                                                                      10:
11:
                                                                                                                                                                                                                                                                                                                                                                                                         12:
13:
14:
                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242.5
130.5
130.5
130.5
130.5
130.5
110.5
110.5
110.5
110.5
110.5
100.5
99.5
99.5
99.5
98.5
88.5
                                                                                                              Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                             Minimum DB :
Maximum DB :
                                       OM protein
                                                                                                                      Sequence:
                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                    Database
                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
```

099hbv2 gallus gall 096647 mus musculu 0966478 mus musculu 090dd3 trichinella 090dd3 trichinella 090dd2 trichinella 090dd2 trichinella 0910d1 mus musculu 099y6 leishmania 081015 arabidopsis 090x7 homo sapien 015424 homo sapien 015424 homo sapien 015424 homo sapien 0164151 homo sapien 096x81 mus musculu 080x18 drosophila 090x18 drosophila 090x18 tulchobus 090x18 tulchobus 090x19 tulchobus 090x19 tulchobus 090x19 tulchobus 090x19 tulchobus 090x10 tulchobus 090x10 musculu 090x10 musculu 090x10 musculu 090x10 musculu 090x10 musculu 00x10 musculu	Ogg103 sus scrofa Ogxej6 escherichia Og5338 tupala glis O28040 archaeoglob O9vjc5 drosophila
09YHV2 09D647 09D647 09DD3 09PDC6 09PWL2 091WJ1 091WJ1 091015 091015 091015 091151 094116 096WH18 099WH18	Q9GL03 Q8XEJ6 Q95338 Q28040 Q9VJC5
113 111 111 111 111 111 111 111 111	
11163 5893 3642 3642 4293 3686 3686 3646 3646 3646 3646 373 3710 3710 3710 3710 3710 3710 3710	578 1047 342 414 667
00000000000000000000000000000000000000	88888 7.7.000
88 88 88 88 88 88 88 88 88 88 88 88 88	80.5 80.5 80 80 80
111 122 133 133 133 133 133 133 133 133	

## ALIGNMENTS

```
.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 GGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 RLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTE 175
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            1 RPRPVLLVPRAVGKILSEKLCLLQG---FKKCLAEYLSQEEYEAWSQRGDII--QEGEVS 55
                                                                                                                                                                                                                                           Ohara O., Nagase T., Kikuno R., Okumura K.; "The nucleotide sequence of a long cDNA clone isolated from human
                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                               26.1%; Score 242.5; DB 4; Length 1171; 31.5%; Pred. No. 7.6e-14; ive 41; Mismatches 76; Indels 7;
                                                                                                                                                                                                                                                                                                                                    1171 AA; 134966 MW; FA567ABBC8A703FF CRC64;
                                                                                                                                                                                                                                                                         spleen.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK074049; BAB84875.1; -.
                                                        01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                              PRT; 1171 AA
                                                                                                     FLJ00120 protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                              PRELIMINARY;
                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
TISSUE-SPLEEN;
Ohara O., Nagase T.
                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 57; Conser
                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                      FLJ00120
                                                                                                                                                                                                                                                                                                                       NON_TER
                            Q8TES3
RESULT 1
               O8TES3
                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

```
Q8TDM6
       Q8TDM7
                                                                                                                                                                                                                                               1685
                                                                                                                                                                                                                                                                                                  153
                                                                                                                                                                                                                                                                                                                                                                                                   DLG5.
                                                                                                                                                                                                                                                                                                                                          RESULT 4
                                                                                                                                                                                                                                                                                                                                                  Q8TDM6
28TDM7
                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                AC
DT
DT
DT
DDT
OC
OC
OC
OC
NT
RP
RP
RP
SQ
SQ
                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                              Q
                                                                                                                                                                                                                               δλ
                                                                                                                                                                                                                                              Dp
                                                                                                                                                                                                                                                               οy
                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                            43 SQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSV 102
                                                                                                                                                                                      MEDLINE-98290545; PubMed-9628581;
Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 RPVL------LVPRAVGK-----ILSEKLCLLQGFKKCLAEYLSQEEYEAW 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 NEKMAKKLK------KGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSD
                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 14.0%; Score 130.5; DB 4; Length 1281; Best Local Similarity 26.7%; Pred. No. 0.0021; Matches 55; Conservative 31; Mismatches 63; Indels 57;
                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER 1 1 SEQUENCE 1281 AA; 140286 MW; 4CC150D03F3ED8B9 CRC64;
                                                                                             01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       31; Mismatches
                                                                    1281 AA
                                                                                                                                                                                                                                                                                                                                        SWART; SM00072; GuKC; 1.
SMART; SM00228; PDZ; 4.
SWART; SM00326; SH3: 1.
PROSITE; PSS0105; GUANYLATE_KINASE_2; 2.
PROSITE; PSS0106; PDZ; 4.
PROSITE; PSS00626; RCC1_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1255 LSSICTQILAMVNQEQNKVLWIPACP 1280
                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 LDGLLSCVRQAIADEQKKVVWTEQSP 178
                                                                                                          KIAA0583 protein (Fragment).
KIAA0583.
                                                                                     01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       55; Conservative
                                                                     PRELIMINARY;
                                                                                                                               Homo sapiens (Human).
                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                TISSUE-BRAIN;
                          1168 E 1168
                                                                                                                                                                                                                                                                                                                                                                                                      domain
          176 9 176
                                                                                                                                                                                                         Ohara O.;
                                                    RESULT 2
Q9Y4E3
                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
           ò
```

RESULT 3

```
10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1685 SGHFDV------TTVASIKEITEKNRHCLLDIAPHAIERLHHMHIYPIVIF--I 1730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1630 RPVLILGPLLDVVKEMLVNEAPGKFCRCPLEVMKASQQAIERGVKDCLF----VDYKRR 1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43 SQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSV 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 NEKMAKKLK------KGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSD 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 NEKMAKKLK-----KGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSD 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43 SQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSV 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 RPVL-----LVPRAVGK----ILSEKLCLLQGFKKCLAEYLSQEEYEAW 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 RPVL------LVPRAVGK-----ILSEKICLLQGFKKCLAEYLSQEEYEAW 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.0%; Score 130.5; DB 4; Length 1809; 26.7%; Pred. No. 0.0032; Live 31; Mismatches 63; Indels 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 1809;
                                                                                                                                                                                                                                                                                                           Shah G., Brugada R., Roberts R.; "Complete cloning and genetic organization of KIAA0583."; "Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF352033; AAL83371.1; "SEQUENCE 1809 AA; 202039 MW; 4794A6C8561CD905 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shah G., Brugada R., Roberts R.;
"Complete CDNA of KIAA0583/DLG5.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF352034; AAL83938.1; -
SEQUENCE 1809 AA: 202066 WW; 3B77B3DCAD6FD6E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.0%; Score 130.5; DB 4; 26.7%; Pred. No. 0.0032; Live 31; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1809 AA.
1809 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1783 LSSICTQILAMVNQEQNKVLWIPACP 1808
                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LDGLLSCVRQAIADEQKKVVWTEQSP 178
                   QRIDM7;
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 26.78
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 26.73
Matches 55; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
```

```
Q96IN2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q96IN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138
Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
Nakamura H., Sudo T., Tsuiki H., Miyake H., Morisaki T., Sasaki J., Masuko N., Kochi M., Ushio Y., Saya H.; "Identification of a novel human homolog of the Drosophila dlg, P-dlg, specifically expressed in the gland tissues and interacting with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  495 RPVLILGPLLDVVKEMLVNEAPGKFCRCPLEVMKASQQAIERGVKDCLF-----VDYKRR 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSV 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 NEKMAKKLK------KGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSD 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 RPVL------LVPRAVGK-----ILSEKLCLLQGFKKCLAEYLSQEEYEAW 42
                                                                                                                       01-MAY-2000 (TEMBLE1. 13, Created)
01-JUN-2002 (TEMBLE1. 13, Last sequence update)
Discs large protein P-dig.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              674 AA; 74892 MW; C4C006B0A4F7E8E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.8%; Score 128.5; DB (26.7%; Pred. No. 0.0015; iive 30; Mismatches 64
                                                                                                       674 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50052; GUANYLATE_KINASE_2; 1. PROSITE; PS501062; PS. 2. PROSITE; PS00626; RCC1_2; UNKNOWN_1. PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                      FEBS Lett. 433:63-67(1998).
-1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
EMBL: 001843; AAC61295.1; -.
HSSP: Q12959; 1PDR.
                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001478; PDZ.
InterPro; IPR000408; Reg_chr_condens.
InterPro; IPR001452; SH3.
                                                 1783 LSSICTQILAMVNQEQNKVLWIPACP 1808
                             153 LDGLLSCVRQAIADEQKKVVWTEQSP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 LDGLLSCVRQAIADEQKKVVWTEQSP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000619; Guanylate_kin.
                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00625; Guanylate_kin; 1.
Pfam; PF00595; PDZ; 2.
Pfam; PF00018; SH3; 1.
SMART; SM00072; GUKC; 1.
SMART; SM00228; PDZ; 2.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                          MEDLINE-98409314; PubMed-9738934;
                                                                                                                O9UE73;
01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
ses 55; Conserv
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 TISSUE-BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                       Q9UE73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                RESULT 5
Q9UE73
                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Op
                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

RESULT 6 Q9D3X0

```
Carralle-C57BL/63; TISSUE=TESTIS;

KRAIN-C57BL/64; TISSUE=TESTIS;

KRAIN-C57BL/64; TISSUE=TESTIS;

RAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shinagawa A., Shibata K., Yoshino H., Adachi J., Fukuda S., Arawa T., Hara A., Fukunishi Y., Konno H., Kaodo S., Yamanaka I., Saito T., Okazaki Y., Gojobri T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Sahurner M., Batalov S., Casavant T., Rubil P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Browstein M.J., Bult C., Fletcher C., Fullita M., Gariboldi M., Brownstein M.J., Hume D.A., Kamiya M., Lee N. H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Androhe P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sakai H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Wanshaw-Bonis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., A., Wanshay-Bonis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSV 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 NEKMAKKLK------KGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSD 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 RPVLLLGPLLDVVKEMLVNEAPGKFCRCPLEVMKASOQAIERGVKDCLF-----VDYKRR 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 RPVL-----LVPRAVGK-----ILSEKLCLLQGFKKCLAEYLSQEEYEAW 42
                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.6%; Score 126.5; DB 11; Length 262; 25.7%; Pred. No. 0.00075; Live 32; Mismatches 64; Indels 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 4 09: 685-690 (2001).

EMBL; ARO16979; BAB30534.1; -.

EMBL; ARO16979; BAB30534.1; -.

EMBL; ARO16979; BAB30534.1; -.

EMBL; ARO16979; BAB30534.1; -.

EMBL; ARO16979; BAB3063.1; -.

SMART; SM00072; Guanylate_kin; 1.

SMART; SM00072; GuKC; 1.

SEQUENCE 262 AA; 30033 MW; A2A5629478469514 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DR-2002 (TrEMBLrel. 20, Last annotation update)
Similar to quanylate kinase 1 (Fragment).
Homo sapiens (Human).
                                                                                           Last sequence update)
Last annotation update)
262 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 AA
                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 LDGLLSCVRQAIADEQKKVVWTEQSP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 LSSICTQILAMVSQEQSKVLWIPACP 261
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
PRELIMINARY;
                                                                                        01-JUN-2001 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                                                                                                                                                         4933429D20Rik protein.
DLG5 OR 4933429D20RIK.
                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090
                           Q9D3X0;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
0961N2
1D 0961N
AC 0961N
DT 01-DI
DT 01-DI
DE SIMI.
```

```
120 SEEQLLEAARQEEGDLDRAPCLYSSLAPDGW-----SDLDGLLSCVRQAIADEQK 169
                                                                                                                                                                                                                                                                                                                                                                PYD OR TAMOU OR CG9763.
Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Euteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilade; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 RHA-VESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEK-MAKKLKKGLQRLG-T 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takahisa M., Togashi S., Suzuki T., Kobayashi M., Murayama A., Kondo K., Miyake T., Ueda R.;
"The Drosophila tamou gene, a component of the activating pathway of extramacrochaetae expression, encodes a protein homologous to mammalian cell-cell junction-associated protein ZO-1.";
Genes Dev. 10:1783-1795(1996).
EMBL, D83477, BAA11923.1;
---ATSGKCRIV 847
                                63 RHA-VESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEK-MAKKLKKGLQRLG-T 119
                                                                                             120 SEEQLLEAARQEEGDLDRAPCLYSSLAPDGW-----SDLDGLLSCVRQAIADEQK 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 RPVLLVPRAVGKILSEKLCLLQGFKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGRCWVT 62
                                                 Length 1367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148347 MW; 571C4566C6B68BF8 CRC64;
                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.9%; Score 110.5; DB 5; 23.4%; Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64;
 803 RPVVLF-GPVSDLARERLA--KDFPDKFSTPLQDDDKSA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50052; GUANVLATE_KINASE_2; 1. PROSITE; PS50106; PDZ; 3. SEQUENCE 1367 AA; 148347 MW; 571C456
                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FlyBase; FBgn0003177; pyd.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96312452; PubMed=8698238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00625; Guanylate_kin; 1. Pfam; PF00595; PDZ; 2. SmART; SM00072; Gukc; 1. SMART; SM00228; PDZ; 3. SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37;
                                                                                                                                                                                                                                                                                                    02,
02,
21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44; Conservative
                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                    01-FEB-1997 (TrEMBLrel. 01-FEB-1997 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q12923; 3PDZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          782 GAVWMSES 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 KVVWTEQS 177
                                                                                                                                                                                           953 GAVWMSES 960
                                                                                                                                                             170 KVVWTEQS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CANTON-S
                                                                                                                                                                                                                                                                       Q94880
Q94880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                         RESULT 9
                                                                                                                                                                                                                                                                        δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Óγ
                                                                                                                                                                                         g
                                                              qq
                                                                                                                             q
                                                                                                                                                            Ω
                                    δy
                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
6
                                                                                                                                                                                                                                                                                                        4 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DD43161p.
PVD OR CG9763.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                  93 IFPIVIHVSVNEKMAKKLKKGLQRLGT-SEEQLLE--AARQEEGDLDRAPCLYSSLAPDG 149
                                                                                                                                                                                                                                                                                                                                                                                                                    43 FVTREVMORDIAAGDFIEHAEFSGNLYGTSKVAVQAVQAMNRICVLDVDLQGVRNIKATD 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 RPVLLVPRAVGKILSEKLCLLQGFKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGRCWVT 62
                                                                                                                                                                                                                                                                                                                                     33 YLSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Gharin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K. Y. C., Lewis S.E., Rubin G.M., Celniker S., Submitted (Aug-2001) to the EMBL/GenBank/DDBJ databases.
      Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                        12.2%; Score 113.5; DB 4; Length 185; 26.2%; Pred. No. 0.0079; Live 36; Mismatches 61; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                    Strausberg R.; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases. Submitted (MAY-2001); -.
InterPro; IPR000619; Guanylate_kin.
Pfam: PF00025; Guanylate_kin.
PROSTITE: PS000856; GUANYLATE_KINNSE]; PROSTITE: PS500856; GUANYLATE_KINNSE].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5FA3A7D7D0922C2E CRC64;
                                                                                                                                                                                                                                   1
20646 MW; 3FF55B058C757184 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 11.9%; Score 110.5; DB 5; Best Local Similarity 23.4%; Pred. No. 0.11; Matches 44; Conservative 37; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            974 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50052; GUANYLATE_KINASE_2; 1. PROSITE; PS50106; PDZ; 3. SEQUENCE 974 AA; 107338 MW; 5FA3A7D71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FlyBase; FBgn0003177; pyd.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00625; Guanylate_kin; 1. Pfam; PF00595; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 -DSLDQAYAELKEALSEEIKK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 WSDLDGLLSCVRQAIADEQKK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                          Local Similarity 26.29 hes 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                            185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BERKELEY;
                                       NCBI_TaxID=9606;
                                                                                        TISSUE=OVARY;
                                                                                                                                                                                                                               NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                  Kinase.
                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               рp
                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

6

1445 AA; 156723 MW; A5675FB66676A40E CRC64;

S

```
PROSITE; PS50106; PDZ; 6. SEQUENCE 1445 AA; 1567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9VKG8
                                                                                                                                                                                g
                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                               Q
                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                               RA Adams M.D., Celniker S.E., II P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., II P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
R. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
R. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
R. George R.A., Forder E.G., Blazej R.G., Champe M., Pfeiffer B.D.,
R. Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
R. Barlew R.M. Basu A. Baxendala J., Bayrakaroglu L., Beasley B.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
R.A. Cherry J.M., Cawley S., Dalhke C., Davenport L.B., Davies P.,
R.A. Cherry J.M., Cawley S., Dalhke C., Davenport L.B., Davies P.,
A cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A cherry J.M., Cawley L.E., Downes M., Dayan-Rocha S., Pleischman W.,
R.A. Godor R., Downes M., Dayan-Rocha S., Pleischman W.,
R.A. Godor C., Ferraz C., Ferraz C., Ferraz C., Reriston D.,
A Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
A Jalali M., Kalush F., Karpen G.H., Ke Z., Gubar W., McDeck M.,
A Jalali M., Kalush F., Karpen G.H., Ke Z., Gubar W., Mattei B.,
A Liu X., Mattei B., McIntosh T.C., Morris J., Mount S.M., Nelson D.L.,
A Merkulov G., Mlishima N.V., Mobarry C., Morris J., Mount S.M.,
A hount S.M., Moy M., Murphy B., Murphy L., Muzray D.M., Nelson D.L.,
A hount S.M., Moy M., Murphy B., Murphy L., Muzray D.M., Nelson D.K.,
A spier E., Speradling A.C., Staplecton M., Strong R., Sun E.,
A Wasaaman D.A., Walner R., Worley K.C., Wu D., Yang S., Zho Q.,
A Yeh R.F., Zaveri J.S., Zhan M., Zhong G., Zhao Q., Zhao Q., Zhao G., Zhan S., Zha
                                                                                                                                                                                                                                                             Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
                                                                                                                                                                              PYD protein.
PYD OR CG9763.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Musay
                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                PRT; 1445 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00218; ZU5; 1.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0003177; pyd.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001452; SH3.
InterPro; IPR000906; ZU5.
Pfam; PP00625; Guanylate_kin; 1.
Pfam; PP00595; PDZ; 2.
Pfam; PP00791; ZU5; 1.
SMART; SM0072; GuKc; 1.
SMART; SM00228; PDZ; 3.
SMART; SM00228; SH3; 1.
SMART; SM00218; ZU5; 1.
                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 287:2185-2195(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE003680; AAF54300.1;
                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; Q12923; 3PDZ
                                        RESULT 10
                                                             09 УНК
```

```
Amanatides P.G., Scherer S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Holf R.A., Hoskins R.A., Galle R.F.,
Accorde R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
B. Gocaye R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
B. Sutton G.G., Worthman J.R., Yandall M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Balazej K.G., Champe M., Pfeilfer B.D.,
R.A. Abril J.F., Agbayani A., An H.-J., Andrews-Perdonnco, C., Baldwin D.,
B. Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,
B. Ballew R.M., Cawley S., Dahlke C., Davenport L.B., Doriter P.,
B. Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
B. Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
B. Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
B. Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
B. Borkova D., Botchar A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
B. Borkova D., Botchar A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
B. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Duukov B.C., Dunn P.,
B. Borkov D., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
B. Harris N.L., Harvey D., Heiman T.J., Wennison J.A., Ketchum K.A.,
B. Harris N.L., Harvey D., Heiman T.J., Wennison J.A., Ketchum K.A.,
B. Hostin D., Molson K.A., Liu Y., Mocheck D.,
B. McIntosh T.C., McLedod M.P., Mochecon D.L.,
R. Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
R. Maltei B., McIntosh T.C., Cheeler F., Shen H.,
R. Reinert K., Remighton K., Saunders R., Dellard J., Puri V., Resee M.G.,
R. Reinert K., Remighton K., Saunders R., Sune E.,
Spier E., Spradling A.C., Staeleler M., Strong R., W., Wang X.,
Spier E., Spradling A.C., Staeleler E., Spradling A.C., Staeler K., Nelson D...
Spier E., Spradling A.C., Staeler K., Venter E., Wang X.,
                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                            | : : : | : : | | | | | | : : | : | | | : | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                                                                                                                                                                                                                 632 RPVVLF-GPVSDLARERLA--KDFPDKFSTPLQDDDKSA------ATSGKCRIV 676
                                                                                                                                                                                                                                                                                                                                      RHA-VESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEK-MAKKLKKGLQRLG-T 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEEQLLEAARQEEGDLDRAPCLYSSLAPDGW-----SDLDGLLSCVRQAIADEQK 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota; Neoptera, Endopterygota; Diptera, Brachycera, Muscomorpha;
Ephydroidea, Drosophilidae; Drosophila.
                                                                                             Gaps
                                                                                                                                                                     3 RPVLLVPRAVGKILSEKLCLLQGFKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGRCWVT 62
                                                                                         43;
            Length 1445;
                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CG6509 protein (LD32687p).
                                                                                    64;
            DB 5;
11.9%; Score 110.5; DE 23.4%; Pred. No. 0.18; Live 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1916 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=BERKELEY;
MEDLINE=20196006; Pubmed=10731132;
                                                                                         44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                 Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            782 GAVWMSES 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 KVVWTEQS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7227;
            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9VKG8
                                                                                                                                                                                                                                                                                                                                      63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
```

```
1 SH3 DOMAIN.
                                                                InterPro; IPR000619; Guanylate_kin
                                                                                                     InterPro: IPR000906; ZU5.
Pfam: PF00625; Guanylate_kin; 1.
Pfam: PF00595; PD2; 3.
Pfam: PF00018; SH3; 1.
Pfam; PF00791; ZU5; 1.
             Exp. Cell Res. 248:97-109(1999).
                   EMBL, US5935; AAD11529.1;
HSSP, P31016; 1BE9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                             InterPro; IPR001478;
InterPro; IPR001452;
                                                                                                                                                                                                                                                                                                          SH3 domain.
                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P70625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
P70625
  δ
                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            á
                                                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BREED: COCKER SPANIEL;
MEDLINE-99196918; PubMed-10094817;
GONZALEZ-MATISCAL L., ISLAS S., CONTECTAS R.G., GARCÍA-VIllegas M.R.,
Betanzos A., Vega J., Diaz-Quinonez A., Martin-Orozco N.,
Ortiz-Navarrete V., Cereijido M., Valdes J.;
"Molecular characterization of the tight junction protein ZO-1 in MDCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1738 RPVLIIGP----LSECLMVRLTIDFSNLFKLCEVTAMDCSQEAMEEGLKENIFVDYRRR 1792
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., "The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 GDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 MAKKLKKGLQRLGTSE-----EQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLSC 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 RPVLLVPRAVGKILSE-------KLCLLQGF---KKCLAEYLSQEEYEAWSQR 45
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                Champe M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nuncoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S., Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AE003632; AAF53102.1;

ESBL, AV069586; AAL39731.1;

ESSP; P31016; LBE9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis
                                                                                                                                                                                                                                                                                                                                                                                                                                           44;
                                                                                                                                                                                                                                                                                                                                                                                                                                         70; Indels
                                                                                                                                                                                                                                                                                                                                                                                      1916 AA; 209863 MW; 32B2A61ABA6848F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                ..
20
                                                                                                                                                                                                                                                                                                                                                                                                               11.4%; Score 106; DB 5
22.7%; Pred. No. 0.65;
ive 39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1769 AA
                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PDZ; 4.
                                                                                                                                                                                                                                                   FIYBASE: FBRN0032363; CG6509.
InterPro: IPR000619; Guanylate_kin.
InterPro: IPR001478; PDZ.
InterPro: IPR001452; SH3.
Pfam; PF00555; PDZ; 3.
SMART: SM002075 GMCs; 1.
SMART: SM00328; PDZ; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1999 (TrEMBLrel. 10, Created) 01-MAY-1999 (TrEMBLrel. 10, Last seq 01-JUN-2002 (TrEMBLrel. 21, Last ann 20-1 MDCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1897 IKDAVDKEQDKLLWVPVS 1914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 VRQAIADEQKKVVWTEQS 177
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 22.7<sup>5</sup>
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZO1-MDCK.
Canis familiaris (Dog).
                                                                                                       SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      097758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-WISTARA-KYOTO:
STRAIN-WISTARA-KYOTO:
MEDLINE-20027749; PubMed-10559001;
Adams L.D., Lemire J.M., Schwartz S.M.;
"A systematic analysis of 40 random genes in cultured vascular smooth muscle subtypes reveals a heterogeneity of gene expression and identifies the tight junction gene zonula occludens 2 as a marker of epithelioid 'pup' smooth muscle cells and a participant in carotid neointimal formation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 658 EKLAREEPDIYQIAKSEPRDAGTDQRSSG---IIRLHTIKQIIDQDKHALLDVTPNAVDR 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 LHRMDIFPIVIHVSVNEKMAKKL------KKGLQRLGTSEEQLLEAARQEEGDLDRA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          27; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 EYLSQEE---YE-AWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCT 87
                                                                                                                                                                                                                                                                                                                                                                                                 Length 1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                      1769 AA; 197606 MW; 181E9F36CEBC96EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arterioscler. Thromb. Vasc. Biol. 19:2600-2608(1999).
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
EMBL; U75916; AAB46979.1; -.
HSSP: P31016; 1BE9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 10.8%; Score 100.5; DB 6; Best Local Similarity 24.1%; Pred. No. 1.9; Matches 38; Conservative 35; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 PCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTEQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zonula occludens 2 protein (Fragment).
                                                                                                                                                                                                               PROSITE; PS50052; GUANVLATE_KINASE_2; PROSITE; PS50106; PDZ; 3. PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P70625; P97625;
01-FEB-1997 (T.FEMBLEE]. 02, Created)
01-JAN-1998 (T.FEMBLEE]. 05, Last seq
01-JUN-2002 (T.FEMBLEE]. 21, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
InterPro; IPR001452; SH3.
PRINTS; PRO1597; ZONOCCLUDNS.
PRINTS; PRO1598; ZONOCCLUDNS1.
PRINTS; PRO1500; ZONOCCLUDNS3.
SMART; SM00072; GUKC; 1.
SMART; SM00228; PDZ; 3.
SMART; SM00226; SH3; 1.
```

```
STRAIN-BERKELEY
                                                                                       172 VWTEQ 176
                                                                                                                                                        09VTB3
                                                                                                                                      RESULT 15
                                                                                                                                                                 Dp
                                                                 Dp
                                                                                      δ
                                                  ò
                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                                                                                                   347 EKVLLREAGFKKPVVLFGPIADIAMERLT--TELPDLFQTAKTEPKDAGSEKSSG--VVR 402
                                                                                                                                                                                                                        63 RHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRLGTSEE 122
                                                                                                                                                                                                                                                              123 QLLEAARQ--EEGDLDRAPC-----LYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVW 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                  18 EKLCLLQ-GFKKCLAEY----LSQEEYEAWSQRGDIIQE------GEVSGGRCWVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
                                                                                                                                                                 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.2%; Score 94.5; DB 5; Length 1034; 25.6%; Pred. No. 3.6; Live 29; Mismatches 47; Indels 17
                                                                                                                                               Length 813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE . 1034 AA; 116053 MW; 7E29646264FCD5BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                  1 1 813 AA; 90776 MW; 30EA78F19DE9C852 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                               DB 11;
                                                                                                                                             Score 99.5; DB Pred. No. 0.94;
                                                                                                                                                                                                                                                                                                                                                                     PRT; 1034 AA.
Pfam; PF00625; Guanylate_kin; 1.
Pfam; PF00595; PDZ; 1.
Pfam; PF0018; SH3; 1.
PRINTS; PR01597; ZONOCCLUDNS.
PRINTS; PR0072; GUKC; 1.
SMART; SM0072; GUKC; 1.
SMART; SM00328; PDZ; 1.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50025; GUANYLATE_KINASE_2; 1.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PD2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            investigating biology.";
Sclence 282:2012-2018(1998).
EMBL, 268298, CAA92607.1; -.
InterPro; IPR000619, Guanylate_kin.
InterPro; IPR001478; PDZ.
Ff.an, PR00595; PDZ.
SWART; SM00072; GuKc; 1.
SMART; SM00228; PDZ; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-99069613; PubMed-9851916;
                                                                                                                                              10.7%;
23.5%;
                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   F44D12.1 protein.
                                                                                                                                                                                                                                                                                                   174 TEQ 176
                                                                                                                                                                                                                                                                                                                      512 VSE 514
                                                                                                         SH3 domain.
                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                           F44D12.1
                                                                                                                                                                                                                                                                                                                                                                     020398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coles
                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                             qq
   Db
                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                         Db
                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                   ò
```

```
Oy 116 RLGTESHANENHALLDOUGNCTHANDENFITIUNINGNEARKIKE.——GLO 1115
D) 912 TAHIND-ITAGGARCAYODSAIDRIKECREPTI--VARIANDENGKRANENGKIKE.——GLO 1115
D) 912 TAHIND-ITAGGARCAYODSAIDRIKECREPTI--VARIANDENGKRANGIKEL TO 1171
D) 969 ISSERRANGIEDRIANGEDDARGARCAYORSHINDLIS----(HOPINING TO 1171
D) 969 ISSERRANGIEDRIANGEDDARGARCAYORSHINDLIS----(HOPINING TO 1172
D) 97172 WWED 175
D) 97173 WWED 175
D) 97172 WWED 175
D) 97172 WWED 175
D) 97173 WWED 175
D) 97173 WWED 175
D) 97173 WWED 175
D) 97174 WRED 175
D) 97175 WWED 175
D) 97177 WWED 175
D) 97175 WW
```

```
9
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farian D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Celniker S.,
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, ARC03547; AAF50139-1; --
EMBL, AV070035; AAL48657.1; --
HSSP; P15454; IGKY.
                                                                                                                                                                                                                                                                                                                                                                                                      9.9%; Score 92.5; DB 5; Length 233; 22.6%; Pred. No. 0.94; tive 32; Mismatches 81; Indels 47
                                                                                                                                                                                               FIGURE PROPOSED CG11811.
InterPro; IPR0003199; ADH_short.
InterPro; IPR000619; Guanylate_kin.
Pfam. PF00625; Guanylate_kin; 1.
SMART; SM00072; GuKc; 1.
PROSITE; PS00066; ADH_SHORT; UNKNOWN_1.
PROSITE; PS00086; GUANYLATE_KINASE_1; 1.
SEQUENCE 233 AA; 25898 MW; 12C4C5CC715C2885 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 22.69
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
```

Db 204 DIDVAYEEFRNFVVQELKE 222 Search completed: January 22, 2003, 08:56:48 Job time : 30.9086 secs

152 DLDGLLSCVRQAIADEQKK 170

g &

ò

90 Q

δ